CGT 250 v1.2

Gene	Disease	Transcript	Mutations	Disease.description	products
ABCA4	Stargardt disease type 1; Cone-rod dystrophy type 3	NM_000350.2	NM_000350.2:c.6449G>A, NM_000350.2:c.6394G>T, NM_000350.2:c.6320G>A, NM_000350.2:c.6118C>T, NM_000350.2:c.6089G>A, NM_000350.2:c.5912T>G, NM_000350.2:c.5882G>A, NM_000350.2:c.5881G>A, NM_000350.2:c.5819T>C, NM_000350.2:c.5714+5G>A, NM_000350.2:c.5512delC, NM_000350.2:c.5461-10T>C, NM_000350.2:c.5338C>G, NM_000350.2:c.4793C>A, NM_000350.2:c.4469G>A, NM_000350.2:c.4457C>T, NM_000350.2:c.4429C>T, NM_000350.2:c.4139C>T, NM_000350.2:c.3970delG, NM_000350.2:c.3364G>A, NM_000350.2:c.3322C>T, NM_000350.2:c.3210_3211dupGT, NM_000350.2:c.3106G>A, NM_000350.2:c.3083C>T, NM_000350.2:c.2791G>A, NM_000350.2:c.2616_2617delCT, NM_000350.2:c.2588G>C, NM_000350.2:c.2300T>A, NM_000350.2:c.2160+1G>T, NM_000350.2:c.1964T>G, NM_000350.2:c.1938-1G>A, NM_000350.2:c.1848delA, NM_000350.2:c.1804C>T, NM_000350.2:c.1771delT, NM_000350.2:c.1755delA, NM_000350.2:c.1622T>C, NM_000350.2:c.1225delA, NM_000350.2:c.1222C>T, NM_000350.2:c.1018T>G, NM_000350.2:c.763C>T, NM_000350.2:c.634C>T, NM_000350.2:c.286A>G, NM_000350.2:c.67-2A>G, NM_000350.2:c.52C>T	Stargardt disease type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ABCA4 gene located on chromosomal region 1p22. The age of onset is infantile. This disease is characterized by progressive central vision loss, mild loss of color vision, delayed dark adaptation and macular atrophy with or without paramacular flecks and degeneration of the underlying retinal pigment ephitelium. The estimated prevalence is 1:8,000-10,000. Mutations in the ABCA4 gene account also for 30 to 60 percent of cases of cone-rod dystrophy that are inherited in an autosomal recessive pattern. The problems associated with this condition include a loss of visual sharpness (acuity), an increased sensitivity to light (photophobia), and impaired color vision. These vision problems worsen over time.	600,25
ACAD9	Mitochondrial complex I deficiency due to ACAD9	NM_014049.4	NM_014049.4:c.23delT, NM_014049.4:c.130T>A, NM_014049.4:c.359delT, NM_014049.4:c.453+1G>A, NM_014049.4:c.797G>A, NM_014049.4:c.976G>C, NM_014049.4:c.1240C>T, NM_014049.4:c.1249C>T, NM_014049.4:c.1594C>T	Mitochondrial complex I deficiency due to ACAD9 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ACAD9 gene located on chromosomal region 3q21.3. The age of onset is neonatal/infantile. This disease is a multisystem disorder characterized by infantile onset of acute metabolic acidosis, hypertrophic cardiomyopathy, and muscle weakness associated with a deficiency of mitochondrial complex I activity in muscle, liver, and fibroblasts (summary by Haack et al., 2010).	600,25
ACADM	Medium-chain acyl-CoA dehydrogenase deficiency	NM_001286043.1	NM_001286043.1:c.250C>T, NM_001286043.1:c.386-2A>G, NM_001286043.1:c.461C>T, NM_001286043.1:c.548_551delCTGA, NM_001286043.1:c.546G>A, NM_001286043.1:c.715C>T, NM_001286043.1:c.716G>A, NM_001286043.1:c.833C>T, NM_001286043.1:c.896A>G, NM_001286043.1:c.898G>A, NM_001286043.1:c.916_928delGCAATGGGAGCTT, NM_001286043.1:c.1083delG, NM_001286043.1:c.1084A>G, NM_001286043.1:c.1201_1204delTTAG	Medium-chain acyl-CoA dehydrogenase (MCAD) deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ACADM gene located on chromosomal region 1p31. Inherited deficiency of MCAD is a condition that prevents the body from converting certain fats to energy, particularly during periods without food (fasting). Signs and symptoms of MCAD deficiency typically appear during infancy or early childhood and can include vomiting, lack of energy (lethargy), and low blood sugar (hypoglycemia). Individuals with MCAD deficiency are at risk of serious complications such as seizures, breathing difficulties, liver problems, brain damage, coma, and sudden death. The estimated prevalence is 1:4,900-1:27,000 in Caucasian populations and 1:14,600 in worldwide populations.	600,25
ACADS	Short-chain acyl-CoA dehydrogenase deficiency	NM_000017.3	NM_000017.3:c.136C>T, NM_000017.3:c.319C>T, NM_000017.3:c.417G>C, NM_000017.3:c.529T>C, NM_000017.3:c.561_568delCAATGCCT, NM_000017.3:c.1095G>T, NM_000017.3:c.1147C>T	Short-chain acyl-CoA dehydrogenase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ACADS gene located on chromosomal region 12q24.31. The age of onset is infantile. This disease is characterized by seizures, developmental delay, failure to grow with poor feeding, and usually muscle weakness and hypotonia. The prevalence is <1:50,000.	600,25
ACADSB	Short/branched-chain acyl-CoA dehydrogenase deficiency	NM_001609.3	NM_001609.3:c.303+1G>A, NM_001609.3:c.443C>T, NM_001609.3:c.621G>A, NM_001609.3:c.763C>T	Short/branched-chain acyl-CoA dehydrogenase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ACADSB gene located on chromosomal region 10q26.3. The age of onset is neonatal/infantile. This disease is characterized by muscle hypotonia, cerebral palsy, developmental delay, lethargy, hypoglycemia, and metabolic acidosis. The prevalence is <1:1,000,000.	600,25

ACADVL	Very long-chain acyl-CoA dehydrogenase deficiency	NM_001270447.1	NM_001270447.1:c.347-1G>A, NM_001270447.1:c.367_368delCA, NM_001270447.1:c.412delG, NM_001270447.1:c.469C>T, NM_001270447.1:c.546+1G>C, NM_001270447.1:c.589G>A, NM_001270447.1:c.754C>T, NM_001270447.1:c.822-2A>C, NM_001270447.1:c.917T>C, NM_001270447.1:c.965_967delAGA, NM_001270447.1:c.1165C>T, NM_001270447.1:c.1166G>A, NM_001270447.1:c.1175T>C, NM_001270447.1:c.1210_1212delGAG, NM_001270447.1:c.1251+1G>A, NM_001270447.1:c.1426C>T, NM_001270447.1:c.1444dupC, NM_001270447.1:c.1458dupG, NM_001270447.1:c.1475G>A, NM_001270447.1:c.1537G>C, NM_001270447.1:c.1601+1G>A, NM_001270447.1:c.1906C>T, NM_001270447.1:c.1912C>T, NM_001270447.1:c.1951delC	Very long-chain acyl-CoA dehydrogenase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ACADVL gene located on chromosomal region 17p13.1. The age of onset is neonatal/infantile. This disease is characterized by cardiomyopathy, hypoketotic hypoglycemia, liver disease, exercise intolerance and rhabdomyolysis. The prevalence is 1:100,000-9:100,000.	600,25
ACE	Renal tubular dysgenesis	NM_000789.3	NM_000789.3:c.798C>G, NM_000789.3:c.1319_1322delTGGA, NM_000789.3:c.1486C>T, NM_000789.3:c.1511delC, NM_000789.3:c.1587-2A>G, NM_000789.3:c.2371C>T	Renal tubular dysgenesis deficiency follows an autosomal recessive pattern of inheritance and the most common cause are pathogenic variants in the ACE (chromosomal region 17q23.3). The age of onset is fetal. This disease is characterized by absent or poorly developed proximal tubules of the kidneys, persistent oligohydramnios, leading to Potter sequence, and skull ossification defects.	600,25
ADA	Adenosine deaminase deficiency / Severe combined immunodeficiency due to ADA deficiency	NM_000022.3	NM_000022.3:c.986C>T, NM_000022.3:c.956_960delAAGAG, NM_000022.3:c.890C>A, NM_000022.3:c.872C>T, NM_000022.3:c.632G>A, NM_000022.3:c.320T>C	Adenosine deaminase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ADA gene located on chromosomal region 20q13.12. The age of onset is neonatal/infantile. This disease is characterized by profound lymphopenia and very low immunoglobulin levels of all isotypes resulting in severe and recurrent opportunistic infections. The annual incidence is 1:200,000-1:1,000,000. The prevalence is 1:100,000-9:100,000.	600,25
ADGRV1	Usher syndrome, type 2C	NM_032119.3	NM_032119.3:c.2258_2270delAAGTGCTGAAATC, NM_032119.3:c.2864C>A, NM_032119.3:c.5357_5358delAA, NM_032119.3:c.6275-1G>A, NM_032119.3:c.6312dupT, NM_032119.3:c.6901C>T, NM_032119.3:c.8713_8716dupAACA, NM_032119.3:c.8790delC, NM_032119.3:c.11377G>T, NM_032119.3:c.14973-1G>C, NM_032119.3:c.15196_15199dupCAAA, NM_032119.3:c.17668_17669delAT, NM_032119.3:c.18131A>G	Usher syndrome type 2C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ADGRV1 and PDZD7 genes located on chromosomal regions 5q14.3 and 10q24.32 respectively. The age of onset is infantile. This disease is characterized by the association of sensorineural prelingual deafness (usually congenital) with retinitis pigmentosa and progressive vision loss. The prevalence is 1/30,000.	600,25
AGL	Glycogen storage disease type 3	NM_000028.2	NM_000028.2:c.16C>T, NM_000028.2:c.18_19delGA, NM_000028.2:c.294-2A>T, NM_000028.2:c.1222C>T, NM_000028.2:c.1485delT, NM_000028.2:c.1783C>T, NM_000028.2:c.1999delC, NM_000028.2:c.2039G>A, NM_000028.2:c.2590C>T, NM_000028.2:c.3216_3217delGA, NM_000028.2:c.3980G>A, NM_000028.2:c.4260-12A>G, NM_000028.2:c.4260-1G>T, NM_000028.2:c.4342G>C, NM_000028.2:c.4456delT, NM_000028.2:c.4529dupA	Glycogen storage disease (GSD) type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the AGL gene located on chromosomal region 1p21.2. The age of onset is infantile. This metabolic disorder is caused by deficiency of the glycogen debrancher enzyme and is associated with an accumulation of abnormal glycogen with short outer chains. Most patients are enzyme-deficient in both liver and muscle (IIIa), but about 15% are enzyme-deficient in liver only (IIIb) (Shen et al., 1996). These subtypes have been explained by differences in tissue expression of the deficient enzyme (Endo et al., 2006). In rare cases, selective loss of only 1 of the 2 debranching activities, glucosidase or transferase, results in type IIIc or IIId, respectively (Van Hoof and Hers, 1967; Ding et al., 1990). Clinically, patients with GSD type 3 present in infancy or early childhood with hepatomegaly, hypoglycemia, and growth retardation. Muscle weakness in those with IIIa is minimal in childhood but can become more severe in adults; some patients develop cardiomyopathy (Shen et al., 1996).	600,25
AGXT	Hyperoxaluria, primary, type 1	NM_000030.2	NM_000030.2:c.33dupC, NM_000030.2:c.121G>A, NM_000030.2:c.166-2A>G, NM_000030.2:c.245G>A, NM_000030.2:c.248A>G, NM_000030.2:c.322T>C, NM_000030.2:c.454T>A, NM_000030.2:c.466G>A, NM_000030.2:c.508G>A, NM_000030.2:c.560C>T, NM_000030.2:c.613T>C, NM_000030.2:c.697C>T, NM_000030.2:c.698G>A, NM_000030.2:c.731T>C, NM_000030.2:c.738G>A	Primary hyperoxaluria type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the AGXT gene located on chromosomal region 2q37.3. The age of onset is variable. This disease is characterized by variable clinical presentation, ranging from occasional symptomatic nephrolithiasis to nephrocalcinosis and end-stage renal disease with systemic involvement. The prevalence is 1:1,000,000-9:1,000,000.	600,25

AHI1	Joubert syndrome type 3	NM_001134830.1	NM_001134830.1:c.3263_3264delGG, NM_001134830.1:c.2295dupA, NM_001134830.1:c.2168G>A, NM_001134830.1:c.1484G>A, NM_001134830.1:c.1303C>T, NM_001134830.1:c.1052G>T, NM_001134830.1:c.1051C>T, NM_001134830.1:c.985C>T	Joubert syndrome type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the AHI1 gene located on chromosomal region 6q23.3. The age of onset is variable. This disease is characterized by the neurological features of Joubert syndrome (neonatal hypotonia, developmental delay, mild to severe intellectrual disability, ataxia, and abnormal eye movements including oculomotor apraxia and primary position nystagmus) associated with retinal dystrophy.	600,25
AIPL1	Leber congenital amaurosis type 4	NM_014336.4	NM_014336.4:c.1053_1064delTGCAGAGCCACC, NM_014336.4:c.834G>A, NM_014336.4:c.715T>C, NM_014336.4:c.589G>C	Leber congenital amaurosis type 4 (LCA4) is a severe dystrophy of the retina, typically becoming evident in the first years of life. Visual function is usually poor and often accompanied by nystagmus, sluggish or near-absent pupillary responses, photophobia, high hyperopia and keratoconus. Mutations in the AIPL1 gene may cause approximately 20% of recessive LCA. Other conditions caused by pathogenic variants in the AIPL1 gene are cone rod dystrophy and the less agressive form, juvenile retinitis pigmentosa. Cone-rod dystropy is characterized by decreased visual acuity, color vision defects, photoaversion and decreased sensitivity in the central visual field, later followed by progressive loss in peripheral vision and night blindness.	600,25
ALDOB	Fructose intolerance, hereditary	NM_000035.3	NM_000035.3:c.1067C>A, NM_000035.3:c.1013C>T, NM_000035.3:c.1005C>G, NM_000035.3:c.720C>A, NM_000035.3:c.612T>A, NM_000035.3:c.524C>A, NM_000035.3:c.448G>C, NM_000035.3:c.442T>C, NM_000035.3:c.360_363delCAAA, NM_000035.3:c.178C>T, NM_000035.3:c.113-1_115delGGTA, NM_000035.3:c.10C>T, NM_000035.3:c.2T>C	Hereditary fructose intolerance follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ALDOB gene located on chromosomal region 9q21.3-q22.2. The age of onset is neonatal/infantile. This disease is characterized by severe abdominal pain, vomiting, and hypoglycemia following ingestion of fructose or other sugars metabolised through fructose-1-phosphate. The prevalence is 1:100,000-9:100,000.	600,25
ALG6	Congenital disorder of glycosylation, type 1c	NM_013339.3	NM_013339.3:c.316C>T, NM_013339.3:c.897_899delAAT, NM_013339.3:c.998C>T, NM_013339.3:c.1432T>C	Congenital disorder of glycosylation type 1c follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ALG6 gene located on chromosomal region 1p31.3. The age of onset is neonatal/infantile. This disease is characterized by psychomotor delay and muscular hypotonia, and possible coagulation anomalies, hormonal abnormalities and seizures. The prevalence is <1:1,000,000.	600,25
ALMS1	Alstrï¿½m syndrome	NM_015120.4	NM_015120.4:c.2323C>T, NM_015120.4:c.4246delC, NM_015120.4:c.5584C>T, NM_015120.4:c.8383C>T, NM_015120.4:c.9614_9618delCAGAA, NM_015120.4:c.11443C>T, NM_015120.4:c.11453dupA, NM_015120.4:c.11612_11613delCT, NM_015120.4:c.12439C>T, NM_015120.4:c.12445C>T	Alstrï¿½m syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ALMS1 gene located on chromosomal region 2p13.1. The age of onset is neonatal/infantile. This disease is characterized by cone-rod dystrophy, hearing loss, obesity, insulin resistance and hyperinsulinemia, type 2 diabetes mellitus, dilated cardiomyopathy and progressive hepatic and renal dysfunction. The prevalence is 1:10,000-1:1,000,000.	600,25
ANO5	Limb-girdle muscular dystrophy type 12 (LGMDR12; formerly LGMD2L)	NM_213599.2	NM_213599.2:c.172C>T, NM_213599.2:c.191dupA, NM_213599.2:c.206_207delAT, NM_213599.2:c.692G>T, NM_213599.2:c.1210C>T, NM_213599.2:c.1295C>G, NM_213599.2:c.1407+5G>A, NM_213599.2:c.1627dupA, NM_213599.2:c.1733T>C, NM_213599.2:c.1887delA, NM_213599.2:c.1898+1G>A, NM_213599.2:c.1914G>A	Limb-girdle muscular dystrophy type 12 (LGMDR12, formerly LGMD2L) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ANO5 gene located on chromosomal region 11p14.3. This disease is characterized by weakness and wasting restricted to the limb musculature. Most often is characterized by an adult onset (but ranging from 11 to 51 years) of mainly proximal lower limb weakness, with difficulties standing on tiptoes being one of the initial signs. Proximal upper limb and distal lower limb weakness is also common, as well as atrophy of the quadriceps (most commonly), biceps brachii, and lower leg muscles. Calf hypertrophy has also been reported in some cases. LGMDR12 progresses slowly, with most patients remaining ambulatory until late adulthood. The estimated prevalence is <1:1,000,000.	600,25
APTX	Ataxia, early-onset, with oculomotor apraxia and hypoalbuminemia	NM_001195248.1	NM_001195248.1:c.917-1G>A, NM_001195248.1:c.879G>A, NM_001195248.1:c.830T>G, NM_001195248.1:c.659C>T, NM_001195248.1:c.362delC, NM_001195248.1:c.209delT, NM_001195248.1:c.176-2A>G, NM_001195248.1:c.166C>T	Ataxia, early-onset, with oculomotor apraxia and hipoalbuminemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the APTX gene located on chromosomal region 9p13.1. Ataxia-oculomotor apraxia syndrome is an early-onset autosomal recessive, progressive, cerebellar ataxia with peripheral axonal neuropathy, oculomotor apraxia (defined as the limitation of ocular movements on command), and hypoalbuminemia. The prevalence is unknown.	600,25

AR	Androgen insensitivity syndrome, complete	NM_000044.3	NM_000044.3:c.340C>T, NM_000044.3:c.1771A>T, NM_000044.3:c.2323C>T, NM_000044.3:c.2391G>A, NM_000044.3:c.2395C>G, NM_000044.3:c.2567G>A, NM_000044.3:c.2650A>T	The complete androgen insensitivity syndrome (CAIS) follows an X-linked pattern of inheritance and is caused by pathogenic variants in the AR gene located on chromosomal region Xq12. Affected males have female external genitalia, female breast development, blind vagina, absent uterus and female adnexa, and abdominal or inguinal testes, despite a normal male 46,XY karyotype. There is unresponsiveness to age-appropriate levels of androgens. There is also a partial androgen insensitivity syndrome (PAIS; OMIM 312300) caused by mutations in the AR gene, called Reifenstein syndrome, which results in hypospadias and micropenis with gynecomastia. Note: A specific type of mutation in the AR gene (a CAG repeat expansion) also cause a rare condition known as Spinal and bulbar muscular atrophy or Kennedy disease; this mutation is not tested by this carrier test.	600,25
ARSA	Metachromatic leukodystrophy	NM_000487.5	NM_000487.5:c.1408_1418delGCAGCTGTGAC, NM_000487.5:c.1401_1411delGTTAGACGCAG, NM_000487.5:c.1283C>T, NM_000487.5:c.1241delC, NM_000487.5:c.1232C>T, NM_000487.5:c.1210+1G>A, NM_000487.5:c.1175G>A, NM_000487.5:c.1174C>T, NM_000487.5:c.1150G>A, NM_000487.5:c.1125_1126delCT, NM_000487.5:c.1108-2A>G, NM_000487.5:c.991G>T, NM_000487.5:c.986C>T, NM_000487.5:c.979G>A, NM_000487.5:c.938G>A, NM_000487.5:c.937C>T, NM_000487.5:c.931G>A, NM_000487.5:c.899T>C, NM_000487.5:c.883G>A, NM_000487.5:c.869G>A, NM_000487.5:c.854+1G>A, NM_000487.5:c.827C>T, NM_000487.5:c.763G>A, NM_000487.5:c.739G>A, NM_000487.5:c.737G>A, NM_000487.5:c.641C>T, NM_000487.5:c.583delT, NM_000487.5:c.582delC, NM_000487.5:c.542dupT, NM_000487.5:c.542T>G, NM_000487.5:c.465+1G>A, NM_000487.5:c.346C>T, NM_000487.5:c.302G>A, NM_000487.5:c.293C>T, NM_000487.5:c.257G>A, NM_000487.5:c.195delC, NM_000487.5:c.34delG	Metachromatic leukodystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ARSA gene located on chromosomal region 22q13.33. The age of onset is variable. This disease is characterized by hypotonia, walking difficulties, optic atrophy and motor regression preceding mental impairment in the late infantile form, arrested intellectual development, followed by motor regression, epileptic seizures and ataxia in the juvenile form, and motor or psychiatric disorders, but with slow progression in the adult form. The incidence is 0.5:5,000-1:50,000ï¾ and the prevalence is 1:10,000 -5/10,000.	600,25
ARSB	Mucopolysaccharidosis type 6 (Maroteaux-Lamy)	NM_000046.3	NM_000046.3:c.1438dupG, NM_000046.3:c.1366C>T, NM_000046.3:c.1214G>A, NM_000046.3:c.1178A>C, NM_000046.3:c.1161dupC, NM_000046.3:c.1143-1G>C, NM_000046.3:c.1143-8T>G, NM_000046.3:c.979C>T, NM_000046.3:c.971G>T, NM_000046.3:c.944G>A, NM_000046.3:c.937C>G, NM_000046.3:c.921delA, NM_000046.3:c.753C>G, NM_000046.3:c.629A>G, NM_000046.3:c.589C>T, NM_000046.3:c.571C>T, NM_000046.3:c.427delG, NM_000046.3:c.349T>C	Mucopolysaccharidosis type 6 (Maroteaux-Lamy) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ARSB gene located on chromosomal region 5q14.1. The age of onset is infantile. This lysosomal storage disorder resulting from a deficiency of arylsulfatase B is characterized by educed pulmonary function, hepatosplenomegaly, hearing loss, sleep apnea, corneal clouding, carpal tunnel disease and occasionally central nervous system findings may include cervical cord compression caused by cervical spinal instability, meningeal thickening and/or bony stenosis, communicating hydrocephalus, optic nerve atrophy and blindness. The prevalence is 1:250,000-1:600,000 newborns.	600,25
ARSE	Chondrodysplasia punctata, X-linked recessive	NM_001282628.1	NM_001282628.1:c.1807C>T, NM_001282628.1:c.1517C>T, NM_001282628.1:c.1504delG, NM_001282628.1:c.485G>T, NM_001282628.1:c.194T>G, NM_001282628.1:c.99-1G>A	X-linked chondrodysplasia punctata follows an X-linked pattern of inheritance and is caused by pathogenic variants in the ARSE gene located on chromosomal region Xp22.33. The age of onset is neonatal. Thisï¾ is a disorder of cartilage and bone development that occurs almost exclusively in males. Include short stature and unusually short fingertips and ends of the toes. This condition is also associated with distinctive facial features, particularly a flattened-appearing nose with crescent-shaped nostrils and a flat nasal bridge. People with X-linked chondrodysplasia punctata 1 typically have normal intelligence and a normal life expectancy. However, some affected individuals have had serious or life-threatening complications including abnormal thickening (stenosis) of the cartilage that makes up the airways, which restricts breathing. Also, abnormalities of spinal bones in the neck can lead to pinching (compression) of the spinal cord, which can cause pain, numbness, and weakness. Other, less common features of X-linked chondrodysplasia punctata 1 include delayed development, hearing loss, vision abnormalities, and heart defects. The prevalence is 1:500,000.	600,25

ASL	Argininosuccinic aciduria	NM_000048.3	NM_000048.3:c.35G>A, NM_000048.3:c.337C>T, NM_000048.3:c.346C>T, NM_000048.3:c.446+1G>A, NM_000048.3:c.525-2A>T, NM_000048.3:c.532G>A, NM_000048.3:c.539T>G, NM_000048.3:c.544C>T, NM_000048.3:c.578G>A, NM_000048.3:c.602+1G>A, NM_000048.3:c.857A>G, NM_000048.3:c.1045_1057delGTCATCTCTACGC, NM_000048.3:c.1060C>T, NM_000048.3:c.1135C>T, NM_000048.3:c.1144-2A>G, NM_000048.3:c.1153C>T, NM_000048.3:c.1255_1256delCT, NM_000048.3:c.1369dupG	Argininosuccinic aciduria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ASL gene located on chromosomal region 7q11.21. The age of onset is infantile. This disease is characterized by severe hyperammonemic coma, hypotonia, growth failure, anorexia and chronic vomiting or behavioral disorders during childhood, and hyperammonemic coma or behavioral disorders that simulate psychiatric disorders later in life. The prevalence is 1:70,000 newborns.	600,25
ASPA	Canavan disease	NM_000049.2	NM_000049.2:c.212G>A, NM_000049.2:c.433-2A>G, NM_000049.2:c.654C>A, NM_000049.2:c.693C>A, NM_000049.2:c.854A>C, NM_000049.2:c.914C>A	Canavan disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ASPA gene located on chromosomal region 17p13.3. The age of onset is neonatal/infantile. This disease is characterized by a variable spectrum between severe forms with leukodystrophy, macrocephaly and severe developmental delay, and a very rare mild/juvenile form characterized by mild developmental delay. The prevalence is 1:6,400- 1:13,500 in Askenazis Jewis.	600,25
ASPM	Primary microcephaly type 5, autosomal recessive	NM_018136.4	NM_018136.4:c.10059C>A, NM_018136.4:c.9789T>A, NM_018136.4:c.9754delA, NM_018136.4:c.9747_9748delCT, NM_018136.4:c.9730C>T, NM_018136.4:c.9697C>T, NM_018136.4:c.9685delA, NM_018136.4:c.9677dupG, NM_018136.4:c.9557C>G, NM_018136.4:c.9492T>G, NM_018136.4:c.9319C>T, NM_018136.4:c.9238A>T, NM_018136.4:c.9190C>T, NM_018136.4:c.9178C>T, NM_018136.4:c.9159delA, NM_018136.4:c.9115_9118dupCATT, NM_018136.4:c.8844delC, NM_018136.4:c.8711_8712delAA, NM_018136.4:c.8668C>T, NM_018136.4:c.8508_8509delGA, NM_018136.4:c.8378delT, NM_018136.4:c.8230dupA, NM_018136.4:c.8131_8132delAA, NM_018136.4:c.7894C>T, NM_018136.4:c.7860_7861delGA, NM_018136.4:c.7782_7783delGA, NM_018136.4:c.7761T>G, NM_018136.4:c.7491_7495delTATTA, NM_018136.4:c.6732delA, NM_018136.4:c.6337_6338delAT, NM_018136.4:c.6232C>T, NM_018136.4:c.6189T>G, NM_018136.4:c.6073delG, NM_018136.4:c.5439_5440delAG, NM_018136.4:c.5149delA, NM_018136.4:c.5136C>A, NM_018136.4:c.4858_4859delAT, NM_018136.4:c.4795C>T, NM_018136.4:c.4583delA, NM_018136.4:c.4195dupA, NM_018136.4:c.3979C>T, NM_018136.4:c.3978G>A, NM_018136.4:c.3811C>T, NM_018136.4:c.3796G>T, NM_018136.4:c.3710C>G, NM_018136.4:c.3663delG, NM_018136.4:c.3527C>G, NM_018136.4:c.3477_3481delCGCTA, NM_018136.4:c.3188T>G, NM_018136.4:c.3082G>A, NM_018136.4:c.3055C>T, NM_018136.4:c.2967G>A, NM_018136.4:c.2389C>T, NM_018136.4:c.1990C>T, NM_018136.4:c.1959_1962delCAAA, NM_018136.4:c.1729_1730delAG, NM_018136.4:c.1590delA, NM_018136.4:c.1406_1413delATCCTAAA, NM_018136.4:c.1366G>T, NM_018136.4:c.1260_1266delTCAAGTC, NM_018136.4:c.1179delT, NM_018136.4:c.1154_1155delAG, NM_018136.4:c.1002delA, NM_018136.4:c.719_720delCT, NM_018136.4:c.577C>T, NM_018136.4:c.349C>T	Primary autosomal recessive microcephaly type 5 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ASPM gene located on chromosomal region 1q31. The age of onset is neonatal/infantile. This disease is characterized by a reduction in head circumference at birth, mild to moderate non-progressive intellectual impairment and delay in early motor milestones, speech delay and hyperactive behavior are common.ï¼ The annual incidence is 1:1,000,000.	600,25
ASS1	Citrullinemia type 1	NM_000050.4	NM_000050.4:c.40G>A, NM_000050.4:c.256C>T, NM_000050.4:c.257G>A, NM_000050.4:c.349G>A, NM_000050.4:c.421-2A>G, NM_000050.4:c.470G>A, NM_000050.4:c.496-2A>G, NM_000050.4:c.535T>C, NM_000050.4:c.539G>A, NM_000050.4:c.571G>A, NM_000050.4:c.787G>A, NM_000050.4:c.793C>T, NM_000050.4:c.794G>A, NM_000050.4:c.805G>A, NM_000050.4:c.814C>T, NM_000050.4:c.835C>T, NM_000050.4:c.836G>A, NM_000050.4:c.910C>T, NM_000050.4:c.919C>T, NM_000050.4:c.970G>A, NM_000050.4:c.970+5G>A, NM_000050.4:c.1085G>T, NM_000050.4:c.1087C>T, NM_000050.4:c.1088G>A, NM_000050.4:c.1168G>A, NM_000050.4:c.1194-1G>C	Citrullinemia type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ASS1 gene located on chromosomal region 9q34.1. The age of onset is variable. This disease is characterized by hyperammonemia, progressive lethargy, poor feeding and vomiting in the neonatal form and by variable hyperammonemia in the later-onset form. The prevalence is 1:100,000-9:100,000.	600,25
ATIC	AICA-ribosiduria due to ATIC deficiency	NM_004044.6	NM_004044.6:c.1277A>G	AICA-ribosiduria due to ATIC deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ATIC gene located on chromosomal region 2q35. The age of onset is neonatal/infantile. This disease is characterized by profound intellectual deficit, epilepsy, dysmorphic features of the knees, elbows, and shoulders and congenital blindness. The prevalence is <1:1,000,000.	600,25

ATP7B	Wilson disease	NM_000053.3	NM_000053.3:c.4088C>T, NM_000053.3:c.4058G>A, NM_000053.3:c.3990_3993delTTAT, NM_000053.3:c.3955C>T, NM_000053.3:c.3809A>G, NM_000053.3:c.3796G>A, NM_000053.3:c.3694A>C, NM_000053.3:c.3359T>A, NM_000053.3:c.3207C>A, NM_000053.3:c.3083delA, NM_000053.3:c.2975C>T, NM_000053.3:c.2972C>T, NM_000053.3:c.2930C>T, NM_000053.3:c.2906G>A, NM_000053.3:c.2807T>A, NM_000053.3:c.2804C>T, NM_000053.3:c.2795C>A, NM_000053.3:c.2755C>T, NM_000053.3:c.2755C>G, NM_000053.3:c.2621C>T, NM_000053.3:c.2605G>A, NM_000053.3:c.2532delA, NM_000053.3:c.2356-2A>G, NM_000053.3:c.2305A>G, NM_000053.3:c.2297C>G, NM_000053.3:c.2123T>C, NM_000053.3:c.2071G>A, NM_000053.3:c.1934T>G, NM_000053.3:c.1846C>T, NM_000053.3:c.1745_1746delTA, NM_000053.3:c.1512dupT, NM_000053.3:c.1145_1151delCCCAACT, NM_000053.3:c.915T>A, NM_000053.3:c.562C>T, NM_000053.3:c.19_20delCA	Wilson disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ATP7B gene located on chromosomal region 13q14.3. The age of onset is infantile. This disease is characterized by the toxic accumulation of copper, mainly in the liver and central nervous system, and symptomatic patients may present with hepatic, neurologic or psychiatric forms. The birth incidence is 1:30,000-1:100,000 in France and The prevalence is 1:10,000-1:30,000.	600,25
ATR	Seckel syndrome type 1	NM_001184.3	NM_001184.3:c.6488delT, NM_001184.3:c.6037dupA, NM_001184.3:c.5645delA, NM_001184.3:c.5635G>T, NM_001184.3:c.2341+1G>A, NM_001184.3:c.975_976delCT	Seckel syndrome type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ATR gene located on chromosomal region 3q23. The age of onset is neonatal/infantile. This disease is characterized by a proportionate dwarfism of prenatal onset, a severe microcephaly with a bird-headed like appearance and mental retardation.ï¾ The prevalence is <1:1,000,000.	600,25
BCKDHA	Maple syrup urine disease, type 1a	NM_000709.3	NM_000709.3:c.14delT, NM_000709.3:c.632C>T, NM_000709.3:c.659C>T, NM_000709.3:c.741dupT, NM_000709.3:c.797delA, NM_000709.3:c.853G>C, NM_000709.3:c.868G>A, NM_000709.3:c.905A>C, NM_000709.3:c.909_910delGT, NM_000709.3:c.917delT, NM_000709.3:c.929C>G, NM_000709.3:c.964C>T, NM_000709.3:c.979G>A, NM_000709.3:c.1036C>T, NM_000709.3:c.1037G>A, NM_000709.3:c.1234G>A	Maple syrup urine disease type 1A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the BCKDHA gene located on chromosomal region 19q13.1-13.2. The age of onset is neonatal/infantile. This disease is characterized by poor feeding, lethargy, vomiting, a maple syrup odor in the cerumen and urine, encephalopathy and central respiratory failure if untreated. The prevalence is 1:1,000,000-9:1,000,000.	600,25
BCS1L	BCS1L-related disorders, including Leigh syndrome	NM_001079866.1	NM_001079866.1:c.103G>C, NM_001079866.1:c.133C>T, NM_001079866.1:c.148A>G, NM_001079866.1:c.166C>T, NM_001079866.1:c.232A>G, NM_001079866.1:c.547C>T, NM_001079866.1:c.548G>A, NM_001079866.1:c.550C>T, NM_001079866.1:c.696delT, NM_001079866.1:c.830G>A, NM_001079866.1:c.1057G>A	Leigh syndrome caused by mutations in the BCS1L gene -located on chromosomal region 2q35- follows an autosomal recessive pattern of inheritance. Leigh syndrome is a clinically and genetically heterogeneous disorder resulting from defective mitochondrial energy generation; It presents extensive genetic heterogeneity (more than 75 different genes) with mutations identified in both nuclear- and mitochondrial-encoded genes involved in energy metabolism, including mitochondrial respiratory chain complexes I, II, III, IV, and V. It most commonly presents as a progressive and severe neurodegenerative disorder with onset within the first months or years of life, and may result in early death. Affected individuals usually show global developmental delay or developmental regression, hypotonia, ataxia, dystonia, and ophthalmologic abnormalities, such as nystagmus or optic atrophy. The BCS1L protein is critical for the formation of mitochondrial complex III. This syndrome affects at least 1 in 40,000 newborns.	600,25
BEST1	Bestrophinopathy, AR	NM_001139443.1	NM_001139443.1:c.242G>A, NM_001139443.1:c.341_342delTG, NM_001139443.1:c.344delG, NM_001139443.1:c.418C>T, NM_001139443.1:c.434T>C, NM_001139443.1:c.502G>A, NM_001139443.1:c.754G>A, NM_001139443.1:c.769G>A, NM_001139443.1:c.1129_1130insCCAAAGA, NM_001139443.1:c.1203_1204insGCCTTGATGGA, NM_001139443.1:c.1311_1317dupCAAAGAC	Bestrophinopathy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the BEST1 gene located on chromosomal region 11q13. The age of onset is variable. This disease is characterized by central visual loss in the first 2 decades of life associated with an absent electrooculogram light rise, and a reduced electroretinogram. Genetic heterogeneity: Mutations in this gene may cause dominant phenotypes like Macular dystrophy, vitelliform, 2 (OMIM 153700) and Vitreoretinochoroidopathy (193220).	600,25
BEST1	Bestrophinopathy, AR	NM_004183.3	NM_004183.3:c.122T>C	Bestrophinopathy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the BEST1 gene located on chromosomal region 11q13. The age of onset is variable. This disease is characterized by central visual loss in the first 2 decades of life associated with an absent electrooculogram light rise, and a reduced electroretinogram. Genetic heterogeneity: Mutations in this gene may cause dominant phenotypes like Macular dystrophy, vitelliform, 2 (OMIM 153700) and Vitreoretinochoroidopathy (193220).	600,25

BSND	Bartter syndrome, type 4a	NM_057176.2	NM_057176.2:c.1A>T, NM_057176.2:c.3G>A, NM_057176.2:c.10G>T, NM_057176.2:c.22C>T, NM_057176.2:c.23G>T, NM_057176.2:c.35T>C, NM_057176.2:c.139G>A	Bartter syndrome type 4A with deafness follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the BSND gene located on chromosomal region 1p32.3. The age of onset is neonatal/infantile. This disease is characterized by maternal polyhydramnios, premature delivery, polyuria, sensorineural deafness and is associated with hypokalemic alkalosis, increased levels of plasma renin and aldosterone, low blood pressure, and vascular resistance to angiotensin II.	600,25
BTD	Biotinidase deficiency	NM_001281723.2	NM_001281723.2:c.190G>A, NM_001281723.2:c.241C>T, NM_001281723.2:c.340G>C, NM_001281723.2:c.449G>A, NM_001281723.2:c.517G>A, NM_001281723.2:c.534G>T, NM_001281723.2:c.563G>A, NM_001281723.2:c.589A>G, NM_001281723.2:c.601G>A, NM_001281723.2:c.635A>G, NM_001281723.2:c.637C>T, NM_001281723.2:c.649C>T, NM_001281723.2:c.670G>A, NM_001281723.2:c.761A>G, NM_001281723.2:c.800A>T, NM_001281723.2:c.939delT, NM_001281723.2:c.1330delG, NM_001281723.2:c.1345C>T, NM_001281723.2:c.1358G>A, NM_001281723.2:c.1374A>C, NM_001281723.2:c.1495C>T, NM_001281723.2:c.1514_1518delGGATG, NM_001281723.2:c.1601C>T, NM_001281723.2:c.1618C>T	Biotinidase deficiency an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the BTD gene located on chromosomal region 3p25. The age of onset is neonatal/infantile. This disease is characterized by seizures, breathing difficulties, hypotonia, skin rash, alopecia, hearing loss and delayed development.	600,25
CAPN3	Limb-girdle muscular dystrophy type 1 (LGMDR1; formerly LGMD2A)	NM_000070.2	NM_000070.2:c.133G>A, NM_000070.2:c.223dupT, NM_000070.2:c.257C>T, NM_000070.2:c.328C>T, NM_000070.2:c.550delA, NM_000070.2:c.580delT, NM_000070.2:c.598_612delTTCTGGAGTGCTCTG, NM_000070.2:c.855_864dupGTTGATTGCA, NM_000070.2:c.956C>T, NM_000070.2:c.1322delG, NM_000070.2:c.1466G>A, NM_000070.2:c.1468C>T, NM_000070.2:c.1469G>A, NM_000070.2:c.1599_1602delGAGC, NM_000070.2:c.1715G>A, NM_000070.2:c.1795dupA, NM_000070.2:c.1838delA, NM_000070.2:c.2120A>G, NM_000070.2:c.2212C>T, NM_000070.2:c.2243G>A, NM_000070.2:c.2251_2254dupGTCA, NM_000070.2:c.2306G>A, NM_000070.2:c.2362_2363delAGinsTCATCT	Limb-girdle muscular dystrophy type 1 (LGMDR1; formerly LGMD2A) follows an autosomal recessive pattern of inheritance and is caused by biallelic pathogenic variants in the CAPN3 gene located on chromosomal region 15q15.1. The age of onset is variable. This disease is characterized by a variable age of onset of progressive, typically symmetrical and selective weakness and atrophy of proximal shoulder- and pelvic-girdle muscles (gluteus maximus, thigh adductors, and muscles of the posterior compartment of the limbs are most commonly affected) without cardiac or facial involvement. Clinical manifestations include exercise intolerance, a waddling gait, scapular winging and calf pseudo-hypertrophy.The prevalence is 1:100,000-9:100,000. Genetic heterogeneity: Heterozygous mutation in the CAPN3 gene can cause autosomal dominant limb-girdle muscular dystrophy-4 (LGMDD4; OMIM 618129), which has a later onset and milder features.	600,25
CBS	Homocystinuria, B6-responsive and nonresponsive types	NM_000071.2	NM_000071.2:c.1330G>A, NM_000071.2:c.1280C>T, NM_000071.2:c.1150A>G, NM_000071.2:c.1136G>A, NM_000071.2:c.1058C>T, NM_000071.2:c.1006C>T, NM_000071.2:c.992C>A, NM_000071.2:c.969G>A, NM_000071.2:c.959T>C, NM_000071.2:c.919G>A, NM_000071.2:c.833T>C, NM_000071.2:c.797G>A, NM_000071.2:c.689delT, NM_000071.2:c.676G>A, NM_000071.2:c.572C>T, NM_000071.2:c.526G>T, NM_000071.2:c.502G>A, NM_000071.2:c.434C>T, NM_000071.2:c.430G>A, NM_000071.2:c.415G>A, NM_000071.2:c.393G>C, NM_000071.2:c.374G>A, NM_000071.2:c.341C>T, NM_000071.2:c.325T>C, NM_000071.2:c.162G>A, NM_000071.2:c.146C>T	Homocystinuria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CBS gene located on chromosomal region 21q22.3. The age of onset is infantile. This disease is characterized by the multiple involvement of the eye, skeleton, central nervous system and vascular system. The prevalence is 1:200,000-1:335,000.	600,25
CC2D2A	Joubert syndrome type 9; Meckel syndrome type 6	NM_001080522.2	NM_001080522.2:c.2486+1G>C, NM_001080522.2:c.2848C>T, NM_001080522.2:c.3145C>T, NM_001080522.2:c.3289delG, NM_001080522.2:c.3364C>T, NM_001080522.2:c.3594+1G>A, NM_001080522.2:c.4179+1delG, NM_001080522.2:c.4181delG, NM_001080522.2:c.4333C>T, NM_001080522.2:c.4582C>T, NM_001080522.2:c.4667A>T	Joubert syndrome type 9 defect follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CC2D2A gene located on chromosomal region 4p15.32. The age of onset is neonatal/infantile. This disease is characterized neonatal hypotonia, developmental delay, intellectrual disability, ataxia, and abnormal eye movements including oculomotor apraxia, primary position nystagmus and congenital hepatic fibrosis.	600,25
CDH23	Usher syndrome, type 1D	NM_022124.5	NM_022124.5:c.146-2A>G, NM_022124.5:c.193delC, NM_022124.5:c.288+1G>A, NM_022124.5:c.1858+2T>G, NM_022124.5:c.3141C>A, NM_022124.5:c.3516_3519delATCC, NM_022124.5:c.3579+2T>C, NM_022124.5:c.4504C>T, NM_022124.5:c.5237G>A, NM_022124.5:c.5663T>C, NM_022124.5:c.6050-9G>A, NM_022124.5:c.6393delC, NM_022124.5:c.6442G>A	Non-syndromic autosomal recessive deafness type 12 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CDH23 gene located on chromosomal region 10p22.1. The age of onset is neonatal/infantile. This disease is characterized by congenital, non-progressive, mild-to-profound sensorineural hearing impairment.	600,25

CDHR1	Cone-rod dystrophy, type 15	NM_033100.3	NM_033100.3:c.338delG, NM_033100.3:c.524dupA, NM_033100.3:c.640delG, NM_033100.3:c.1112delC, NM_033100.3:c.1463delG, NM_033100.3:c.1485+2T>C, NM_033100.3:c.1485+2T>G	Cone-rod dystrophy, type 15 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CDHR1 gene located on chromosomal region 10q23.1. This disease is characterized by decreased visual acuity and sensitivity in the central visual field, followed by loss of peripheral vision. The overall prevalence of all types of cone-rod dystrophy is 1-9:100,000.	600,25
CENPJ	Primary microcephaly type 6, autosomal recessive	NM_018451.4	NM_018451.4:c.3842_3843dupTA, NM_018451.4:c.3704A>T, NM_018451.4:c.3699_3702dupAATA, NM_018451.4:c.3568_3571dupGTCA, NM_018451.4:c.3415G>T, NM_018451.4:c.3243_3246delTCAG, NM_018451.4:c.2968_2972delAAAAA, NM_018451.4:c.2614delT, NM_018451.4:c.2460_2463delGACG, NM_018451.4:c.1949_1952dupAGTG, NM_018451.4:c.757_760delGTCT, NM_018451.4:c.289dupA, NM_018451.4:c.232_236delCAGAA, NM_018451.4:c.40C>T	Primary autosomal recessive microcephaly type 6 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CENPJ gene located on chromosomal region 13q12.12.ï¾ The age of onset is neonatal/infantile. This disease is characterized by reduced head circumference at birth with no gross anomalies of brain architecture and variable degrees of intellectual impairment.	600,25
CEP290	Meckel syndrome type 4; Joubert syndrome type 5	NM_025114.3	NM_025114.3:c.7341dupA, NM_025114.3:c.7341delA, NM_025114.3:c.7324G>T, NM_025114.3:c.6798G>A, NM_025114.3:c.6645+1G>A, NM_025114.3:c.6624delG, NM_025114.3:c.6448_6455delCAGTTGAA, NM_025114.3:c.5668G>T, NM_025114.3:c.5611_5614delCAAA, NM_025114.3:c.4962_4963delAA, NM_025114.3:c.4916C>A, NM_025114.3:c.4723A>T, NM_025114.3:c.4705-1G>T, NM_025114.3:c.4656delA, NM_025114.3:c.4393C>T, NM_025114.3:c.3185delT, NM_025114.3:c.2249T>G, NM_025114.3:c.1681C>T, NM_025114.3:c.1665_1666delAA, NM_025114.3:c.1501G>T, NM_025114.3:c.613C>T, NM_025114.3:c.384_387delTAGA, NM_025114.3:c.164_167delCTCA, NM_025114.3:c.21G>T	Meckel syndrome type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CEP290 gene located on chromosomal region 12q21.32. The age of onset is neonatal. This disease is characterized by a combination of renal cysts and variably associated features including developmental anomalies of the central nervous system (typically occipital encephalocele), hepatic ductal dysplasia and cysts, and postaxial polydactyly. The prevalence is <1/1,000,000.	600,25
CERKL	Retinitis pigmentosa type 26	NM_001030311.2	NM_001030311.2:c.1090C>T, NM_001030311.2:c.858delT, NM_001030311.2:c.847C>T, NM_001030311.2:c.312delA	Retinitis pigmentosa 26 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CERKL gene located on chromosomal region 2q31.3. The age of onset is variable. This disease is characterized by night blindness (nyctalopia), peripheral visual field impairment and over time loss of central vision. The prevalence is 1:10,000-5:10,000.	600,25
CFH	Complement factor H deficiency	NM_000186.3	NM_000186.3:c.380G>T, NM_000186.3:c.1606T>C, NM_000186.3:c.2876G>A	Complement factor H deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CFH gene located on chromosomal region 1q32. This disease is characterized by increased susceptibility to recurrent, usually severe, infections (particularly by Neisseria meningitidis, Escherichia coli, and Haemophilus influenzae), renal impairment and/or autoimmune diseases.	600,25

CFTR	Cystic fibrosis	NM_000492.3	NM_000492.3:c.1A>G, NM_000492.3:c.4C>T, NM_000492.3:c.11C>A, NM_000492.3:c.50delT, NM_000492.3:c.44T>C, NM_000492.3:c.53+1G>T, NM_000492.3:c.57G>A, NM_000492.3:c.79G>T, NM_000492.3:c.88C>T, NM_000492.3:c.115C>T, NM_000492.3:c.137C>A, NM_000492.3:c.164+1G>A, NM_000492.3:c.164+1G>T, NM_000492.3:c.164+2T>C, NM_000492.3:c.164+4dupT, NM_000492.3:c.165-3C>T, NM_000492.3:c.165-1G>A, NM_000492.3:c.166G>A, NM_000492.3:c.169T>G, NM_000492.3:c.170G>A, NM_000492.3:c.171G>A, NM_000492.3:c.174_177delTAGA, NM_000492.3:c.175dupA, NM_000492.3:c.178G>A, NM_000492.3:c.178G>T, NM_000492.3:c.200C>T, NM_000492.3:c.223C>T, NM_000492.3:c.233dupT, NM_000492.3:c.254G>A, NM_000492.3:c.262_263delTT, NM_000492.3:c.263T>A, NM_000492.3:c.263T>G, NM_000492.3:c.271G>A, NM_000492.3:c.273+1G>A, NM_000492.3:c.273+3A>C, NM_000492.3:c.274-2A>G, NM_000492.3:c.274-1G>A, NM_000492.3:c.274G>A, NM_000492.3:c.274G>T, NM_000492.3:c.292C>T, NM_000492.3:c.305T>G, NM_000492.3:c.310delA, NM_000492.3:c.313delA, NM_000492.3:c.325_327delTATinsG, NM_000492.3:c.328G>C, NM_000492.3:c.328G>T, NM_000492.3:c.349C>T, NM_000492.3:c.350G>A, NM_000492.3:c.350G>T, NM_000492.3:c.366T>A, NM_000492.3:c.409delC, NM_000492.3:c.413_415dupTAC, NM_000492.3:c.416A>G, NM_000492.3:c.442delA, NM_000492.3:c.445G>A, NM_000492.3:c.445G>T, NM_000492.3:c.446G>T, NM_000492.3:c.489+1G>T, NM_000492.3:c.531delT, NM_000492.3:c.532G>A, NM_000492.3:c.543_546delTAGT, NM_000492.3:c.571T>G, NM_000492.3:c.577G>T, NM_000492.3:c.579+1G>T, NM_000492.3:c.579+3A>G, NM_000492.3:c.579+5G>A, NM_000492.3:c.580-1G>T, NM_000492.3:c.595C>T, NM_000492.3:c.613C>T, NM_000492.3:c.617T>G, NM_000492.3:c.647G>A, NM_000492.3:c.658C>T, NM_000492.3:c.680T>G, NM_000492.3:c.695T>A, NM_000492.3:c.708delT, NM_000492.3:c.717delG, NM_000492.3:c.803delA, NM_000492.3:c.825C>G, NM_000492.3:c.828C>A, NM_000492.3:c.850dupA, NM_000492.3:c.861_865delCTTAA, NM_000492.3:c.935_937delTCT, NM_000492.3:c.933C>G, NM_000492.3:c.948delT, NM_000492.3:c.987delA, NM_000492.3:c.988G>T, NM_000492.3:c.1000C>T, NM_000492.3:c.1001G>T, NM_000492.3:c.1006_1007insG, NM_000492.3:c.1007T>A, NM_000492.3:c.1013C>T	Cystic fibrosis follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CFTR gene located on chromosomal region 7q31.2. The age of onset of severe form is neonatal or infantile but there are also variants associated with moderate clinical or late onset. This disease is characterized by the production of sweat with a high salt content, mucus secretions with an abnormal viscosity, chronic bronchitis, pancreatic insufficiency, adolescent diabetes and, more rarely, stercoral obstruction and cirrhosis. Male sterility is a constant feature. Late-onset forms, which are usually only mild or monosymptomatic. The prevalence is 1:10,000-9:10,000.	600,25
CHST6	Macular corneal dystrophy	NM_021615.4	NM_021615.4:c.853delC, NM_021615.4:c.820G>T, NM_021615.4:c.392C>A, NM_021615.4:c.327_328delCT	Macular corneal dystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CHST6 gene located on chromosomal region 16q22. The age of onset is variable. This disease is characterized by bilateral ill-defined cloudy regions within a hazy stroma, and eventually severe visual impairment. The prevalence is 1:100,000-9:100,000.	600,25
CLCN1	Myotonia congenita, recessive	NM_000083.2	NM_000083.2:c.180+3A>T, NM_000083.2:c.225dupC, NM_000083.2:c.409T>G, NM_000083.2:c.871G>A, NM_000083.2:c.1238T>G, NM_000083.2:c.1453A>G, NM_000083.2:c.2680C>T	Myotonia congenita follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CLCN1 gene located on chromosomal region 7q35. The age of onset is neonatal/infantile. This is a nondystrophic skeletal muscle disorder characterized by muscle stiffness and an inability of the muscle to relax after voluntary contraction. Most patients have symptom onset in the legs, which later progresses to the arms, neck, and facial muscles. Many patients show marked hypertrophy of the lower limb muscles. The prevalence is 1:100,000.	600,25
CLDN19	Rena hypomagnesemia type 5, with ocular involvement	NM_148960.2	NM_148960.2:c.425_437delCCCTGGTGACCCA, NM_148960.2:c.269T>C, NM_148960.2:c.169C>G, NM_148960.2:c.59G>A	Renal hypomagnesemia type 5, with ocular involvement follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CLDN19 gene located on chromosomal region 1p34.2. The age of onset is infantile. This disease is characterized by excessive magnesium and calcium renal wasting, bilateral nephrocalcinosis, progressive renal failure and severe ocular abnormalities. The prevalence is <1:1,000,000.	600,25
CLRN1	Usher syndrome, type 3A	NM_001195794.1	NM_001195794.1:c.669_670insT, NM_001195794.1:c.630dupT, NM_001195794.1:c.189C>A, NM_001195794.1:c.144T>G, NM_001195794.1:c.118T>G, NM_001195794.1:c.92C>T	Usher syndrome type 3A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CLRN1 gene located on chromosomal region 3q25.1. The age of onset is neonatal/infantile. This disease is characterized by the association of sensorineural deafness with retinitis pigmentosa and progressive vision loss. The prevalence is 1:1.000.000- 9/1.000.000.	600,25

CNGA1	Retinitis pigmentosa type 49	NM_001142564.1	NM_001142564.1:c.2179delA, NM_001142564.1:c.2134C>T, NM_001142564.1:c.1747C>T, NM_001142564.1:c.1166C>T, NM_001142564.1:c.1001G>A, NM_001142564.1:c.656+2T>C, NM_001142564.1:c.445G>T, NM_001142564.1:c.304dupA	Retinitis pigmentosa 49 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CNGA1 gene located on chromosomal region 4p12. The age of onset is variable. This disease is characterized by night blindness (nyctalopia), peripheral visual field impairment and over time loss of central vision. The prevalence is 1:10,000-5:10,000.	600,25
CNGB1	Retinitis pigmentosa type 45	NM_001297.4	NM_001297.4:c.3462+1G>A, NM_001297.4:c.3425delT, NM_001297.4:c.3150delG, NM_001297.4:c.2762_2765delACGA, NM_001297.4:c.2653delG, NM_001297.4:c.2492+2T>G, NM_001297.4:c.1958-1G>A, NM_001297.4:c.1122-2A>T, NM_001297.4:c.952C>T, NM_001297.4:c.413-1G>A, NM_001297.4:c.218-2A>G	Retinitis pigmentosa 45 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CNGB1 gene located on chromosomal region 16q13. The age of onset is variable. This disease is characterized by night blindness, peripheral visual field impairment and over time loss of central vision. The prevalence is 1:10,000 to 5:10,000.	600,25
CNGB3	Achromatopsia type 3	NM_019098.4	NM_019098.4:c.2048_2049delCA, NM_019098.4:c.2011G>T, NM_019098.4:c.1148delC, NM_019098.4:c.1063C>T, NM_019098.4:c.893_897delCAAAA, NM_019098.4:c.887_896delCTTCTACAAA, NM_019098.4:c.886_890delACTTC, NM_019098.4:c.819_826delCAGACTCC, NM_019098.4:c.446_447insT	Achromatopsia type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CNGB3 gene located on chromosomal region 8q21.3. The age of onset is neonatal/Infantile. This disease is characterized by reduced visual acuity, pendular nystagmus, increased sensitivity to light (photophobia), a small central scotoma, and reduced or complete loss of color discrimination. Most individuals have complete form, with total lack of function in all three types of cones. Rarely, individuals have incomplete form, with similar, but generally less severe symptoms. The prevalence is 1/30,000-1/50,000.	600,25
COL17A1	Epidermolysis bullosa, junctional, non-Herlitz type	NM_000494.3	NM_000494.3:c.4319dupC, NM_000494.3:c.4003_4004delGG, NM_000494.3:c.3908G>A, NM_000494.3:c.3897_3900delATCT, NM_000494.3:c.3827dupC, NM_000494.3:c.3795delC, NM_000494.3:c.3676C>T, NM_000494.3:c.3277+1G>A, NM_000494.3:c.3067C>T, NM_000494.3:c.3043C>T, NM_000494.3:c.2965delA, NM_000494.3:c.2944_2947+1delGAAGG, NM_000494.3:c.2564T>G, NM_000494.3:c.2551+1G>T, NM_000494.3:c.2430_2431insCCGA, NM_000494.3:c.2383C>T, NM_000494.3:c.2336-1G>T, NM_000494.3:c.2336-2A>G, NM_000494.3:c.2228-3_2235delCAGGTCCTGCTinsTTG, NM_000494.3:c.1898G>A, NM_000494.3:c.1706delC, NM_000494.3:c.520_521delAG, NM_000494.3:c.433C>T	Epidermolysis bullosa, junctional, non-Herlitz type follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COL17A1 gene located on chromosomal region 10q24.3. The age of onset is neonatal/infantile. This disease is characterized by a generalized skin blistering, atrophic scarring, nail dystrophy or nail absence, and enamel hypoplasia, with extracutaneous involvement.	600,25
COL18A1	Knobloch syndrome, type 1	NM_130444.2	NM_130444.2:c.1700_1701insGACGTGAAAGAGGGG, NM_130444.2:c.2240_2241insGACGTGAAAGAGGGG, NM_130444.2:c.3294_3295delAG, NM_130444.2:c.3502C>T, NM_130444.2:c.4072_4084delCCCCCAGGCCCAC, NM_130444.2:c.4214_4223delCAGGGCCCCC, NM_130444.2:c.4222_4223delCC, NM_130444.2:c.4323_4323+1delGG, NM_130444.2:c.4759_4760delCT, NM_130444.2:c.5168dupG	Knobloch syndrome type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COL18A1 gene located on chromosomal region 21q22.3. The age of onset is neonatal/infantile. This disease is characterized by vitreoretinal and macular degeneration, and occipital encephalocele.ï¾ The prevalence is <1:1,000,000.	600,25
COL4A3	Alport syndrome, autosomal recessive	NM_000091.4	NM_000091.4:c.345delG, NM_000091.4:c.898G>A, NM_000091.4:c.2083G>A, NM_000091.4:c.2111delC, NM_000091.4:c.2954G>T, NM_000091.4:c.4420_4424delCTTTT, NM_000091.4:c.4441C>T, NM_000091.4:c.4571C>G	Alport syndrome, autosomal recessive follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COL4A3 and COL4A4 genes located on chromosomal region 2q36.3. The age of onset is infantile. This disease is characterized by renal, cochlear, and ocular involvement. Renal disease progresses from microscopic hematuria to proteinuria, progressive renal insufficiency, and end-stage renal disease. Progressive sensorineural hearing loss is usually present by late childhood or early adolescence. Ocular findings include anterior lenticonus, maculopathy, corneal endothelial vesicles, and recurrent corneal erosion. The prevalence is 1:50,000 newborn.	600,25
COL4A4	Alport syndrome, autosomal recessive	NM_000092.4	NM_000092.4:c.4923C>A, NM_000092.4:c.4129C>T, NM_000092.4:c.3713C>A, NM_000092.4:c.3601G>A, NM_000092.4:c.2312delG, NM_000092.4:c.71+1G>A	Alport syndrome, autosomal recessive follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COL4A3 and COL4A4 genes located on chromosomal region 2q36.3. The age of onset is infantile. This disease is characterized by renal, cochlear, and ocular involvement. Renal disease progresses from microscopic hematuria to proteinuria, progressive renal insufficiency, and end-stage renal disease. Progressive sensorineural hearing loss is usually present by late childhood or early adolescence. Ocular findings include anterior lenticonus, maculopathy, corneal endothelial vesicles, and recurrent corneal erosion. The prevalence is 1:50,000 newborn.	600,25

COL7A1	Epidermolysis bullosa dystrophica, AR	NM_000094.3	NM_000094.3:c.8524_8527+10delGAAGGTGAGGACAG, NM_000094.3:c.8479C>T, NM_000094.3:c.8440C>T, NM_000094.3:c.8393T>A, NM_000094.3:c.8245G>A, NM_000094.3:c.7957G>A, NM_000094.3:c.7930-1G>C, NM_000094.3:c.7912G>T, NM_000094.3:c.7411C>T, NM_000094.3:c.7345-1G>A, NM_000094.3:c.6946G>A, NM_000094.3:c.6859G>A, NM_000094.3:c.6752G>A, NM_000094.3:c.6670G>T, NM_000094.3:c.6573+1G>T, NM_000094.3:c.6527dupC, NM_000094.3:c.6205C>T, NM_000094.3:c.6187C>T, NM_000094.3:c.6091G>A, NM_000094.3:c.5821-1G>A, NM_000094.3:c.5532+1G>A, NM_000094.3:c.5287C>T, NM_000094.3:c.5096C>T, NM_000094.3:c.5052+1G>A, NM_000094.3:c.4888C>T, NM_000094.3:c.4783G>C, NM_000094.3:c.4373C>T, NM_000094.3:c.4119+1G>T, NM_000094.3:c.4039G>C, NM_000094.3:c.3831+1G>T, NM_000094.3:c.2471dupG, NM_000094.3:c.933C>A, NM_000094.3:c.887delG, NM_000094.3:c.706C>T, NM_000094.3:c.425A>G, NM_000094.3:c.336C>G	Epidermolysis bullosa dystrophica follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COL7A1 gene located on chromosomal region 3p21.1. The age of onset is neonatal/infantile. This disease is characterized by generalized cutaneous and mucosal blistering and scarring associated with severe deformities and major extracutaneous involvement. The prevalence is <1:1,000,000.	600,25
COQ2	Primary coenzyme Q10 deficiency, type 1	NM_015697.7	NM_015697.7:c.1197delT, NM_015697.7:c.890A>G, NM_015697.7:c.723delT, NM_015697.7:c.683A>G, NM_015697.7:c.590G>A	Primary coenzyme Q10 deficiency type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COQ2 gene located on chromosomal region 4q21.23. The age of onset is neonatal/infantile. The phenotypes include an encephalomyopathic form with seizures and ataxia; a multisystem infantile form with encephalopathy, cardiomyopathy and renal failure; a predominantly cerebellar form with ataxia and cerebellar atrophy; Leigh syndrome with growth retardation; and an isolated myopathic form.	600,25
COQ8A	Primary coenzyme Q10 deficiency, type 4	NM_020247.4	NM_020247.4:c.589-3C>G, NM_020247.4:c.637C>T, NM_020247.4:c.815G>A, NM_020247.4:c.815G>T, NM_020247.4:c.911C>T, NM_020247.4:c.1541A>G, NM_020247.4:c.1645G>A, NM_020247.4:c.1651G>A, NM_020247.4:c.1750_1752delACC, NM_020247.4:c.1813dupG	Primary coenzyme Q10 deficiency type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COQ8A gene located on chromosomal region 1q42.13. The age of onset is infantile. This disease is characterized by progressive ataxia, cerebellar atrophy, and often exercise intolerance with elevated lactate levels and mild intellectual deficit.	600,25
CPT2	Carnitine palmitoyltransferase type 2 deficiency, lethal neonatal	NM_000098.2	NM_000098.2:c.149C>A, NM_000098.2:c.338C>T, NM_000098.2:c.359A>G, NM_000098.2:c.370C>T, NM_000098.2:c.452G>A, NM_000098.2:c.464dupT, NM_000098.2:c.520G>A, NM_000098.2:c.638A>G, NM_000098.2:c.680C>T, NM_000098.2:c.725_726delAC, NM_000098.2:c.886C>T, NM_000098.2:c.1148T>A, NM_000098.2:c.1237C>T, NM_000098.2:c.1239_1240delGA, NM_000098.2:c.1369A>T, NM_000098.2:c.1437C>G, NM_000098.2:c.1784delC, NM_000098.2:c.1883A>C, NM_000098.2:c.1891C>T	Carnitine palmitoyltransferase deficiency, type 2, lethal neonatal form follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CPT2 gene located on chromosomal region 1p32. The age of onset is neonatal/infantile. This disease is characterized by a severe fasting intolerance leading to metabolic derangements of hypoketotic hypoglycemia, resulting in coma and seizures, and hepatic encephalopathy leading to liver failure.ï¾ The prevalence is <1:1,000,000.	600,25
CRB1	Retinitis pigmentosa type 12, AR; Leber congenital amaurosis type 8	NM_201253.2	NM_201253.2:c.498_506delAATTGATGG, NM_201253.2:c.613_619delATAGGAA, NM_201253.2:c.2290C>T, NM_201253.2:c.2401A>T, NM_201253.2:c.2416G>T, NM_201253.2:c.2688T>A, NM_201253.2:c.2983G>T, NM_201253.2:c.3055_3059dupTATAT, NM_201253.2:c.3122T>C, NM_201253.2:c.3299T>C, NM_201253.2:c.3299T>G, NM_201253.2:c.3383delT, NM_201253.2:c.3419T>A, NM_201253.2:c.3997G>T	Retinitis pigmentosa type 12 and leber congenital amaurosis type 8 follow an autosomal recessive pattern of inheritance and are caused by pathogenic variants in the CRB1 gene located on chromosomal region 1q31-q32.1. Retinitis pigmentosa type 12 is characterized by night blindness, peripheral visual field impairment and over time loss of central visionm, and its prevalence is 1-5:10,000. Leber congenital amaurosis, with a neonatal/infantile age of onset, comprises a group of early-onset childhood retinal dystrophies characterized by vision loss, nystagmus, and severe retinal dysfunction. Patients usually present at birth with profound vision loss and pendular nystagmus. Other clinical findings of this disease may include high hypermetropia, photodysphoria, oculodigital sign, keratoconus, cataracts, and a variable appearance to the fundus.	600,25
CTNS	Cystinosis (atypical/juvenile/ocular) nephropathic	NM_001031681.2	NM_001031681.2:c.283G>T, NM_001031681.2:c.329G>T, NM_001031681.2:c.357_360delCAGC, NM_001031681.2:c.397_398delAT, NM_001031681.2:c.414G>A, NM_001031681.2:c.416C>T, NM_001031681.2:c.506G>A, NM_001031681.2:c.589G>A, NM_001031681.2:c.646dupA, NM_001031681.2:c.853-3C>G, NM_001031681.2:c.1015G>A	Nephropathic cystinosis follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CTNS gene located on chromosomal region 17p13. The age of onset is neonatal/infantile. This disease is characterized by hypothyroidism, insulin-dependent diabetes, hepatosplenomegaly with portal hypertension, and muscle, cerebral and ocular involvement, caused by cystine deposits in various organs. The prevalence is 1:100,000-1:200,000.	600,25

CTSK	Pycnodysostosis	NM_000396.3	NM_000396.3:c.926T>C, NM_000396.3:c.721C>T, NM_000396.3:c.436G>C, NM_000396.3:c.236G>A, NM_000396.3:c.154A>T	Pycnodysostosis follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CTSK gene located on chromosomal region 1q21. The age of onset is variable. This disease is characterized by osteosclerosis, short stature or dwarfism, acroosteolysis of the distal phalanges, fragile bones associated with spontaneous fractures and dysplasia of the clavicles. The prevalence is 1/1,000,000 to 9/1,000,000.	600,25
CYP4V2	Bietti crystalline corneoretinal dystrophy	NM_207352.3	NM_207352.3:c.130T>A, NM_207352.3:c.327+1G>A, NM_207352.3:c.332T>C, NM_207352.3:c.1523G>A	Bietti crystalline corneoretinal dystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CYP4V2 gene located on chromosomal region 4q35.2. The age of onset is adult. This disease is characterized by nightblindness, decreased vision, paracentral scotoma, and, in the end stages of the disease, legal blindness.	600,25
CYP7B1	Spastic paraplegia type 5A, autosomal recessive	NM_004820.4	NM_004820.4:c.1460dupT, NM_004820.4:c.1456C>T, NM_004820.4:c.1162C>T, NM_004820.4:c.889A>G, NM_004820.4:c.825T>A, NM_004820.4:c.321_324delACAA, NM_004820.4:c.187C>T	Spastic paraplegia type 5A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CYP7B1 gene located on chromosomal region 8q21.3. The age of onset is neonatal/infantile. This disease is characterized by a slow, gradual, progressive weakness and spasticity of the lower limbs. Rate of progression and the severity of symptoms are quite variable. Initial symptoms may include difficulty with balance, weakness and stiffness in the legs, muscle spasms, and dragging the toes when walking. In some forms of the disorder, bladder symptoms (such as incontinence) may appear, or the weakness and stiffness may spread to other parts of the body. The prevalence is below 1,000,000.	600,25
D2HGDH	D-2-hydroxyglutaric aciduria	NM_152783.4	NM_152783.4:c.440T>G, NM_152783.4:c.1123G>T, NM_152783.4:c.1315A>G, NM_152783.4:c.1331T>C, NM_152783.4:c.1333_1334delAC	D-2-Hydroxyglutaric aciduria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the D2HGDH gene located on chromosomal region 2q37.3. The age of onset is variable. This disease is characterized by extremely variable clinical manifestations, with severe cases characterized by neonatal or early infantile-onset epileptic encephalopathy, and marked hypotonia, and cerebral visual failure, developmental delay, seizures, involuntary movements, and cardiomyopathy are also common in these cases. The prevalence is below 1,000,000.	600,25
DBT	Maple syrup urine disease, type 2	NM_001918.3	NM_001918.3:c.1281+1G>A, NM_001918.3:c.939G>C, NM_001918.3:c.901C>T, NM_001918.3:c.871C>T, NM_001918.3:c.827T>G, NM_001918.3:c.772+1G>A, NM_001918.3:c.670G>T, NM_001918.3:c.581C>G, NM_001918.3:c.294C>G, NM_001918.3:c.272_275delCAGT, NM_001918.3:c.126T>G	Maple syrup urine disease, type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DBT gene located on chromosomal region 1p21.2. The age of onset in neonatal/infantil. This disease is characterized by a maple syrup odor to the urine, deficient diet, lethargy and focal dystonia, followed by progressive encephalopathy and central respiratory failure if not treated. The prevalence is 1-5/10,000.	600,25
DCLRE1C	Omenn syndrome; Severe combined immunodeficiency, Athabascan type	NM_001033855.2	NM_001033855.2:c.1639G>T, NM_001033855.2:c.1558dupA, NM_001033855.2:c.780+1delG, NM_001033855.2:c.597C>A, NM_001033855.2:c.2T>C	Omenn syndrome and Athabascan type severe combined immunodeficiency follow an autosomal recessive pattern of inheritance and are caused by pathogenic variants in the DCLRE1C gene located on chromosomal region 10p13. Omenn syndrome has an early age of onset and it is characterized by erythroderma, desquamation, alopecia, chronic diarrhea, failure to thrive, lymphadenopathy, and hepatosplenomegaly, associated with severe combined immunodeficiency. The age of onset of Athabascan type severe combined immunodeficiency is neonatal/infantile and it is characterized by severe and recurrent infections, diarrhea, failure to thrive, and cell sensitivity to ionizing radiation. The prevalence is 1-9/1,000,000.	600,25
DGUOK	DGUOK-related mitochondrial DNA depletion syndrome	NM_080916.2	NM_080916.2:c.137A>G, NM_080916.2:c.313C>T, NM_080916.2:c.425G>A, NM_080916.2:c.494A>T, NM_080916.2:c.707+2T>G, NM_080916.2:c.763G>T	Mitochondrial DNA depletion syndrome type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DGUOK gene located on chromosomal region 2p13. The age of onset is neonatal/infantile. This disease is characterized by progressive liver failure, hypoglycemia and neurologic abnormalities including hypotonia, encephalopathy and peripheral neuropathy	600,25

DHCR7	Smith-Lemli-Opitz syndrome	NM_001163817.1	NM_001163817.1:c.1342G>A, NM_001163817.1:c.1337G>A, NM_001163817.1:c.1228G>A, NM_001163817.1:c.1210C>T, NM_001163817.1:c.1055G>A, NM_001163817.1:c.1054C>T, NM_001163817.1:c.976G>T, NM_001163817.1:c.964-1G>C, NM_001163817.1:c.907G>A, NM_001163817.1:c.866C>T, NM_001163817.1:c.841G>A, NM_001163817.1:c.839A>G, NM_001163817.1:c.832-1G>C, NM_001163817.1:c.744G>T, NM_001163817.1:c.730G>A, NM_001163817.1:c.725G>A, NM_001163817.1:c.724C>T, NM_001163817.1:c.506C>T, NM_001163817.1:c.461C>G, NM_001163817.1:c.453G>A, NM_001163817.1:c.452G>A, NM_001163817.1:c.356A>T, NM_001163817.1:c.292C>T, NM_001163817.1:c.278C>T, NM_001163817.1:c.151C>T, NM_001163817.1:c.1A>G	Smith-Lemli-Opitz syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DHCR7 gene located on chromosomal region 11q13.4. The age of onset is neonatal/infantile. This disease is characterized by multiple congenital anomalies, intellectual deficit, and behavioral problems.ï¾ The prevalence is 1/20,000 to 1/40,000 newborn.	600,25
DPYD	Dihydropyrimidine dehydrogenase deficiency	NM_000110.3	NM_000110.3:c.1905+1G>A, NM_000110.3:c.1679T>G, NM_000110.3:c.1109_1110delTA, NM_000110.3:c.299_302delTCAT	Dihydropyrimidine dehydrogenase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DPYD gene located on chromosomal region 1p22. This disease shows large phenotypic variability, ranging from no symptoms to a convulsive disorder with motor and mental retardation in homozygous patients. In people with severe dihydropyrimidine dehydrogenase deficiency, the disorder becomes apparent in infancy. These affected individuals have recurrent seizures (epilepsy), intellectual disability, a small head size (microcephaly), increased muscle tone (hypertonia), delayed development of motor skills such as walking, and autistic behaviors that affect communication and social interaction. The prevalence is unknow. In addition, homozygous and heterozygous mutation carriers can develop severe toxicity after the administration of the antineoplastic drug 5-fluorouracil (5FU).	600,25
DSP	Cardiomyopathy, dilated, with woolly hair and keratoderma; Epidermolysis bullosa, lethal acantholytic	NM_004415.3	NM_004415.3:c.3098delA, NM_004415.3:c.5800C>T, NM_004415.3:c.6370_6371delCT, NM_004415.3:c.7000C>T, NM_004415.3:c.7180_7181delAG, NM_004415.3:c.8188C>T	Dilated cardiomyopathy with woolly hair and keratoderma, known as Carvajal syndrome, follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DSP gene located on chromosomal region 6p24. The age of onset is neonatal/infantile. This disease is characterized by woolly hair is present at birth and the palmoplantar keratoderma appears during the first year of life. The cardiac anomaly presents during childhood and is marked by dilation of the left ventricle accompanied by alterations in muscle contractility. The dilated cardiomyopathy may lead to life-threatening congestive heart failure and death. The prevalence is below 1,000,000. Furthermore, mutations in the DSP gene have been identified in people with an autosomal recessive disorder called lethal acantholytic epidermolysis bullosa. Features of this condition include very fragile skin that blisters and detaches easily, a complete absence of hair (alopecia), abnormal or missing fingernails, teeth that are present from birth (neonatal teeth), and abnormalities of the heart muscle (cardiomyopathy). The skin abnormalities lead to a severe loss of fluids and death in early infancy.	600,25
DYSF	Miyoshi muscular dystrophy, type 1; Muscular dystrophy, limb-girdle, autosomal recessive, type 2	NM_001130978.1	NM_001130978.1:c.1481-1G>A	Miyoshi muscular dystrophy, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DYSF gene located on chromosomal region 2p13.3. The age of onset is young adulthood. This disease is characterized by weakness and atrophy in the distal lower extremity posterior compartment (gastrocnemius and soleus muscles) and is associated with difficulties in standing on tip toes. The prevalence is 1/1,000,000 to 9/1,000,000. Mutations in the DYSF gene can also cause muscular dystrophy, limb-girdle, autosomal recessive, type 2. This disease is characterized by an onset in late adolescence or early adulthood of slowly progressive, proximal weakness and atrophy of shoulder and pelvic girdle muscles. Cardiac and respiratory muscles are not involved. Hypertrophy of the calf muscles and highly elevated serum creatine kinase levels are frequently observed.	600,25

DYSF	Miyoshi muscular dystrophy, type 1; Muscular dystrophy, limb-girdle, autosomal recessive, type 2	NM_001130987.1	NM_001130987.1:c.203_204delTGinsAT, NM_001130987.1:c.396_397delCC, NM_001130987.1:c.706C>T, NM_001130987.1:c.759+1G>C, NM_001130987.1:c.797G>A, NM_001130987.1:c.853C>T, NM_001130987.1:c.991G>A, NM_001130987.1:c.991G>T, NM_001130987.1:c.1033+1G>A, NM_001130987.1:c.1149+1G>A, NM_001130987.1:c.1372G>A, NM_001130987.1:c.1380+2T>C, NM_001130987.1:c.1464C>A, NM_001130987.1:c.1488dupA, NM_001130987.1:c.1494-2A>G, NM_001130987.1:c.1494-1G>A, NM_001130987.1:c.1609G>A, NM_001130987.1:c.1674delA, NM_001130987.1:c.1692+2T>A, NM_001130987.1:c.1717C>T, NM_001130987.1:c.1867C>T, NM_001130987.1:c.1888C>T, NM_001130987.1:c.1927G>T, NM_001130987.1:c.2924_2928delAGACC, NM_001130987.1:c.2923C>T, NM_001130987.1:c.3051G>T, NM_001130987.1:c.3095A>G, NM_001130987.1:c.3166C>T, NM_001130987.1:c.3229-2A>T, NM_001130987.1:c.3498_3499delTGinsAA, NM_001130987.1:c.3531C>A, NM_001130987.1:c.3532C>T, NM_001130987.1:c.3695delC, NM_001130987.1:c.3762delA, NM_001130987.1:c.3859G>T, NM_001130987.1:c.3957+1delG, NM_001130987.1:c.4011delC, NM_001130987.1:c.4144C>T, NM_001130987.1:c.4162_4163delGT, NM_001130987.1:c.4307G>A, NM_001130987.1:c.4873C>T, NM_001130987.1:c.4989_4993delGCCCGinsCCCC, NM_001130987.1:c.5194C>T, NM_001130987.1:c.5318A>G, NM_001130987.1:c.5383C>T, NM_001130987.1:c.5458-2A>C, NM_001130987.1:c.5546G>A, NM_001130987.1:c.5546+1G>T, NM_001130987.1:c.5614G>T, NM_001130987.1:c.5626G>A, NM_001130987.1:c.5642+1G>A, NM_001130987.1:c.5711delG, NM_001130987.1:c.5761C>T, NM_001130987.1:c.5815_5816delAG, NM_001130987.1:c.5830C>T, NM_001130987.1:c.5953_5956delCAGC, NM_001130987.1:c.6096dupA, NM_001130987.1:c.6109G>T, NM_001130987.1:c.6241C>T	Miyoshi muscular dystrophy, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DYSF gene located on chromosomal region 2p13.3. The age of onset is young adulthood. This disease is characterized by weakness and atrophy in the distal lower extremity posterior compartment (gastrocnemius and soleus muscles) and is associated with difficulties in standing on tip toes. The prevalence is 1/1,000,000 to 9/1,000,000. Mutations in the DYSF gene can also cause muscular dystrophy, limb-girdle, autosomal recessive, type 2. This disease is characterized by an onset in late adolescence or early adulthood of slowly progressive, proximal weakness and atrophy of shoulder and pelvic girdle muscles. Cardiac and respiratory muscles are not involved. Hypertrophy of the calf muscles and highly elevated serum creatine kinase levels are frequently observed.	600,25
EDA	Ectodermal dysplasia, type 1, hypohidrotic, X-linked	NM_001399.4	NM_001399.4:c.181T>C, NM_001399.4:c.183C>G, NM_001399.4:c.187G>A, NM_001399.4:c.463C>T, NM_001399.4:c.466C>T, NM_001399.4:c.467G>A, NM_001399.4:c.573_574insT, NM_001399.4:c.671G>C, NM_001399.4:c.826C>T, NM_001399.4:c.1045G>A	Hypohidrotic ectodermal dysplasia, type 1, hypohidrotic, X-linked follows an X-linked pattern of inheritance and is caused by pathogenic variants in the EDA gene located on chromosomal region Xq12-q13.1. The age of onset is neonatal/infantile. This disease is characterized by malformation of ectodermal structures such as skin, hair, teeth and sweat glands. The prevalence is 1/5,000 to 1/10,000 newborns.	600,25
ERCC2	Trichothiodystrophy, type 1	NM_000400.3	NM_000400.3:c.2230_2233dupCTAG, NM_000400.3:c.2176C>T, NM_000400.3:c.2047C>T, NM_000400.3:c.1972C>T, NM_000400.3:c.1703_1704delTT, NM_000400.3:c.1621A>C, NM_000400.3:c.1454T>C, NM_000400.3:c.1381C>G, NM_000400.3:c.1354C>T, NM_000400.3:c.1308-1G>A, NM_000400.3:c.950-2A>G, NM_000400.3:c.949+1G>A, NM_000400.3:c.719-1G>A, NM_000400.3:c.567G>A, NM_000400.3:c.183+2T>A	Trichothiodystrophy (TTD), type 1 is a heterogeneous group of disorders that follows an autosomal recessive pattern of inheritance. It is caused by pathogenic variants in the ERCC2 gene located on chromosomal region 19q13.32. The age of onset is neonatal or infantile. This disease, with variable clinical expression, is characterized by brittle and fragile hair, often combined with growth retardation and intellectual deficit, congenital ichthyosis and nail abnormalities, among other symptoms. About half of the patients with TTD exhibit marked photosensitivity.	600,25
ERCC5	Cerebrooculofacioskeletal syndrome, type 3	NM_000123.3	NM_000123.3:c.88+2T>C, NM_000123.3:c.215C>A, NM_000123.3:c.381-2A>G, NM_000123.3:c.406C>T, NM_000123.3:c.464dupA, NM_000123.3:c.526C>T, NM_000123.3:c.787C>T, NM_000123.3:c.2144dupA, NM_000123.3:c.2375C>T, NM_000123.3:c.2573T>C, NM_000123.3:c.2751delA	Cerebrooculofacioskeletal syndrome type 3, also known as COFS syndrome, follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ERCC5 gene located on chromosomal region 13q33.1. COFS syndrome is characterized by prenatal onset of arthrogryposis, microcephaly and growth failure. Postnatal features include severe developmental delay, congenital cataracts (in some), and marked UV sensitivity of the skin. Survival beyond 6 years of age is rare. The prevalence is below 1/1,000,000.	600,25
ERCC6	Cockayne syndrome, type B; Cerebrooculofacioskeletal syndrome, type 1	NM_000124.3	NM_000124.3:c.3862C>T, NM_000124.3:c.3591_3592dupGA, NM_000124.3:c.2587C>T, NM_000124.3:c.2203C>T, NM_000124.3:c.2047C>T, NM_000124.3:c.1550G>A, NM_000124.3:c.1357C>T, NM_000124.3:c.422+1G>A, NM_000124.3:c.207dupG, NM_000124.3:c.48_49delCT	Cockayne syndrome (CS), type B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ERCC6 gene located on chromosomal region 10q11.23. The age of onset is variable. This disease is characterized by short stature, a characteristic facial appearance, premature aging, photosensitivity, progressive neurological dysfunction, and intellectual deficit. Mutations in the ERRC6 gene have been also found in patients with COFS syndrome type 1, an extreme prenatal form of the CS clinical spectrum. This autosomal recessive progressive neurodegenerative disorder is characterized by microcephaly, congenital cataracts, severe mental retardation, facial dysmorphism, and arthrogryposis.	600,25

EYS	Retinitis pigmentosa, type 25	NM_001292009.1	NM_001292009.1:c.9468T>A, NM_001292009.1:c.9362_9365delCTCA, NM_001292009.1:c.9099delT, NM_001292009.1:c.8711_8718delCATGCAGA, NM_001292009.1:c.8692_8695dupACAG, NM_001292009.1:c.8632G>T, NM_001292009.1:c.8471dupA, NM_001292009.1:c.7822C>T, NM_001292009.1:c.7095T>G, NM_001292009.1:c.6170delA, NM_001292009.1:c.6102dupT, NM_001292009.1:c.5928-2A>G, NM_001292009.1:c.5857G>T, NM_001292009.1:c.5757dupT, NM_001292009.1:c.4462_4469dupAGCCCCTC, NM_001292009.1:c.4350_4356delTATAGCT, NM_001292009.1:c.4120C>T, NM_001292009.1:c.4045C>T, NM_001292009.1:c.2826_2827delAT, NM_001292009.1:c.1211dupA, NM_001292009.1:c.571dupA, NM_001292009.1:c.490C>T, NM_001292009.1:c.232delT, NM_001292009.1:c.103C>T	Retinitis pigmentosa, type 25 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the EYS gene located on chromosomal region 6q12. The age of onset is variable. This disease is characterized by night blindness (nyctalopia), peripheral visual field impairment and over time loss of central vision. The prevalence is 1/10,000 to 5/10,000.	600,25
F11	Factor XI deficiency, autosomal recessive	NM_000128.3	NM_000128.3:c.166T>C, NM_000128.3:c.403G>T, NM_000128.3:c.438C>A, NM_000128.3:c.595+3A>G, NM_000128.3:c.901T>C, NM_000128.3:c.1211C>A, NM_000128.3:c.1613C>T, NM_000128.3:c.1693G>A	Factor XI deficiency, autosomal recessive follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the F11 gene located on chromosomal region 4q35. The age of onset is variable. This disease is characterized by reduced levels and activity of factor XI resulting in moderate bleeding symptoms, usually occurring after trauma or surgery. The prevalence is 1/1,000,000 to 9/1,000,000.	600,25
F9	Hemophilia B	NM_000133.3	NM_000133.3:c.82T>C, NM_000133.3:c.1031T>C, NM_000133.3:c.1136G>A, NM_000133.3:c.1150C>T	Hemophilia B follows an X-linked pattern of inheritance and is caused by pathogenic variants in the F9 gene located on chromosomal region Xq27.1-q27.2. The age of onset is neonatal/infantile. This disease is characterized by spontaneous or prolonged hemorrhages due to factor IX deficiency. The prevalence is 1/100,000 to 9/100,000.	600,25
FAH	Tyrosinemia, type 1	NM_000137.2	NM_000137.2:c.47A>T, NM_000137.2:c.192G>T, NM_000137.2:c.401C>A, NM_000137.2:c.456G>A, NM_000137.2:c.554-1G>T, NM_000137.2:c.707-1G>A, NM_000137.2:c.782C>T, NM_000137.2:c.786G>A, NM_000137.2:c.837+1G>A, NM_000137.2:c.939delC, NM_000137.2:c.982C>T, NM_000137.2:c.1009G>A, NM_000137.2:c.1027G>T, NM_000137.2:c.1062+5G>A, NM_000137.2:c.1069G>T, NM_000137.2:c.1090G>T, NM_000137.2:c.1141A>G	Tyrosinemia, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FAH gene located on chromosomal region 15q25.1. The age of onset is variable. This disease is characterized by progressive liver disease, renal tubular dysfunction, porphyria-like crises and a dramatic improvement in prognosis following treatment with nitisinone. The birth incidence is 1/100,000, notably in Quï¿½bec, Canada, and the prevalence is 1/100,000 to 1/120,000 newborns.	600,25
FANCA	Fanconi anemia, complementation group A	NM_000135.2	NM_000135.2:c.4130C>G, NM_000135.2:c.3788_3790delTCT, NM_000135.2:c.3763G>T, NM_000135.2:c.3558dupG, NM_000135.2:c.2303T>C, NM_000135.2:c.1115_1118delTTGG, NM_000135.2:c.233_236delTTGA, NM_000135.2:c.131dupA	Fanconi anemia, complementation group A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FANCA gene located on chromosomal region 16q24.3. The age of onset is infantile. This disease is characterized by progressive pancytopenia with bone marrow failure, variable congenital malformations and predisposition to develop hematological or solid tumors. The prevalence is 1/1,000,000 to 9/1,000,000.	600,25
FANCC	Fanconi anemia, complementation group C	NM_000136.2	NM_000136.2:c.1642C>T, NM_000136.2:c.1487T>G, NM_000136.2:c.1103_1104delTG, NM_000136.2:c.1015delA, NM_000136.2:c.996+1G>T, NM_000136.2:c.67delG, NM_000136.2:c.37C>T	Fanconi anemia, complementation group C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FANCC gene located on chromosomal region 9q22.3. The age of onset is infantile. This disease is characterized by progressive pancytopenia with bone marrow failure, variable congenital malformations and predisposition to develop hematological or solid tumors. The prevalence is 1/1,000,000 to 9/1,000,000.	600,25
FANCG	Fanconi anemia, complementation group G	NM_004629.1	NM_004629.1:c.1852_1853delAA, NM_004629.1:c.1795_1804delTGGATCCGTC, NM_004629.1:c.1480+1G>C, NM_004629.1:c.1077-2A>G, NM_004629.1:c.907_908dupCT, NM_004629.1:c.637_643delTACCGCC, NM_004629.1:c.510+1G>A, NM_004629.1:c.313G>T	Fanconi anemia, complementation group G follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FANCG gene located on chromosomal region 9p13. The age of onset is infantile. This disease is characterized by progressive pancytopenia with bone marrow failure, variable congenital malformations and predisposition to develop hematological or solid tumors. The prevalence is 1/1,000,000 to 9/1,000,000.	600,25
FGB	Congenital afibrinogenemia	NM_005141.4	NM_005141.4:c.1148T>G, NM_005141.4:c.1289G>A	Congenital afibrinogenemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FGB gene located on chromosomal region 4q28. The age of onset is variable. This disease is characterized by bleeding symptoms ranging from mild to severe resulting from reduced quantity and/or quality of circulating fibrinogen. The prevalence is 1/1,000,000 to 9/1,000,000.	600,25

FIG4	Charcot-Marie-Tooth disease, type 4J; Yunis-Varon syndrome	NM_014845.5	NM_014845.5:c.122T>C, NM_014845.5:c.311G>A, NM_014845.5:c.501C>G, NM_014845.5:c.547C>T, NM_014845.5:c.592C>T, NM_014845.5:c.737G>A, NM_014845.5:c.831_838delTAAATTTG, NM_014845.5:c.2299dupG	Charcot-Marie-Tooth disease, type 4J follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FIG4 gene located on chromosomal region 6q.21. The age of onset is neonatal/infantile. This disease is characterized by rapidly progressive, asymmetric motor neuron degeneration with slow nerve conduction velocities, weakness and paralysis, without sensory loss. The prevalence is 4/100,000 to 8/100,000. Mutations in the FIG4 gene have been also found in patient with Yunis-Varon syndrome. This disease is a severe autosomal recessive disorder characterized by skeletal defects, including cleidocranial dysplasia and digital anomalies, and severe neurologic involvement with neuronal loss. Enlarged cytoplasmic vacuoles are found in neurons, muscle, and cartilage. The disorder is usually lethal in infancy.	600,25
FKRP	Muscular dystrophy-dystroglycanopathy, type 5A, 5B and 5C	NM_001039885.2	NM_001039885.2:c.160C>T, NM_001039885.2:c.1154C>A, NM_001039885.2:c.1343C>T, NM_001039885.2:c.1387A>G	Muscular dystrophy-dystroglycanopathy type 5 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FKRP gene located on chromosomal region 19q13.32. The age of onset is neonatal or early infancy. There are three subtypes of dystroglycanopathies related to FKRP gene: subtype 5A, 5B and 5C. Subtype 5A is the most severe phenotype and is associated with congenital brain and eye anomalies, cobblestone lissencephaly, profound mental retardation, and death usually in the first years of life. Included diseases are the more severe Walker-Warburg syndrome and the slightly less severe muscle-eye-brain disease. Subtype 5B represents an intermediate phenotype with or without congenital mental retardation, white matter changes and structural brain abnormalities. Finally, subtype 5C is the less severe phenotype characterized by limb-girdle muscular dystrophy, variable age at onset, normal cognition, and no structural brain changes.	600,25
FMR1	Fragile X syndrome	0	(CGG)n pre-mutated allele	Fragile X syndrome follows an X-linked pattern of inheritance and is caused by pathogenic variants in the FMR1 gene located on chromosomal region Xq27.3. The symptoms are variable depending on the range of CGG triplet expansion. In complete mutation the onset is infantile in men and is characterized by intellectual disability, characteristic appearance (large head, long face, prominent forehead and chin, protruding ears) joint laxity and large testes after puberty. In carrier female, the symptoms are milder and include primary ovarian insufficiency. The prevalence is 1/2,500 (full mutation allele) to 1/4,000 (prevalence of symptomatic cases) for both genders.	600,25
FRAS1	Fraser syndrome, type 1	NM_025074.6	NM_025074.6:c.835_838delGTGT, NM_025074.6:c.3799C>T, NM_025074.6:c.5605_5606insT, NM_025074.6:c.6433C>T, NM_025074.6:c.6991_6992insGG, NM_025074.6:c.7813C>T, NM_025074.6:c.11160_11167delGCTGGAGA	Fraser syndrome, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the gene FRAS1 located on chromosomal region 4q21.21. The age of onset is early infancy. Twenty-five per cent of affected infants are stillborn, while 20 % die before the age of 1 year. This disease is characterized mainly by cryptophthalmos and syndactyly, besides urinary and genital anormalities. The prevalence is <1:1,000,000.	600,25
G6PC	Glycogen storage disease, type 1A	NM_000151.3	NM_000151.3:c.113A>T, NM_000151.3:c.229T>C, NM_000151.3:c.230+1G>C, NM_000151.3:c.247C>T, NM_000151.3:c.248G>A, NM_000151.3:c.370G>A, NM_000151.3:c.379_380dupTA, NM_000151.3:c.447-1G>A, NM_000151.3:c.497T>G, NM_000151.3:c.508C>T, NM_000151.3:c.562G>C, NM_000151.3:c.883C>T, NM_000151.3:c.1039C>T	Glycogen storage disease, type 1A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the G6PC gene located on chromosomal region 17q21.31. The age of onset is infantile. This disease is characterized by poor tolerance to fasting, significant hepatomegaly and growth retardation. The incidence is 1/100,000.	600,25
G6PC	Glycogen storage disease, type 1A	NM_001270397.1	NM_001270397.1:c.474G>A	Glycogen storage disease, type 1A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the G6PC gene located on chromosomal region 17q21.31. The age of onset is infantile. This disease is characterized by poor tolerance to fasting, significant hepatomegaly and growth retardation. The incidence is 1/100,000.	600,25

GALC	Krabbe disease	NM_000153.3	NM_000153.3:c.2056T>C, NM_000153.3:c.1964delC, NM_000153.3:c.1814dupA, NM_000153.3:c.1796T>G, NM_000153.3:c.1723_1724insT, NM_000153.3:c.1700A>C, NM_000153.3:c.1695delT, NM_000153.3:c.1592G>A, NM_000153.3:c.1591C>T, NM_000153.3:c.1586C>T, NM_000153.3:c.1543G>A, NM_000153.3:c.1489+1_1489+2delGT, NM_000153.3:c.1488_1489+2delTGGT, NM_000153.3:c.1488_1489delTG, NM_000153.3:c.1472delA, NM_000153.3:c.1161+2T>G, NM_000153.3:c.1153G>T, NM_000153.3:c.953C>G, NM_000153.3:c.658C>T, NM_000153.3:c.655C>T, NM_000153.3:c.628A>T, NM_000153.3:c.582+1G>A, NM_000153.3:c.453G>A, NM_000153.3:c.430delA, NM_000153.3:c.388G>A, NM_000153.3:c.205C>T	Krabbe disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GALC gene located on chromosomal region 14q31.3. There are two forms of the disease: infantile form (2-6 months onset) more severe and adult form less severe. It is a degenerative disorder that affects the nervous system characterized by a muscle stiffness, blindness, deafness, and eventually death. The incidence is 1/100,000-1/250,000 and the prevalence is 1/100,000.	600,25
GALT	Galactosemia	NM_000155.3	NM_000155.3:c.18delC, NM_000155.3:c.41delCinsTT, NM_000155.3:c.71_72insA, NM_000155.3:c.113A>C, NM_000155.3:c.118G>T, NM_000155.3:c.130G>A, NM_000155.3:c.132delG, NM_000155.3:c.152G>A, NM_000155.3:c.158G>A, NM_000155.3:c.199C>T, NM_000155.3:c.203A>C, NM_000155.3:c.220_221delCT, NM_000155.3:c.221T>C, NM_000155.3:c.253-2A>G, NM_000155.3:c.265T>G, NM_000155.3:c.289_291delAAC, NM_000155.3:c.290A>G, NM_000155.3:c.292G>A, NM_000155.3:c.329-2A>C, NM_000155.3:c.367C>T, NM_000155.3:c.386T>C, NM_000155.3:c.400delT, NM_000155.3:c.404C>T, NM_000155.3:c.413C>T, NM_000155.3:c.425T>A, NM_000155.3:c.428C>T, NM_000155.3:c.445dupG, NM_000155.3:c.442C>T, NM_000155.3:c.443G>A, NM_000155.3:c.502_504delGTG, NM_000155.3:c.505C>A, NM_000155.3:c.508-1G>C, NM_000155.3:c.512T>C, NM_000155.3:c.547C>A, NM_000155.3:c.552C>A, NM_000155.3:c.563A>G, NM_000155.3:c.565_578delGTATGGGCCAGCAG, NM_000155.3:c.568T>C, NM_000155.3:c.580T>C, NM_000155.3:c.584T>C, NM_000155.3:c.598delC, NM_000155.3:c.601C>T, NM_000155.3:c.602G>A, NM_000155.3:c.607G>A, NM_000155.3:c.610C>T, NM_000155.3:c.619C>T, NM_000155.3:c.626A>G, NM_000155.3:c.634C>T, NM_000155.3:c.688-2A>C, NM_000155.3:c.692G>A, NM_000155.3:c.719_728delTAGTACTGGT, NM_000155.3:c.772C>T, NM_000155.3:c.775C>T, NM_000155.3:c.790delC, NM_000155.3:c.790_792delCTAinsTAG, NM_000155.3:c.820+13A>G, NM_000155.3:c.844C>G, NM_000155.3:c.855G>T, NM_000155.3:c.904+1G>T, NM_000155.3:c.905-2A>G, NM_000155.3:c.939G>A, NM_000155.3:c.947G>A, NM_000155.3:c.957C>A, NM_000155.3:c.985T>C, NM_000155.3:c.997C>G, NM_000155.3:c.997C>T, NM_000155.3:c.998G>A, NM_000155.3:c.1006A>T, NM_000155.3:c.1030C>A, NM_000155.3:c.1048delA, NM_000155.3:c.1052delC, NM_000155.3:c.1138T>C	Galactosemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GALT gene located on chromosomal region 9p13.3. The age of onset is neonatal. This disease is characterized by feeding difficulties, lethargy, and severe liver disease. Long-term complications appear including cognitive impairments, motor deficits, and ovarian dysfunction with reduced fertility in women and diminished bone density. The prevalence is 1/40,000-1/60,000.	600,25
GAN	Giant axonal neuropathy, type 1	NM_022041.3	NM_022041.3:c.413G>A, NM_022041.3:c.505G>A, NM_022041.3:c.601C>T, NM_022041.3:c.1268T>C, NM_022041.3:c.1429C>T, NM_022041.3:c.1447C>T, NM_022041.3:c.1456G>A	Giant axonal neuropathy, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GAN gene located on chromosomal region 16q23.2. The age of onset is infantile. This disease is characterized by a progressive motor and sensitive peripheral and central nervous system neuropathy. Twenty families have been reported with this disease but the frequency is likely to be under-estimated.	600,25

GBA	Gaucher disease	NM_000157.3	NM_000157.3:c.1604G>A, NM_000157.3:c.1504C>T, NM_000157.3:c.1448T>G, NM_000157.3:c.1448T>C, NM_000157.3:c.1361C>G, NM_000157.3:c.1348T>A, NM_000157.3:c.1343A>T, NM_000157.3:c.1342G>C, NM_000157.3:c.1319C>T, NM_000157.3:c.1309G>T, NM_000157.3:c.1307T>C, NM_000157.3:c.1301G>C, NM_000157.3:c.1297G>T, NM_000157.3:c.1295G>T, NM_000157.3:c.1274dupA, NM_000157.3:c.1246G>A, NM_000157.3:c.1240G>T, NM_000157.3:c.1240G>C, NM_000157.3:c.1228C>G, NM_000157.3:c.1226A>G, NM_000157.3:c.1208G>C, NM_000157.3:c.1192C>T, NM_000157.3:c.1184C>T, NM_000157.3:c.1174C>G, NM_000157.3:c.1171G>C, NM_000157.3:c.1141T>G, NM_000157.3:c.1098dupA, NM_000157.3:c.1090G>A, NM_000157.3:c.1085C>T, NM_000157.3:c.1060G>C, NM_000157.3:c.1053G>T, NM_000157.3:c.1049A>G, NM_000157.3:c.1043C>T, NM_000157.3:c.914delC, NM_000157.3:c.586A>C, NM_000157.3:c.509G>T, NM_000157.3:c.508C>T, NM_000157.3:c.487delG, NM_000157.3:c.481C>T, NM_000157.3:c.476G>A, NM_000157.3:c.475C>T, NM_000157.3:c.431T>G, NM_000157.3:c.407C>A, NM_000157.3:c.354G>C, NM_000157.3:c.259C>T, NM_000157.3:c.254G>A, NM_000157.3:c.160G>T, NM_000157.3:c.115+1G>A, NM_000157.3:c.84dupG	Gaucher disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GBA gene located on chromosomal region 1q22. Gaucher disease encompasses a continuum of clinical findings from a perinatal lethal disorder to an asymptomatic type. There are three major clinical types (1, 2, and 3) and two other subtypes (perinatal-lethal and cardiovascular). Type 1 is characterized by the presence of clinical or radiographic evidence of bone disease, hepatosplenomegaly, anemia and thrombocytopenia, lung disease, and the absence of primary central nervous system disease. GD types 2 and 3 are characterized by the presence of primary neurologic disease. Type 2 has an onset before age two years, limited psychomotor development, and a rapidly progressive course with death by age two to four years. Type 3 may have onset before age two years, but often have a more slowly progressive course, with survival into the third or fourth decade. The perinatal-lethal form is associated with ichthyosiform or collodion skin abnormalities or with nonimmune hydrops fetalis. The cardiovascular form is characterized by calcification of the aortic and mitral valves, mild splenomegaly, corneal opacities, and supranuclear ophthalmoplegia. Cardiopulmonary complications have been described with all the clinical subtypes, although varying in frequency and severity. The incidence is 1/60,000 and the prevalence is approximately 1/100,000.	600,25
GBE1	Glycogen storage disease, type 4	NM_000158.3	NM_000158.3:c.2052+1G>A, NM_000158.3:c.1883A>G, NM_000158.3:c.1774G>T, NM_000158.3:c.1604A>G, NM_000158.3:c.1571G>A, NM_000158.3:c.1570C>T, NM_000158.3:c.1543C>T, NM_000158.3:c.986A>C, NM_000158.3:c.771T>A, NM_000158.3:c.466_470delCGTAT	Glycogen storage disease, type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GBE1 gene located on chromosomal region 3p12.2. The age of onset is infantile. This disease is characterized by failure to thrive; hepatomegaly, liver dysfunction, and progressive liver cirrhosis; hypotonia; cardiomyopathy and, finally, death.	600,25
GCDH	Glutaricaciduria, type 1	NM_000159.3	NM_000159.3:c.74C>A, NM_000159.3:c.271+1G>A, NM_000159.3:c.383G>A, NM_000159.3:c.416C>T, NM_000159.3:c.542A>G, NM_000159.3:c.572T>C, NM_000159.3:c.636-1G>A, NM_000159.3:c.680G>C, NM_000159.3:c.743C>T, NM_000159.3:c.751C>T, NM_000159.3:c.764C>T, NM_000159.3:c.769C>T, NM_000159.3:c.877G>A, NM_000159.3:c.883T>C, NM_000159.3:c.914C>T, NM_000159.3:c.1002_1003delGA, NM_000159.3:c.1060G>A, NM_000159.3:c.1093G>A, NM_000159.3:c.1168G>C, NM_000159.3:c.1198G>A, NM_000159.3:c.1199dupT, NM_000159.3:c.1204C>T, NM_000159.3:c.1244-2A>C, NM_000159.3:c.1247C>T, NM_000159.3:c.1262C>T	Glutaricaciduria, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GCDH gene located on chromosomal region 19p13.2. The age of onset is infantile or neonatal. This disease is characterized by encephalopathic crises resulting in striatal injury and a severe dystonic dyskinetic movement disorder. The prevalence is 1 in 100,000 births.	600,25
GJB2	Deafness, autosomal recessive, type 1A	NM_004004.5	NM_004004.5:c.617A>G, NM_004004.5:c.551G>C, NM_004004.5:c.550C>T, NM_004004.5:c.516G>A, NM_004004.5:c.465T>A, NM_004004.5:c.439G>A, NM_004004.5:c.427C>T, NM_004004.5:c.416G>A, NM_004004.5:c.402delG, NM_004004.5:c.365A>T, NM_004004.5:c.358_360delGAG, NM_004004.5:c.334_335delAA, NM_004004.5:c.313_326delAAGTTCATCAAGGG, NM_004004.5:c.310_323delAGGAAGTTCATCAA, NM_004004.5:c.299_300delAT, NM_004004.5:c.299A>T, NM_004004.5:c.270dupA, NM_004004.5:c.269dupT, NM_004004.5:c.269T>C, NM_004004.5:c.250G>T, NM_004004.5:c.250G>C, NM_004004.5:c.239A>C, NM_004004.5:c.238C>T, NM_004004.5:c.235delC, NM_004004.5:c.231G>A, NM_004004.5:c.230G>A, NM_004004.5:c.229T>C, NM_004004.5:c.169C>T, NM_004004.5:c.139G>T, NM_004004.5:c.132G>A, NM_004004.5:c.35delG	Autosomal recessive nonsyndromic sensorineural deafness type 1A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GJB2 gene located on chromosomal region 13q12.11. The age of onset is infantile. This disease is characterized by congenital, non-progressive, mild-to-profound sensorineural hearing impairment. No other associated medical findings are present.	600,25
GJB6	Deafness, autosomal recessive, type 1B	NM_001110219.2	NM_001110219.2:c.485dupA, NM_001110219.2:c.443delC, NM_001110219.2:c.383_384delTA, NM_001110219.2:c.261dupA, NM_001110219.2:c.169C>T, NM_001110219.2:c.14C>T	Autosomal recessive nonsyndromic sensorineural deafness type 1B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GJB6 gene located on chromosomal region 13q12.11. The age of onset is infantile. This disease is characterized by mild-to-profound sensorineural hearing impairment. No other associated medical findings are present.	600,25

GLB1	GM1-gangliosidosis, type 1	NM_001317040.1	NM_001317040.1:c.1877A>G, NM_001317040.1:c.1790C>T, NM_001317040.1:c.1721dupG, NM_001317040.1:c.1693G>T, NM_001317040.1:c.1600_1610dupGGTGCATATAT, NM_001317040.1:c.1589G>A, NM_001317040.1:c.1514G>A, NM_001317040.1:c.1513C>T, NM_001317040.1:c.1499dupA, NM_001317040.1:c.1469G>A, NM_001317040.1:c.1465G>A, NM_001317040.1:c.1457G>A, NM_001317040.1:c.1318_1319delCT, NM_001317040.1:c.1212+1G>T, NM_001317040.1:c.1195C>T, NM_001317040.1:c.1148C>T, NM_001317040.1:c.1091A>G, NM_001317040.1:c.1045G>A, NM_001317040.1:c.962G>T, NM_001317040.1:c.766C>T, NM_001317040.1:c.746G>A, NM_001317040.1:c.745C>T, NM_001317040.1:c.735dupT, NM_001317040.1:c.601+2T>C, NM_001317040.1:c.586C>T, NM_001317040.1:c.586C>A, NM_001317040.1:c.582_584delTCT, NM_001317040.1:c.420G>A, NM_001317040.1:c.346C>T, NM_001317040.1:c.320G>A, NM_001317040.1:c.319C>T, NM_001317040.1:c.315C>G, NM_001317040.1:c.296T>C, NM_001317040.1:c.289C>T	Gangliosidosis GM1, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GLB1 gene located on chromosomal region 3p22.3. Although the three types differ in severity, their features can overlap significantly. The age of onset in type 1 is infantile, in type 2 is late-infantile or juvenile and adult in type3. This disease is characterized by arrest/regression of neurological development, hypotonia, visceromegaly, macular cherry-red spots, dysostosis and coarse facial features. The prevalence is 1:100,000 a 200,000 newborn.	600,25
GLDC	Glycine encephalopathy	NM_000170.2	NM_000170.2:c.2405C>T, NM_000170.2:c.2284G>A, NM_000170.2:c.2216G>A, NM_000170.2:c.1691G>T, NM_000170.2:c.1545G>C, NM_000170.2:c.1166C>T, NM_000170.2:c.322G>T	Glycine encephalopathy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in GLDC gene located on chromosomal region 9p24.1. The age of onset is neonatal/infantile. This disease is characterized by lethargy or even coma, hypotonia, hiccups, myoclonic jerks, and breathing/swallowing disorders, with subsequent intellectual deficit, spasticity and intractable seizures. The prevalence is 1:1,000,000-9:1,000,000.	600,25
GLE1	Lethal congenital contracture syndrome, type 1	NM_001003722.1	NM_001003722.1:c.898-2A>G, NM_001003722.1:c.1412_1413delAG, NM_001003722.1:c.2051T>C, NM_001003722.1:c.2069_2072delTTCT	Lethal congenital contracture syndrome, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GLE1 gene located on chromosomal region 9q34.11. The age of onset is neonatal. This disease is characterized by total fetal akinesia (detectable since the 13th week of gestation) accompanied by hydrops, micrognathia, pulmonary hypoplasia, pterygia and multiple joint contractures (usually flexion contractures in the elbows and extension in the knees), leading invariably to death before the 32nd week of gestation. Lack of anterior horn motoneurons, severe atrophy of the ventral spinal cord and severe skeletal muscle hypoplasia are characteristic neuropathological findings, with no evidence of other organ structural anomalies.	600,25
GNE	Inclusion body myopathy, type 2 (Nonaka myopathy)	NM_001128227.2	NM_001128227.2:c.2228T>C, NM_001128227.2:c.2179G>A, NM_001128227.2:c.1937C>G, NM_001128227.2:c.1891G>A, NM_001128227.2:c.1820G>A, NM_001128227.2:c.1002T>A, NM_001128227.2:c.880C>T, NM_001128227.2:c.830G>A, NM_001128227.2:c.478C>T	Inclusion body myopathy, type 2 (Nonaka myopathy) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GNE gene located on chromosomal region 9p13.3. The age of onset is adult. This disease is characterized by progressive muscle weakness and joint deformity. The prevalence is 1:500-1:1,000.	600,25
GNPTAB	Mucolipidosis 2 alpha/beta	NM_024312.4	NM_024312.4:c.3663delG, NM_024312.4:c.3565C>T, NM_024312.4:c.3560_3561delAG, NM_024312.4:c.3503_3504delTC, NM_024312.4:c.3410T>A, NM_024312.4:c.3326dupA, NM_024312.4:c.3173C>G, NM_024312.4:c.2896delA, NM_024312.4:c.2383delG, NM_024312.4:c.1906dupA, NM_024312.4:c.1759C>T, NM_024312.4:c.1196C>T, NM_024312.4:c.1000C>T, NM_024312.4:c.749dupA, NM_024312.4:c.732_733delAA, NM_024312.4:c.648_651delAGAA, NM_024312.4:c.616_619delACAG, NM_024312.4:c.99delC, NM_024312.4:c.25C>T, NM_024312.4:c.10A>C	Mucolipidosis type 2 alpha/beta follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GNPTAB gene located on chromosomal region 12q23.2. The age of onset is infantile. This disease is characterized by growth retardation, short stature, skeletal abnormalities, facial dysmorphism, stiff skin, developmental delay and cardiomegaly and that is lethal in childhood. The prevalence is 1:123,500-1:625,500.	600,25
GPR179	Night blindness, congenital stationary (complete), type 1E, autosomal recessive	NM_001004334.3	NM_001004334.3:c.6847_6848delCT, NM_001004334.3:c.5763_5764delGA, NM_001004334.3:c.5693dupT, NM_001004334.3:c.4699_4700delAG, NM_001004334.3:c.3233_3234delCT, NM_001004334.3:c.1807C>T, NM_001004334.3:c.1784+1G>A, NM_001004334.3:c.1368delT, NM_001004334.3:c.1236G>A, NM_001004334.3:c.984delC, NM_001004334.3:c.839_842delATCA, NM_001004334.3:c.278dupC, NM_001004334.3:c.278delC	Congenital stationary night blindness type 1E follow an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GPR179 gene located on chromosomal region 17q12. The age of onset is infantile. This disease is characterized by hemeralopia with a moderate loss of visual acuity.	600,25
GRM6	Night blindness, congenital stationary (complete), type 1B, autosomal recessive	NM_000843.3	NM_000843.3:c.2560C>T, NM_000843.3:c.2341G>A, NM_000843.3:c.2213_2219delCCAGAGG, NM_000843.3:c.2122C>T, NM_000843.3:c.1861C>T, NM_000843.3:c.1565G>A, NM_000843.3:c.1336C>T, NM_000843.3:c.1258C>T, NM_000843.3:c.1214T>C, NM_000843.3:c.727dupG, NM_000843.3:c.719_720insG, NM_000843.3:c.712C>T	Congenital stationary night blindness type 1B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GRM6 gene located on chromosomal region 5q35.3. The age of onset is early infancy. This disease is characterized by hemeralopia with a moderate loss of visual acuity.	600,25

GUSB	Mucopolysaccharidosis, type 7	NM_000181.3	NM_000181.3:c.1881G>T, NM_000181.3:c.1856C>T, NM_000181.3:c.1831C>T, NM_000181.3:c.1730G>T, NM_000181.3:c.1618G>T, NM_000181.3:c.1534G>A, NM_000181.3:c.1521G>A, NM_000181.3:c.1429C>T, NM_000181.3:c.1338G>A, NM_000181.3:c.1337G>A, NM_000181.3:c.1244+1G>A, NM_000181.3:c.1219_1220insC, NM_000181.3:c.1144C>T, NM_000181.3:c.1084G>A, NM_000181.3:c.1065+1G>T, NM_000181.3:c.1061C>T, NM_000181.3:c.1050G>C, NM_000181.3:c.866G>A, NM_000181.3:c.820_821delAC, NM_000181.3:c.646C>T, NM_000181.3:c.526C>T, NM_000181.3:c.499C>T, NM_000181.3:c.442C>T	Mucopolysaccharidosis type 7 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GUSB gene located on chromosomal region 7q11.21. The age of onset is variable. There are prenatal forms with non-immune hydrops fetalis, and severe neonatal forms with dysmorphism, hernias, hepatosplenomegaly, club feet, dysostosis, severe hypotonia and neurological disorders that ultimately lead to profound intellectual deficit and small stature in patients that survive. Finally, there are also very mild cases that are discovered during adolescence or adulthood following presentation with thoracic kyphosis. The prevalence is 1:250,000 in newborn.	600,25
HADHA	LCHAD deficiency	NM_000182.4	NM_000182.4:c.2146+1G>A, NM_000182.4:c.2132dupC, NM_000182.4:c.1918C>T, NM_000182.4:c.1793_1794delAT, NM_000182.4:c.1678C>T, NM_000182.4:c.1644delC, NM_000182.4:c.1620+2_1620+6delTAAGG, NM_000182.4:c.1528G>C, NM_000182.4:c.1422dupT, NM_000182.4:c.1132C>T, NM_000182.4:c.919-2A>G, NM_000182.4:c.845T>A, NM_000182.4:c.499delA, NM_000182.4:c.274_278delTCATC	Isolated deficiency of long-chain 3-hydroxyl-CoA dehydrogenase (LCHAD deficiency) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HADHA gene located on chromosomal region 2p23.3. This disease is characterized in infancy/early childhood of hypoketotic hypoglycemia, metabolic acidosis, liver disease, hypotonia and, frequently, cardiac involvement with arrhythmias and/or cardiomyopathy. The prevalence is 1/250,000.	600,25
HBB	HBB-related hemoglobinopathy	NM_000518.4	NM_000518.4:c.*110T>C, NM_000518.4:c.440_441dupAC, NM_000518.4:c.440A>T, NM_000518.4:c.440A>C, NM_000518.4:c.439C>G, NM_000518.4:c.438T>A, NM_000518.4:c.437A>G, NM_000518.4:c.436T>C, NM_000518.4:c.435G>C, NM_000518.4:c.431A>C, NM_000518.4:c.428C>A, NM_000518.4:c.421G>A, NM_000518.4:c.383A>C, NM_000518.4:c.371_378delCCCCACCA, NM_000518.4:c.364G>T, NM_000518.4:c.364G>A, NM_000518.4:c.347C>A, NM_000518.4:c.344T>C, NM_000518.4:c.343_344delCTinsG, NM_000518.4:c.341T>A, NM_000518.4:c.332T>C, NM_000518.4:c.328delG, NM_000518.4:c.328G>A, NM_000518.4:c.323dupG, NM_000518.4:c.320T>G, NM_000518.4:c.316-1G>T, NM_000518.4:c.316-1G>A, NM_000518.4:c.316-2A>G, NM_000518.4:c.316-2A>C, NM_000518.4:c.316-3C>A, NM_000518.4:c.316-106C>G, NM_000518.4:c.316-146T>G, NM_000518.4:c.316-197C>T, NM_000518.4:c.315+2T>G, NM_000518.4:c.315+1G>C, NM_000518.4:c.315+1G>A, NM_000518.4:c.312C>G, NM_000518.4:c.306G>C, NM_000518.4:c.305A>G, NM_000518.4:c.304G>A, NM_000518.4:c.302C>T, NM_000518.4:c.299A>T, NM_000518.4:c.299A>G, NM_000518.4:c.299A>C, NM_000518.4:c.298G>T, NM_000518.4:c.298G>C, NM_000518.4:c.298G>A, NM_000518.4:c.295G>A, NM_000518.4:c.293A>T, NM_000518.4:c.287dupA, NM_000518.4:c.282_283dupTG, NM_000518.4:c.283G>C, NM_000518.4:c.277C>T, NM_000518.4:c.277C>A, NM_000518.4:c.275T>C, NM_000518.4:c.271G>T, NM_000518.4:c.269G>A, NM_000518.4:c.268A>C, NM_000518.4:c.257T>C, NM_000518.4:c.251delG, NM_000518.4:c.248A>T, NM_000518.4:c.248A>C, NM_000518.4:c.247A>G, NM_000518.4:c.230delC, NM_000518.4:c.226delC, NM_000518.4:c.217_221delAGTGAinsT, NM_000518.4:c.217dupA, NM_000518.4:c.216dupT, NM_000518.4:c.208G>A, NM_000518.4:c.206T>A, NM_000518.4:c.203_204delTG, NM_000518.4:c.201delA, NM_000518.4:c.199A>G, NM_000518.4:c.194delG, NM_000518.4:c.190C>T, NM_000518.4:c.184A>T, NM_000518.4:c.182T>A, NM_000518.4:c.179A>C, NM_000518.4:c.176C>G, NM_000518.4:c.162delT, NM_000518.4:c.143_146dupATCT, NM_000518.4:c.143dupA, NM_000518.4:c.135delC, NM_000518.4:c.134C>G, NM_000518.4:c.130G>T, NM_000518.4:c.126_129delCTTT, NM_000518.4:c.128T>C, NM_000518.4:c.127T>G, NM_000518.4:c.127T>C, NM_000518.4:c.114_120delGACCCAG, NM_000518.4:c.117_118delCC, NM_000518.4:c.118C>T, NM_000518.4:c.114G>A, NM_000518.4:c.113G>A, NM_000518.4:c.112delT	DNA variations in the HBB gene result in the production of different versions of beta-globin. Some of these variations may affect a person's health while other variations cause no noticeable signs or symptoms. Two of the most common HBB-related conditions are beta-thalassemia and sickle cell anemia (SCA). Beta thalassemia is caused by HBB gene mutations that prevent or decrease beta-globin production, subunits that make up hemoglobin. A lack of hemoglobin disrupts the normal development of red blood cells. A shortage of mature red blood cells can reduce the amount of oxygen that is delivered to tissues to below what is needed to satisfy the body's energy needs. A lack of oxygen in the body's tissues can lead to poor growth, organ damage, and other health problems associated with beta thalassemia. SCA is a multisystem disease associated with episodes of acute illness and progressive organ damage. SCA-associated mutations cause red blood cells assuming an abnormal, rigid, sickle shape promoting cell break down prematurely, which can lead to anemia. Anemia can cause shortness of breath, fatigue, and delayed growth and development in children.	600,25
HESX1	Growth hormone deficiency with pituitary anomalies	NM_003865.2	NM_003865.2:c.450_451delCA, NM_003865.2:c.445G>A, NM_003865.2:c.77T>C, NM_003865.2:c.18G>C	Growth hormone deficiency with pituitary anomalies follows an autosomal recessive pattern of inheritance and are caused by pathogenic variants in the HESX1 gene located on chromosomal region 3p14.3. The age of onset is infantile. These diseases are characterized by short stature, cognitive alterations or delayed puberty. The incidence is 1:3,000 and 1:4,000 births.	600,25

HEXA	Tay-Sachs disease	NM_000520.5	NM_000520.5:c.254-1G>C	Tay-Sachs disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HEXA gene located on chromosomal region 15q23. The age of onset is infantile. There are three forms, type 1 (infantile), with a psychomotor retardation which is associated with hypotonia, amaurosis and megalencephaly. Type 2 is characterized by locomotor ataxia, behavioural disorders, and progressive loss of intellectual capacities. Type three (chronic form) shows spinocerebellar ataxia or spinal amyotrophy. The prevalence is 1 case per 320 000 live births.	600,25
HEXA	Tay-Sachs disease	NM_001318825.1	NM_001318825.1:c.1570C>T, NM_001318825.1:c.1561C>T, NM_001318825.1:c.1544G>A, NM_001318825.1:c.1543delC, NM_001318825.1:c.1543C>T, NM_001318825.1:c.1532delT, NM_001318825.1:c.1529G>A, NM_001318825.1:c.1528C>T, NM_001318825.1:c.1477G>A, NM_001318825.1:c.1455G>C, NM_001318825.1:c.1311_1312insTATC, NM_001318825.1:c.1307_1310dupTATC, NM_001318825.1:c.1293G>C, NM_001318825.1:c.1247_1248delAAinsG, NM_001318825.1:c.1210C>T, NM_001318825.1:c.1209G>A, NM_001318825.1:c.1020G>A, NM_001318825.1:c.1019+3A>G, NM_001318825.1:c.948_950delCTT, NM_001318825.1:c.838+1G>C, NM_001318825.1:c.838+1G>A, NM_001318825.1:c.838G>A, NM_001318825.1:c.805G>C, NM_001318825.1:c.782G>A, NM_001318825.1:c.705+1G>A, NM_001318825.1:c.665T>C, NM_001318825.1:c.662C>T, NM_001318825.1:c.573C>G, NM_001318825.1:c.571T>C, NM_001318825.1:c.566G>T, NM_001318825.1:c.566G>A, NM_001318825.1:c.565C>T, NM_001318825.1:c.542G>A, NM_001318825.1:c.541C>T, NM_001318825.1:c.492+5G>A, NM_001318825.1:c.413T>G, NM_001318825.1:c.173G>A, NM_001318825.1:c.116T>G, NM_001318825.1:c.78G>A, NM_001318825.1:c.77G>A, NM_001318825.1:c.2T>C, NM_001318825.1:c.1A>T, NM_001318825.1:c.1A>G	Tay-Sachs disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HEXA gene located on chromosomal region 15q23. The age of onset is infantile. There are three forms, type 1 (infantile), with a psychomotor retardation which is associated with hypotonia, amaurosis and megalencephaly. Type 2 is characterized by locomotor ataxia, behavioural disorders, and progressive loss of intellectual capacities. Type three (chronic form) shows spinocerebellar ataxia or spinal amyotrophy. The prevalence is 1 case per 320 000 live births.	600,25
HEXB	Sandhoff disease, infantile, juvenile, and adult forms	NM_000521.3	NM_000521.3:c.115delG, NM_000521.3:c.171delG, NM_000521.3:c.202_203insGG, NM_000521.3:c.298delC, NM_000521.3:c.508C>T, NM_000521.3:c.797A>G, NM_000521.3:c.841C>T, NM_000521.3:c.850C>T, NM_000521.3:c.1238_1242delCAAAG, NM_000521.3:c.1250C>T, NM_000521.3:c.1310_1311delCA, NM_000521.3:c.1345delT, NM_000521.3:c.1375G>T, NM_000521.3:c.1380G>A, NM_000521.3:c.1517_1529dupCAAGTGCTGTTGG, NM_000521.3:c.1539_1540delCT	Sandhoff disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HEXB gene located on chromosomal region 5q13.3. The age of onset is adult or infantile. This disease is characterized by central nervous system degeneration, with startle reactions, early blindness, progressive motor and mental deterioration, macrocephaly and cherry-red spots on the macula. The prevalence is 1/130.000.	600,25
HGD	Alkaptonuria	NM_000187.3	NM_000187.3:c.1189-2A>G, NM_000187.3:c.1111dupC, NM_000187.3:c.1102A>G, NM_000187.3:c.899T>G, NM_000187.3:c.808G>A, NM_000187.3:c.688C>T, NM_000187.3:c.674G>A, NM_000187.3:c.481G>A, NM_000187.3:c.469+2T>C, NM_000187.3:c.342+1G>A, NM_000187.3:c.175delA, NM_000187.3:c.172A>T, NM_000187.3:c.140C>T, NM_000187.3:c.16-1G>A	Alkaptonuria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HGD gene located on chromosomal region 3q13.33. The age of onset is infantile. This disease is characterized by darkening of the urine when it is left exposed to air, grey-blue colouration of the eye sclerae and the ear helix (ochronosis), and a disabling joint disease involving both the axial and peripheral joints (ochronotic arthropathy). The prevalence is 1:250,000-1:1.000.000 newborn.	600,25
HGSNAT	Mucopolysaccharidosis type 3C (Sanfilippo C)	NM_152419.2	NM_152419.2:c.493+1G>A, NM_152419.2:c.607C>T, NM_152419.2:c.848C>T, NM_152419.2:c.1030C>T, NM_152419.2:c.1250+1G>A, NM_152419.2:c.1378-1G>A, NM_152419.2:c.1464+1G>A, NM_152419.2:c.1503delA, NM_152419.2:c.1553C>T, NM_152419.2:c.1622C>T	Mucopolysaccharidosis type 3C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HGSNAT gene located on chromosomal region 8p11.21. The age of onset is infantile. This disease is characterized by defective or missing enzymes to break down mucopolysaccharides are missing or are defective. The prevalence is <1:70.000 newborn.	600,25
HPD	Tyrosinemia, type 3	NM_002150.2	NM_002150.2:c.987delA, NM_002150.2:c.774T>G, NM_002150.2:c.600C>G	Tyrosinemia type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HPD gene located on chromosomal region 12q24.31. The age of onset is infantile. This disease is characterized by intellectual deficit and ataxia. The prevalence is 1:100,000-1:120,000 newborn.	600,25

IGHMBP2	Charcot-Marie-Tooth disease, axonal, type 2S	NM_002180.2	NM_002180.2:c.121C>T, NM_002180.2:c.638A>G, NM_002180.2:c.661delA, NM_002180.2:c.1107C>G, NM_002180.2:c.1488C>A, NM_002180.2:c.1540G>A, NM_002180.2:c.1738G>A, NM_002180.2:c.2362C>T, NM_002180.2:c.2611+1G>T	Charcot-Marie-Tooth disease, axonal, type 2S follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the IGHMBP2 gene located on chromosomal region 11q13.3. The age of onset can be infancy, childhood, adult or adolescent. This disease is characterized by progressive distal muscle weakness and atrophy of both the lower and upper limbs, absent or reduced deep tendon reflexes, mild sensory loss, foot drop, and pes cavus leading eventually to wheelchair dependence. Some patients present with early hypotonia and delayed motor development. Scoliosis and variable autonomic disturbances may be associated. The prevalence is below 1/1,000,000.	600,25
INPP5E	Joubert syndrome, type 1	NM_019892.5	NM_019892.5:c.1879C>T, NM_019892.5:c.1688G>A, NM_019892.5:c.1543C>T, NM_019892.5:c.1304G>A, NM_019892.5:c.1132C>T, NM_019892.5:c.855_856insCG	Joubert syndrome type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the INPP5E gene located on chromosomal region 9q34.3. The age of onset is early infantile. This disease is characterized congenital malformation of the brainstem and agenesis of the cerebellar vermis (molar tooth sign) leading to an abnormal respiratory pattern, nystagmus, hypotonia, mental retardation, ataxia, and delay in achieving motor milestones. Other variable features include retinal dystrophy (manifesting with either Leber congenital amaurosis or progressive retinal dystrophy) and nephronophthisis (usually juvenile). The prevalence is 1:100,000.	600,25
INSR	Diabetes mellitus, insulin-resistant, with acanthosis nigricans, type A	NM_000208.3	NM_000208.3:c.3680G>C, NM_000208.3:c.3079C>T, NM_000208.3:c.2668C>T, NM_000208.3:c.1114C>T, NM_000208.3:c.172G>A	Diabetes mellitus, insulin-resistant, with acanthosis nigricans type A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the INSR gene located on chromosomal region 19p13.2. The age of onset is infantile. This disease is characterized by the triad of hyperinsulinemia, acanthosis nigricans (skin lesions associated with insulin resistance), and signs of hyperandrogenism in females without lipodystrophy and who are not overweight. It is generally diagnosed in young women with marked signs of hyperandrogenism, but insulin resistance and acanthosis nigricans may be observed in men and in childhood. Acromegaloid facies or muscular cramps are sometimes associated. Hyperinsulinemia, a biological marker for insulin resistance, is often associated with glucose tolerance defects over the course of the disease, and diabetes progressively sets in. Hyperandrogenism (associated with polycystic ovarian syndrome (see this term) or ovarian hyperthecoses) leads to fertility problems. The prevalence is <1:1,000,000.	600,25
ITGB4	Epidermolysis bullosa, junctional, with pyloric atresia	NM_000213.4	NM_000213.4:c.112T>C, NM_000213.4:c.182G>A, NM_000213.4:c.1150delG, NM_000213.4:c.1660C>T, NM_000213.4:c.1684T>C, NM_000213.4:c.2608delC, NM_000213.4:c.2792G>A, NM_000213.4:c.3321_3331delACTGGACCGGA, NM_000213.4:c.3674G>A, NM_000213.4:c.3793+1G>A, NM_000213.4:c.3801dupT, NM_000213.4:c.3841C>T, NM_000213.4:c.4620delG, NM_000213.4:c.4643G>A, NM_000213.4:c.4828C>T, NM_000213.4:c.5329+2T>C	Junctional epidermolysis bullosa with pyloric atresia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ITGB4 gene located on chromosomal region 17q25.1. The age of onset is early infantile. This disease is characterized by generalized blistering at birth and congenital atresia of the pylorus and rarely of other portions of the gastrointestinal tract. More than 100 cases have been reported around the world.	600,25
IVD	Isovaleric acidemia	NM_002225.3	NM_002225.3:c.2T>G, NM_002225.3:c.134T>C, NM_002225.3:c.157C>T, NM_002225.3:c.158G>A, NM_002225.3:c.158G>C, NM_002225.3:c.243+1G>A, NM_002225.3:c.367G>A, NM_002225.3:c.390delT, NM_002225.3:c.406_407delTG, NM_002225.3:c.434_437dupATGA, NM_002225.3:c.465+2T>C, NM_002225.3:c.478_479insGT, NM_002225.3:c.507delG, NM_002225.3:c.559+1G>A, NM_002225.3:c.593G>A, NM_002225.3:c.605G>T, NM_002225.3:c.627delT, NM_002225.3:c.793+1G>A, NM_002225.3:c.941C>T, NM_002225.3:c.994_995delAT, NM_002225.3:c.1141T>C, NM_002225.3:c.1145_1147+4delTTGGTGA, NM_002225.3:c.1183C>T, NM_002225.3:c.1188delT, NM_002225.3:c.1192C>T, NM_002225.3:c.1208A>G	Isovaleric academia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the IVD gene located on chromosomal region 15q15.1. The age of onset is neonatal. This disease is characterized by vomiting, dehydration, coma and abnormal movements. The prevalence is 1/100,000.	600,25

JAK3	Severe Combined Immunodeficiency, autosomal recessive, T-negative/B-positive type	NM_000215.3	NM_000215.3:c.1837C>T, NM_000215.3:c.1765G>A, NM_000215.3:c.1695C>A, NM_000215.3:c.1333C>T, NM_000215.3:c.1172_1173insG, NM_000215.3:c.299A>G	Severe combined immunodeficiency, T-B+ type follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the JAK3 gene located on chromosomal region 19p13.11. The age of onset is infantile. This disease is characterized by chronic diarrhea, failure to thrive, recurrent respiratory infections and/or generalized infections due to opportunistic pathogens. The incidence is 1/100,000 and 1/1,000,000.	600,25
KCNJ1	Bartter syndrome, type 2	NM_000220.4	NM_000220.4:c.1014delA, NM_000220.4:c.1012C>T, NM_000220.4:c.996_999delAAAG, NM_000220.4:c.942T>G, NM_000220.4:c.657C>G, NM_000220.4:c.641C>T, NM_000220.4:c.592G>A, NM_000220.4:c.500G>A, NM_000220.4:c.372T>A, NM_000220.4:c.322G>C, NM_000220.4:c.237C>G	Bartter syndrome, type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the KCNJ1 gene located on chromosomal region 11q24.3. The age of onset is antenatal. This disease is characterized by severe polyhydramnios in mother leading to premature delivery, postnatally newborns suffer from recurrent episodes of severe dehydration and electrolyte imbalance which can lead to fatal outcome.	600,25
KCNV2	Retinal cone dystrophy, type 3B	NM_133497.3	NM_133497.3:c.226C>T, NM_133497.3:c.325C>T, NM_133497.3:c.357dupC, NM_133497.3:c.427G>T, NM_133497.3:c.442G>T, NM_133497.3:c.491T>C, NM_133497.3:c.767C>G, NM_133497.3:c.778A>T, NM_133497.3:c.916G>T, NM_133497.3:c.1016_1024delACCTGGTGG, NM_133497.3:c.1133dupT, NM_133497.3:c.1376G>A	Retinal cone dystrophy, type 3B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the KCNV2 gene located on 9p24.2. The age of onset is in the first or second decade of life. This disease is characterized by is characterized by onset in the first or second decade of life of very marked photophobia, myopia, reduced color vision along the red-green axis with relatively preserved tritan discrimination, and central scotomata with peripheral widespread sensitivity loss predominating in the superior visual field. Nyctalopia is a later feature of the disorder. There is often retinal pigment epithelium disturbance at the macula with a normal retinal periphery.	600,25
LAMA2	LAMA2-related muscular dystrophy	NM_000426.3	NM_000426.3:c.112+1G>A, NM_000426.3:c.184G>T, NM_000426.3:c.825delC, NM_000426.3:c.1050delT, NM_000426.3:c.1612C>T, NM_000426.3:c.2049_2050delAG, NM_000426.3:c.2098_2099delTT, NM_000426.3:c.2323-2A>T, NM_000426.3:c.2451-2A>G, NM_000426.3:c.2750-1G>C, NM_000426.3:c.2901C>A, NM_000426.3:c.2962C>T, NM_000426.3:c.3215delG, NM_000426.3:c.3237C>A, NM_000426.3:c.3630delT, NM_000426.3:c.3718C>T, NM_000426.3:c.3976C>T, NM_000426.3:c.4645C>T, NM_000426.3:c.5050G>T, NM_000426.3:c.5227G>T, NM_000426.3:c.6011delA, NM_000426.3:c.6038delT, NM_000426.3:c.6334A>T, NM_000426.3:c.6429+1G>A, NM_000426.3:c.6617delT, NM_000426.3:c.6955C>T, NM_000426.3:c.7147C>T, NM_000426.3:c.7279_7280delCT, NM_000426.3:c.7536delC, NM_000426.3:c.7732C>T, NM_000426.3:c.7810C>T, NM_000426.3:c.7888C>T, NM_000426.3:c.8314delA, NM_000426.3:c.8705delT, NM_000426.3:c.8748delA, NM_000426.3:c.9101_9104dupAACA, NM_000426.3:c.9221delA, NM_000426.3:c.9253C>T	LAMA2-related muscular dystrophy 1A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LAMA2 gene located on chromosomal region 6q22.33. LAMA2-related muscular dystrophy is a disorder that causes weakness and atrophy of skeletal muscles. This condition varies in severity, from a severe, early-onset type to a milder, late-onset form. Early-onset LAMA2-related muscular dystrophy is apparent at birth or within the first few months of life, called merosin-deficient congenital muscular dystrophy type 1A (607855). Patients show hypotonia, poor suck and cry, and delayed motor development; most never achieve independent ambulation. Most patients also have periventricular white matter abnormalities on brain imaging, but mental retardation and/or seizures occur only rarely. Symptoms of late-onset LAMA2-related muscular dystrophy become evident later in childhood or adulthood, and are similar to those of a group of muscle disorders classified as autosomal recessive limb-girdle muscular dystrophies, type 23. This group is characterized by slowly progressive proximal muscle weakness primarily affecting the lower limbs and resulting in gait difficulties. Additional features include white matter abnormalities on brain imaging, increased serum creatine kinase, and dystrophic features, with partial LAMA2 deficiency on muscle biopsy. Some patients may have additional neurologic features, including executive deficits, seizures, and peripheral neuropathy. Patients remain ambulatory well into adulthood. The prevalence is 1/30,000.	600,25

LAMB3	Junctional epidermolysis bullosa, Herlitz and non-Herlitz type	NM_000228.2	NM_000228.2:c.3228+1G>T, NM_000228.2:c.3228+1G>A, NM_000228.2:c.2806C>T, NM_000228.2:c.1903C>T, NM_000228.2:c.1830G>A, NM_000228.2:c.1587_1588delAG, NM_000228.2:c.1438_1442delCCGTG, NM_000228.2:c.1357delT, NM_000228.2:c.904delT, NM_000228.2:c.727C>T, NM_000228.2:c.628+1delG, NM_000228.2:c.628G>A, NM_000228.2:c.565-2A>G, NM_000228.2:c.496C>T, NM_000228.2:c.124C>T	Junctional epidermolysis bullosa follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LAMB3 gene located on chromosomal region 1q32.2. The age of onset is neonatal/infancy. Junctional epidermolysis bullosa (JEB) is a group of genetic conditions that cause the skin to be very fragile and to blister easily. Blisters and skin erosions form in response to minor injury or friction, such as rubbing or scratching. Researchers classify junctional epidermolysis bullosa into two main types based on severity: Herlitz JEB and non-Herlitz JEB. Herlitz type is more severe phenotype characterized by blisters and erosions, localized to the skin and mucous membranes and often results in early death. More than 80 mutations in the LAMB3 gene have been identified in people with Herlitz JEB. Other LAMB3 gene mutations cause the milder form non-Herlitz JEB, disease characterized by generalized skin blistering, atrophic scarring, nail dystrophy or nail absence, and enamel hypoplasia, with extracutaneous involvement.	600,25
LMNA	LMNA-related disorders, autosomal recessive	NM_001282626.1	NM_001282626.1:c.1818+6C>T	LMNA-related disorders, autosomal recessive, are caused by pathogenic variants in the LMNA gene located on chromosomal region 1q22, and include Charcot-Marie-Tooth disease, type 2B1, Emery-Dreifuss muscular dystrophy type 3, mandibuloacral dysplasia, lethal restrictive dermopathy among others. Charcot-Marie-Tooth disease constitutes a clinically and genetically heterogeneous group of hereditary motor and sensory neuropathies. Emery-Dreifuss muscular dystrophy is characterized classically by the triad of weakness of the shoulder and pelvic girdle muscles, contractures of the elbows, neck, and Achilles tendon, and cardiac involvement, most commonly arrhythmias. Mandibuloacral dysplasia is characterized by growth retardation, craniofacial anomalies with mandibular hypoplasia, skeletal abnormalities with progressive osteolysis of the distal phalanges and clavicles, and pigmentary skin changes. Restrictive dermopathy is a rare, lethal genodermatosis characterized by thin, tightly adherent translucent skin with erosions at flexure sites, superficial vessels, typical facial dysmorphism, and generalized joint ankylosis.	600,25
LMNA	LMNA-related disorders, autosomal recessive	NM_170707.3	NM_170707.3:c.419T>C, NM_170707.3:c.1072G>A, NM_170707.3:c.1228C>T, NM_170707.3:c.1366A>C, NM_170707.3:c.1411C>T, NM_170707.3:c.1488+1G>A, NM_170707.3:c.1579C>T, NM_170707.3:c.1580G>A, NM_170707.3:c.1583C>A, NM_170707.3:c.1585G>A, NM_170707.3:c.1586C>T, NM_170707.3:c.1626G>C	LMNA-related disorders, autosomal recessive, are caused by pathogenic variants in the LMNA gene located on chromosomal region 1q22, and include Charcot-Marie-Tooth disease, type 2B1, Emery-Dreifuss muscular dystrophy type 3, mandibuloacral dysplasia, lethal restrictive dermopathy among others. Charcot-Marie-Tooth disease constitutes a clinically and genetically heterogeneous group of hereditary motor and sensory neuropathies. Emery-Dreifuss muscular dystrophy is characterized classically by the triad of weakness of the shoulder and pelvic girdle muscles, contractures of the elbows, neck, and Achilles tendon, and cardiac involvement, most commonly arrhythmias. Mandibuloacral dysplasia is characterized by growth retardation, craniofacial anomalies with mandibular hypoplasia, skeletal abnormalities with progressive osteolysis of the distal phalanges and clavicles, and pigmentary skin changes. Restrictive dermopathy is a rare, lethal genodermatosis characterized by thin, tightly adherent translucent skin with erosions at flexure sites, superficial vessels, typical facial dysmorphism, and generalized joint ankylosis.	600,25
LRP5	Osteoporosis-pseudoglioma syndrome	NM_002335.3	NM_002335.3:c.804_813delGGGGAAGAGG, NM_002335.3:c.1453G>T, NM_002335.3:c.1468delG, NM_002335.3:c.1481G>A, NM_002335.3:c.1708C>T, NM_002335.3:c.1709G>A, NM_002335.3:c.2202G>A, NM_002335.3:c.2254C>G, NM_002335.3:c.2305delG, NM_002335.3:c.2557C>T, NM_002335.3:c.4099G>A, NM_002335.3:c.4651G>A	Osteoporosis-pseudoglioma syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LRP5 gene located on chromosomal region 11q13.2. The age of onset is infantile. This disease is characterized by congenital or infancy-onset blindness and severe juvenile-onset osteoporosis and spontaneous fractures. The prevalence is 1:2,000,000.	600,25

MAN2B1	Mannosidosis, alpha-, types I and II	NM_000528.3	NM_000528.3:c.2686_2687delCTinsG, NM_000528.3:c.2436+2T>C, NM_000528.3:c.2426T>C, NM_000528.3:c.2398G>A, NM_000528.3:c.2368C>T, NM_000528.3:c.2278C>T, NM_000528.3:c.2119C>T, NM_000528.3:c.2013delT, NM_000528.3:c.1929G>A, NM_000528.3:c.1915C>T, NM_000528.3:c.1830+1G>C, NM_000528.3:c.1780C>T, NM_000528.3:c.384G>A, NM_000528.3:c.1A>G	Alpha-mannosidosis follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MAN2B1 gene located on chromosomal region 19p13.2. The age of onset is infantile. This disease is characterized by immunodeficiency, facial and skeletal abnormalities, hearing impairment and intellectual disability. The prevalence is 1:1,000,000-9:1,000,000.	600,25
MCCC2	3-Methylcrotonyl-CoA carboxylase type 2, deficiency	NM_022132.4	NM_022132.4:c.295G>C, NM_022132.4:c.380C>G, NM_022132.4:c.464G>A, NM_022132.4:c.499T>C, NM_022132.4:c.517dupT, NM_022132.4:c.641delG, NM_022132.4:c.735dupC, NM_022132.4:c.838G>T, NM_022132.4:c.929C>G, NM_022132.4:c.994C>T, NM_022132.4:c.1015G>A, NM_022132.4:c.1065A>T, NM_022132.4:c.1072+1G>A, NM_022132.4:c.1577dupT, NM_022132.4:c.1580G>A	3-methylcrotonyl-CoA carboxylase deficiency type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MCCC2 gene located on chromosomal region 5q13.2. The age of onset is neonatal. This disease is characterized by a highly variable clinical picture ranging from neonatal onset with severe neurological involvement to asymptomatic adults. The prevalence is 1:75,000 newborn.	600,25
MED25	Basel-Vanagait-Smirin-Yosef syndrome	NM_030973.3	NM_030973.3:c.320delG, NM_030973.3:c.1366C>T	Basel-Vanagait-Smirin-Yosef syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MED25 gene located on chromosomal region 19q13.33. The age of onset neonatal/infantile. This syndrome is characterized by eye, brain, cardiac and palatal abnormalities as well as growth retardation, microcephaly and severe intellectual disability.	600,25
MEFV	Familial Mediterranean fever, AR	NM_000243.2	NM_000243.2:c.2282G>A, NM_000243.2:c.2230G>T, NM_000243.2:c.2177T>C, NM_000243.2:c.2084A>G, NM_000243.2:c.2082G>A, NM_000243.2:c.2080A>G, NM_000243.2:c.2076_2078delAAT, NM_000243.2:c.2040G>C, NM_000243.2:c.2040G>A, NM_000243.2:c.1958G>A, NM_000243.2:c.1437C>G, NM_000243.2:c.1141C>T, NM_000243.2:c.656dupG, NM_000243.2:c.501G>C, NM_000243.2:c.163dupA	Familial Mediterranean fever follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MEFV gene located on chromosomal region 16p13.3. The age of onset is infantile or adult (before the age of 30). This disease is characterized by recurrent short episodes of fever and serositis resulting in pain in the abdomen, chest, joints and muscles. The prevalence is 1:10,000-5:10,000.	600,25
MERTK	Retinitis pigmentosa type 38	NM_006343.2	NM_006343.2:c.1605-2A>G, NM_006343.2:c.2070_2074delAGGAC, NM_006343.2:c.2189+1G>T, NM_006343.2:c.2211_2214delCTGT, NM_006343.2:c.2323C>T, NM_006343.2:c.2785_2786dupTA	Retinitis pigmentosa type 38 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MERTK gene located on chromosomal region 2q13. The age of onset is infantile. This disease is characterized by. This disease is characterized by night blindness, followed by a progressive loss of peripheral vision in the daylight period and leading to blindness.	600,25
MFRP	Microphthalmia, isolated type 5	NM_031433.3	NM_031433.3:c.1149dupC, NM_031433.3:c.1124+1G>T, NM_031433.3:c.545T>C, NM_031433.3:c.523C>T, NM_031433.3:c.498delC	Microphthalmia, isolated type 5 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MFRP gene located on chromosomal region 11q23.3. The age of onset is infantile. This disease is characterized by posterior microphthalmos, retinitis pigmentosa, foveoschisis, and optic disk drusen.	600,25
MKKS	Bardet-Biedl syndrome type 6	NM_018848.3	NM_018848.3:c.1436C>G, NM_018848.3:c.1225_1226delGG, NM_018848.3:c.830T>C, NM_018848.3:c.353delG	Bardet-Biedl syndrome type 6 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MKKS gene located on chromosomal region 20p12.2. The age of onset is antenatal or infacy. This disease is characterized by a combination of clinical signs: obesity, pigmentary retinopathy, post-axial polydactyly, polycystic kidneys, hypogenitalism, and learning disabilities, many of which appear several years after disease onset. Clinical expression is variable but most patients manifest the majority of clinical signs during the disease course.	600,25
MKS1	Bardet-Biedl syndrome type 13	NM_001321269.1	NM_001321269.1:c.1024+1G>A, NM_001321269.1:c.508C>T	Bardet-Biedl syndrome type 13 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MKS1 gene located on chromosomal region 17q22. The age of onset is antenatal or infacy. This disease is characterized by a combination of clinical signs: obesity, pigmentary retinopathy, post-axial polydactyly, polycystic kidneys, hypogenitalism, and learning disabilities, many of which appear several years after disease onset. Clinical expression is variable but most patients manifest the majority of clinical signs during the disease course.	600,25

MMACHC	Methylmalonic aciduria and homocystinuria, cblC type	NM_015506.2	NM_015506.2:c.271dupA, NM_015506.2:c.331C>T, NM_015506.2:c.347T>C, NM_015506.2:c.388_390delTAC, NM_015506.2:c.394C>T, NM_015506.2:c.440G>C, NM_015506.2:c.481C>T, NM_015506.2:c.482G>A, NM_015506.2:c.547_548delGT, NM_015506.2:c.608G>A, NM_015506.2:c.609G>A, NM_015506.2:c.615C>A, NM_015506.2:c.615C>G, NM_015506.2:c.619dupG, NM_015506.2:c.616C>T, NM_015506.2:c.658_660delAAG, NM_015506.2:c.688C>T	Vitamin B12-responsive methylmalonic acidemia type cbl B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MMAB gene located on chromosomal region 12q24.31. The age of onset is early infantile. This disease is characterized by developmentally delayed with other features that include hypotonia, seizures, hypoglycaemia, metabolic acidosis, cardiomyopathy and diarrhoea. The prevalence is <1:1,000,000.	600,25
MOCS2	Molybdenum cofactor deficiency B	NM_004531.4	NM_004531.4:c.567A>C, NM_004531.4:c.539_540delAA, NM_004531.4:c.502G>A, NM_004531.4:c.377+1G>A, NM_004531.4:c.106_107delAT, NM_004531.4:c.58delT, NM_004531.4:c.3G>A	Molybdenum cofactor deficiency type B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MOCS2 gene located on chromosomal region 5q11.2. This disease is characterized by severe neurological abnormalities, dislocated ocular early death.	600,25
MOCS2	Molybdenum cofactor deficiency B	NM_176806.3	NM_176806.3:c.16C>T	Molybdenum cofactor deficiency type B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MOCS2 gene located on chromosomal region 5q11.2. This disease is characterized by severe neurological abnormalities, dislocated ocular early death.	600,25
MTTP	Abetalipoproteinemia	NM_001300785.1	NM_001300785.1:c.789_790delCA, NM_001300785.1:c.1700G>A, NM_001300785.1:c.1850G>T, NM_001300785.1:c.1948+1G>A, NM_001300785.1:c.2112delC, NM_001300785.1:c.2674G>T	Abetalipoproteinemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MTTP gene located on chromosomal region 4q23. The age of onset is infantile. This disease is characterized by growth delay, malabsorption, hepatomegaly, and neurological and neuromuscular manifestations. The prevalence is <1:1,000,000.	600,25
MUT	Methylmalonic aciduria, mut(0) type	NM_000255.3	NM_000255.3:c.2150G>T, NM_000255.3:c.2080C>T, NM_000255.3:c.1924G>C, NM_000255.3:c.1871A>G, NM_000255.3:c.1867G>A, NM_000255.3:c.1741C>T, NM_000255.3:c.1658delT, NM_000255.3:c.1445-2A>G, NM_000255.3:c.1420C>T, NM_000255.3:c.1399C>T, NM_000255.3:c.1280G>A, NM_000255.3:c.1207C>T, NM_000255.3:c.1181T>A, NM_000255.3:c.1106G>A, NM_000255.3:c.914T>C, NM_000255.3:c.682C>T, NM_000255.3:c.671_678dupAATTTATG, NM_000255.3:c.655A>T, NM_000255.3:c.643G>A, NM_000255.3:c.607G>A, NM_000255.3:c.572C>A, NM_000255.3:c.313T>C, NM_000255.3:c.280G>A, NM_000255.3:c.278G>A, NM_000255.3:c.91C>T	Methylmalonic acidemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MUT gene located on chromosomal region 6p12.3. The age of onset is very early infantile. This disease is characterized by recurrent ketoacidotic comas or transient vomiting, dehydration, hypotonia and intellectual deficit, which does not respond to administration of vitamin B12.	600,25
MVK	Mevalonic aciduria	NM_000431.3	NM_000431.3:c.59A>C, NM_000431.3:c.185G>A, NM_000431.3:c.494C>T, NM_000431.3:c.803T>C, NM_000431.3:c.902A>C, NM_000431.3:c.928G>A, NM_000431.3:c.1000G>A, NM_000431.3:c.1129G>A	Mevalonic aciduria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MVK gene located on chromosomal region 12q24.11. The age of onset is infantile. This disease is characterized by psychomotor retardation, failure to thrive, progressive cerebellar ataxia, dysmorphic features, progressive visual impairment and recurrent febrile crises. The prevalence is <1:1,000,000.	600,25
MYO15A	Deafness, autosomal recessive type 3	NM_016239.3	NM_016239.3:c.625G>T, NM_016239.3:c.755dupA, NM_016239.3:c.3313G>T, NM_016239.3:c.3336delG, NM_016239.3:c.3385C>T, NM_016239.3:c.3693-2A>G, NM_016239.3:c.3756+1G>T, NM_016239.3:c.4751_4752dupTC, NM_016239.3:c.5326C>T, NM_016239.3:c.5492G>T, NM_016239.3:c.6004delG, NM_016239.3:c.6864_6874delGGACCTGGAGC, NM_016239.3:c.8148G>T, NM_016239.3:c.8410A>T, NM_016239.3:c.8548C>T, NM_016239.3:c.9958_9961delGACT, NM_016239.3:c.10573delA	Deafness autosomal recessive type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MYO15A gene located on chromosomal region 17p11.2. The age of onset is infantile, etc/. This disease is characterized by mild-to-profound sensorineural hearing impairment with no associated visible abnormalities of the external ear or any related medical problems.	600,25
MYO3A	Deafness, autosomal recessive type 30	NM_017433.4	NM_017433.4:c.1A>G, NM_017433.4:c.732-2A>G, NM_017433.4:c.770C>G, NM_017433.4:c.1086T>G, NM_017433.4:c.1193C>A, NM_017433.4:c.1777-12G>A, NM_017433.4:c.1953delC, NM_017433.4:c.2243delA, NM_017433.4:c.2506-1G>A, NM_017433.4:c.2793+2T>A, NM_017433.4:c.3112-2A>G, NM_017433.4:c.3154C>T, NM_017433.4:c.4586+2T>G, NM_017433.4:c.4730+1G>A	Deafness autosomal recessive type 30 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MYO3A gene located on chromosomal region 10p12.1. The age of onset is infantile. This disease is characterized by mild-to-profound sensorineural hearing impairment with no associated visible abnormalities of the external ear or any related medical problems.	600,25
MYO6	Deafness, autosomal recessive type 37	NM_004999.3	NM_004999.3:c.1452dupT, NM_004999.3:c.2907_2909delAGA, NM_004999.3:c.3496C>T, NM_004999.3:c.3808C>T	Deafness autosomal recessive type 37 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MYO6 gene located on chromosomal region 6q14.1. The age of onset is infantile. This disease is characterized by mild-to-profound sensorineural hearing impairment with no associated visible abnormalities of the external ear or any related medical problems.	600,25

MYO7A	Usher syndrome, type 1B	NM_000260.3	NM_000260.3:c.3G>A, NM_000260.3:c.133-2A>G, NM_000260.3:c.448C>T, NM_000260.3:c.494C>T, NM_000260.3:c.634C>T, NM_000260.3:c.635G>A, NM_000260.3:c.640G>A, NM_000260.3:c.731G>C, NM_000260.3:c.1184G>A, NM_000260.3:c.1344-1G>A, NM_000260.3:c.1797G>A, NM_000260.3:c.1884C>A, NM_000260.3:c.1996C>T, NM_000260.3:c.2476G>A, NM_000260.3:c.3504-1G>C, NM_000260.3:c.3508G>A, NM_000260.3:c.3596dupT, NM_000260.3:c.3719G>A, NM_000260.3:c.3764delA, NM_000260.3:c.4024delT, NM_000260.3:c.5392C>T, NM_000260.3:c.5618G>A, NM_000260.3:c.5824G>T, NM_000260.3:c.5886_5889delCTTT, NM_000260.3:c.5967C>G, NM_000260.3:c.6025delG	Usher syndrome type 1B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MYO7A gene located on chromosomal region 11q13.5. The age of onset is infantile. This disease is characterized by congenital, bilateral, profound sensorineural hearing loss, vestibular areflexia, and adolescent-onset retinitis pigmentosa. The prevalence is 1:100,000-9:100,000.	600,25
NAGA	Schindler disease, type I	NM_000262.2	NM_000262.2:c.986G>A, NM_000262.2:c.985C>T, NM_000262.2:c.973G>A, NM_000262.2:c.577G>T	Schindler disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NAGA gene located on chromosomal region 22q13.2. The age of onset is infantile. This disease is characterized by early-onset neuroaxonal dystrophy and neurological signs (convulsion during fever, epilepsy, psychomotor retardation and hypotonia). NAGA deficiency is typically classified in three main phenotypes: NAGA deficiency type I (Schindler disease or Schindler disease type I) with severe manifestations; NAGA deficiency type II (Kanzazi disease or Schindler disease type II) which is mild; NAGA deficiency type III (Schindler disease type III) characterized by mild-to-moderate neurologic manifestations. NAGA deficiency results in the increased urinary excretion of glycopeptides and oligosaccharides containing alpha-N-acetylgalactosaminyl moieties.	600,25
NEB	Nemaline myopathy type 2, autosomal recessive	NM_001271208.1	NM_001271208.1:c.12238_12239delAT, NM_001271208.1:c.8031_8041delAAATAAACGAG, NM_001271208.1:c.6105dupT, NM_001271208.1:c.2173G>T, NM_001271208.1:c.843T>G	Nemaline myopathy type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NEB gene located on chromosomal region 2q23.3. The age of onset is infantile or adult. This disease is characterized by hypotonia, weakness and depressed or absent deep tendon reflexes, with pathologic evidence of nemaline bodies (rods) on muscle biopsy. The prevalence is 1:100,000-9:100,000 and the incidence is 1/50.000 newborn.	600,25
NMNAT1	Leber congenital amaurosis type 9	NM_001297778.1	NM_001297778.1:c.25G>A, NM_001297778.1:c.451G>T, NM_001297778.1:c.457C>G, NM_001297778.1:c.507G>A, NM_001297778.1:c.619C>T, NM_001297778.1:c.710G>T, NM_001297778.1:c.769G>A	Leber congenital amaurosis type 9 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NMNAT1 gene located on chromosomal region 1p36.22. The age of onset is early infantile. This disease is characterized by blindness, nystagmus, roving eye movement, leading to severe visual impairment.	600,25
NPC1	Niemann-Pick disease, type C1	NM_000271.4	NM_000271.4:c.3662delT, NM_000271.4:c.3611_3614delTTAC, NM_000271.4:c.3467A>G, NM_000271.4:c.3425T>C, NM_000271.4:c.3182T>C, NM_000271.4:c.3175C>T, NM_000271.4:c.3107C>T, NM_000271.4:c.3104C>T, NM_000271.4:c.3019C>G, NM_000271.4:c.2974G>T, NM_000271.4:c.2974G>A, NM_000271.4:c.2972_2973delAG, NM_000271.4:c.2932C>T, NM_000271.4:c.2873G>A, NM_000271.4:c.2861C>T, NM_000271.4:c.2848G>A, NM_000271.4:c.2842G>A, NM_000271.4:c.2761C>T, NM_000271.4:c.2324A>C, NM_000271.4:c.2072C>T, NM_000271.4:c.1628C>T, NM_000271.4:c.1211G>A, NM_000271.4:c.1042C>T, NM_000271.4:c.813_815delCAT, NM_000271.4:c.530G>A, NM_000271.4:c.352_353delAG, NM_000271.4:c.337T>C	Niemann-Pick disease type C1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NPC1 gene located on chromosomal region 18q11.2. The age of onset varies between the perinatal period and the age of 50 years or more. This disease is characterized by hepatosplenomegaly and progressive neurological involvement. The prevalence is 1/130,000.	600,25
NPC2	Niemann-pick disease, type C2	NM_006432.3	NM_006432.3:c.436C>T, NM_006432.3:c.358C>T, NM_006432.3:c.352G>T, NM_006432.3:c.295T>C, NM_006432.3:c.190+5G>A, NM_006432.3:c.115G>A, NM_006432.3:c.58G>T, NM_006432.3:c.27delG	Niemann-Pick disease type C2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NPC2 gene located on chromosomal region 14q24.3. The age of onset varies between the perinatal period and the age of 50 years or more. This disease is characterized by hepatosplenomegaly and progressive neurological involvement. The prevalence is 1/130,000.	600,25
NPHP3	Meckel syndrome type 7	NM_153240.4	NM_153240.4:c.3406C>T, NM_153240.4:c.3373C>T, NM_153240.4:c.3156dupA, NM_153240.4:c.2694-2_2694-1delAG, NM_153240.4:c.2694-2A>G, NM_153240.4:c.2570+1G>T, NM_153240.4:c.2541delG, NM_153240.4:c.2369T>C, NM_153240.4:c.1985+5G>A, NM_153240.4:c.1817G>A, NM_153240.4:c.1729C>T, NM_153240.4:c.1381G>T, NM_153240.4:c.1119-2A>G, NM_153240.4:c.434_437delAAAG	Meckel syndrome type 7 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NPHP3 gene located on chromosomal region 3q22.1. The age of onset is infantile. This is a disorder characterized by a combination of renal cysts and variably associated features including developmental anomalies of the central nervous system (typically encephalocele), hepatic ductal dysplasia and cysts, and polydactyly.	600,25

NPHP4	Nephronophthisis type 4	NM_015102.4	NM_015102.4:c.3767_3768insAA, NM_015102.4:c.3231+1G>C, NM_015102.4:c.2940_2944dupGCTCC, NM_015102.4:c.2335C>T, NM_015102.4:c.1972C>T, NM_015102.4:c.1120-1G>C, NM_015102.4:c.556_557insT, NM_015102.4:c.517C>T	Nephronophthisis type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NPHP4 gene located on chromosomal region 1p36.31. The age of onset is infantile. This disease results in end-stage renal disease at age ranging between 6 and 35 years. It is a progressive tubulo-interstitial kidney disorder characterized by polydipsia, polyuria, anemia and growth retardation. The prevalence is 1:1,000,000-9:1,000,000.	600,25
NPHS1	Nephrotic syndrome, type 1	NM_004646.3	NM_004646.3:c.3478C>T, NM_004646.3:c.3325C>T, NM_004646.3:c.3250dupG, NM_004646.3:c.3250delG, NM_004646.3:c.3109+1G>A, NM_004646.3:c.2928G>T, NM_004646.3:c.2491C>T, NM_004646.3:c.1715G>A, NM_004646.3:c.1481delC, NM_004646.3:c.1307_1308dupAC, NM_004646.3:c.121_122delCT	Nephrotic syndrome type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NPHS1 gene located on chromosomal region 19q13.12. The age of onset is fetal- infantile. This disease is characterized by fetal proteinuria and nephritic infantile syndrome. The prevalence is 1 in 8 200 births.	600,25
NR2E3	Enhanced S-cone syndrome	NM_014249.3	NM_014249.3:c.119-2A>C, NM_014249.3:c.226C>T, NM_014249.3:c.298_299delTG, NM_014249.3:c.932G>A, NM_014249.3:c.1034_1038delTGCAG	Enhaced S-Cone Syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NR2E3 gene located on chromosomal region 15q23. The age of onset is infantile. This disease is characterized by night blindness, reduced bilateral visual acuity, and typical fundus findings (progressive pigmentary degenerative changes, macular edema, retinoschisis).	600,25
OCA2	Oculocutaneous albinism type 2	NM_000275.2	NM_000275.2:c.2228C>T, NM_000275.2:c.1960delG, NM_000275.2:c.1842+1G>T, NM_000275.2:c.1465A>G, NM_000275.2:c.1364+1G>T, NM_000275.2:c.1327G>A, NM_000275.2:c.1182+2T>C, NM_000275.2:c.1182G>A, NM_000275.2:c.1025A>G, NM_000275.2:c.819_822delCTGGinsGGTC, NM_000275.2:c.157delA, NM_000275.2:c.79G>A	Oculocutaneous albinism type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the OCA2 gene located on chromosomal region 15q12-q13. The age of onset is infantile. This disease is characterized by variable hypopigmentation of the skin and hair, numerous characteristic ocular changes and misrouting of the optic nerves at the chiasm. The prevalence is 1/38,000-1/40,000	600,25
OTOA	Deafness, autosomal recessive type 22	NM_144672.3	NM_144672.3:c.121-1G>A, NM_144672.3:c.828delT, NM_144672.3:c.1725_1726delCA	Deafness, autosomal recessive type 22 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the OTOA gene located on chromosomal region 16p12.2. The age of onset is infantile. This disease is characterized by hearing loss with no associated visible abnormalities of the external ear or any related medical problems.	600,25
OTOF	Auditory neuropathy, autosomal recessive, type 1	NM_001287489.1	NM_001287489.1:c.5474_5475delCC, NM_001287489.1:c.5473C>G, NM_001287489.1:c.5103+2T>A, NM_001287489.1:c.4559G>A, NM_001287489.1:c.4491T>A, NM_001287489.1:c.3032T>C, NM_001287489.1:c.2485C>T, NM_001287489.1:c.2348delG, NM_001287489.1:c.1778delT, NM_001287489.1:c.1544T>C, NM_001287489.1:c.1498C>T, NM_001287489.1:c.766-2A>G, NM_001287489.1:c.584-1G>C, NM_001287489.1:c.227+2T>C, NM_001287489.1:c.149G>A	Auditory neuropathy, autosomal recessive type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the OTOF gene located on chromosomal region 2p23.3. Patients can have varying degrees of hearing loss with poor speech reception out of proportion to the degree of hearing loss.	600,25
OTOF	Auditory neuropathy, autosomal recessive, type 1	NM_004802.3	NM_004802.3:c.3515G>A	Auditory neuropathy, autosomal recessive type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the OTOF gene located on chromosomal region 2p23.3. Patients can have varying degrees of hearing loss with poor speech reception out of proportion to the degree of hearing loss.	600,25

PAH	Phenylketonuria	NM_000277.1	NM_000277.1:c.1315+1G>A, NM_000277.1:c.1243G>A, NM_000277.1:c.1241A>G, NM_000277.1:c.1238G>C, NM_000277.1:c.1222C>T, NM_000277.1:c.1217T>C, NM_000277.1:c.1208C>T, NM_000277.1:c.1199+17G>A, NM_000277.1:c.1199+1G>A, NM_000277.1:c.1197A>T, NM_000277.1:c.1184C>A, NM_000277.1:c.1169A>G, NM_000277.1:c.1166delC, NM_000277.1:c.1162G>A, NM_000277.1:c.1139C>T, NM_000277.1:c.1068C>A, NM_000277.1:c.1066-3C>T, NM_000277.1:c.1066-11G>A, NM_000277.1:c.1045T>C, NM_000277.1:c.1042C>G, NM_000277.1:c.1033G>T, NM_000277.1:c.1030G>A, NM_000277.1:c.955G>T, NM_000277.1:c.926C>T, NM_000277.1:c.926C>A, NM_000277.1:c.912+1G>A, NM_000277.1:c.898G>T, NM_000277.1:c.896T>G, NM_000277.1:c.842+5G>A, NM_000277.1:c.838G>A, NM_000277.1:c.829T>G, NM_000277.1:c.823C>T, NM_000277.1:c.818C>T, NM_000277.1:c.814G>T, NM_000277.1:c.809G>A, NM_000277.1:c.806delT, NM_000277.1:c.782G>A, NM_000277.1:c.764T>C, NM_000277.1:c.755G>A, NM_000277.1:c.754C>T, NM_000277.1:c.745C>T, NM_000277.1:c.737C>A, NM_000277.1:c.734T>C, NM_000277.1:c.733G>C, NM_000277.1:c.728G>A, NM_000277.1:c.727C>T, NM_000277.1:c.722delG, NM_000277.1:c.722G>A, NM_000277.1:c.721C>T, NM_000277.1:c.688G>A, NM_000277.1:c.673C>G, NM_000277.1:c.665A>G, NM_000277.1:c.638T>C, NM_000277.1:c.611A>G, NM_000277.1:c.569T>C, NM_000277.1:c.533A>G, NM_000277.1:c.529G>A, NM_000277.1:c.527G>T, NM_000277.1:c.509+1G>A, NM_000277.1:c.508C>G, NM_000277.1:c.503delA, NM_000277.1:c.490A>G, NM_000277.1:c.482T>C, NM_000277.1:c.473G>A, NM_000277.1:c.472C>T, NM_000277.1:c.450dupA, NM_000277.1:c.442-1G>A, NM_000277.1:c.442-5C>G, NM_000277.1:c.441+5G>T, NM_000277.1:c.441+1G>A, NM_000277.1:c.357delC, NM_000277.1:c.331C>T, NM_000277.1:c.320A>G, NM_000277.1:c.311C>A, NM_000277.1:c.284_286delTCA, NM_000277.1:c.261C>A, NM_000277.1:c.250G>T, NM_000277.1:c.204A>T, NM_000277.1:c.194T>C, NM_000277.1:c.165T>G, NM_000277.1:c.143T>C, NM_000277.1:c.136G>A, NM_000277.1:c.117C>G, NM_000277.1:c.47_48delCT	Phenylketonuria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PAH gene located on chromosomal region 12q23.2. The age of onset is neonatal. This disease is characterized by gradual developmental delay, stunted growth, microcephaly, seizures, tremors, eczema, vomiting, and musty odor. Untreated patients subsequently develop intellectual disability, behavioral disorders (hyperactivity) and motor disorders. The prevalence is 1:2,600-1:200,000.	600,25
PANK2	Neurodegeneration with brain iron accumulation type 1	NM_153638.3	NM_153638.3:c.790C>T, NM_153638.3:c.823_824delCT, NM_153638.3:c.1561G>A, NM_153638.3:c.1583C>T	Neurodegeneration with brain iron accumulation type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PANK2 gene located on chromosomal region 20p13. The age of onset is infantile. This disease is characterized by progressive extrapyramidal dysfunction (dystonia, rigidity, choreoathetosis), iron accumulation on the brain and axonal spheroids in the central nervous system. The prevalence is 1-2/1,000,000.	600,25
PC	Pyruvate carboxylase deficiency	NM_000920.3	NM_000920.3:c.1748G>T, NM_000920.3:c.434T>C	Pyruvate carboxylase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PC gene located on chromosomal region 11q13.2. The age of onset is infantile. This disease is characterized by metabolic acidosis, failure to thrive, developmental delay, and recurrent seizures. The prevalence is 1:250,000.	600,25
PCCA	Propionic acidemia	NM_000282.3	NM_000282.3:c.229C>T, NM_000282.3:c.261dupT, NM_000282.3:c.412G>A, NM_000282.3:c.600+1G>A, NM_000282.3:c.862A>T, NM_000282.3:c.1023dupT, NM_000282.3:c.1118T>A, NM_000282.3:c.1226_1227delTT, NM_000282.3:c.1284+1G>A, NM_000282.3:c.1598_1601delTTGT, NM_000282.3:c.1891G>C, NM_000282.3:c.1899+4_1899+7delAGTA	Propionic acidemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PCCA gene located on chromosomal region 13q32.3. The age of onset is infantile. This disease is characterized by life threatening episodes of metabolic decompensation, neurological dysfunction and may be complicated by cardiomyopathy. The prevalence is 1:100,000.	600,25
PCCB	Propionic acidemia	NM_001178014.1	NM_001178014.1:c.331C>T, NM_001178014.1:c.337C>T, NM_001178014.1:c.562G>A, NM_001178014.1:c.622G>A, NM_001178014.1:c.743C>T, NM_001178014.1:c.1050dupT, NM_001178014.1:c.1233dupT, NM_001178014.1:c.1278_1291delGGGCATCATCCGGCinsTAGAGCACAGGA, NM_001178014.1:c.1279_1284delGGCATCinsAA, NM_001178014.1:c.1283_1286delTCAT, NM_001178014.1:c.1288C>T, NM_001178014.1:c.1289_1290insT, NM_001178014.1:c.1343C>T, NM_001178014.1:c.1364A>G, NM_001178014.1:c.1594C>T, NM_001178014.1:c.1598_1600dupCCC, NM_001178014.1:c.1666A>G	Propionic acidemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PCCB gene located on chromosomal region 3q22.3. The age of onset is infantile. This disease is characterized by life threatening episodes of metabolic decompensation, neurological dysfunction and may be complicated by cardiomyopathy. The prevalence is 1:100,000.	600,25

PCDH15	Deafness, autosomal recessive type 23	NM_001142763.1	NM_001142763.1:c.5680A>T, NM_001142763.1:c.4982_4983insTGAT, NM_001142763.1:c.4958_4961dupTGAT, NM_001142763.1:c.4885delA, NM_001142763.1:c.4569_4572dupATCT, NM_001142763.1:c.3733-2A>G, NM_001142763.1:c.2660_2661delAT, NM_001142763.1:c.1955C>G, NM_001142763.1:c.1752C>G, NM_001142763.1:c.1598T>A, NM_001142763.1:c.1103delT, NM_001142763.1:c.1021C>T, NM_001142763.1:c.800G>A, NM_001142763.1:c.415C>T, NM_001142763.1:c.415C>G, NM_001142763.1:c.7C>T	Deafness, autosomal recessive 23 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PCDH15 gene located on chromosomal region 10q21.1. This is a form of non-syndromic sensorineural hearing loss. Sensorineural deafness results from damage to the neural receptors of the inner ear, the nerve pathways to the brain, or the area of the brain that receives sound information.	600,25
PDE6A	Retinitis pigmentosa type 43	NM_000440.2	NM_000440.2:c.2053G>A, NM_000440.2:c.1749C>G, NM_000440.2:c.1683G>A, NM_000440.2:c.1560dupA, NM_000440.2:c.1113+1G>T, NM_000440.2:c.1113+1G>A	Retinitis pigmentosa type 43 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PDE6A gene located on chromosomal region 5q32. The age of onset is variable. This disease is characterized by night blindness (nyctalopia) due to loss of rod function, often in adolescence or earlier. They then develop peripheral visual field impairment, and overtime loss of central vision, usually at late stages, often around midlife. The prevalence is 1:10,000-5:10,000.	600,25
PDE6B	Retinitis pigmentosa type 40	NM_000283.3	NM_000283.3:c.892C>T, NM_000283.3:c.1540delC, NM_000283.3:c.1572delC, NM_000283.3:c.1580T>C, NM_000283.3:c.1669C>T, NM_000283.3:c.1920+2T>C	Retinitis pigmentosa 40 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PDE6B gene located on chromosomal region 4p16.3. The age of onset is variable. Retinitis pigmentosa 40 is a retinal dystrophy belonging to the group of pigmentary retinopathies.This disease is characterized by night blindness, followed by a progressive loss of peripheral vision in the daylight period and leading to blindness.	600,25
PEX1	Heimler syndrome type 1	NM_000466.2	NM_000466.2:c.3505_3517delCAGTTGTTTTCAC, NM_000466.2:c.2916delA, NM_000466.2:c.2528G>A, NM_000466.2:c.2097dupT, NM_000466.2:c.1991T>C, NM_000466.2:c.1952_1960dupCAGTGTGGA, NM_000466.2:c.1842delA, NM_000466.2:c.1239+1G>T, NM_000466.2:c.877C>T	Heimler syndrome 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PEX1 gene located on chromosomal region 7q21.2. This disease is characterized by sensorineural hearing loss, enamel hyoplasia of the secondary dentition, and nail abnormalities.	600,25
PEX7	Rhizomelic chondrodysplasia punctata, type 1	NM_000288.3	NM_000288.3:c.532C>T, NM_000288.3:c.618G>A, NM_000288.3:c.649G>A, NM_000288.3:c.653C>T, NM_000288.3:c.694C>T, NM_000288.3:c.854A>G, NM_000288.3:c.875T>A, NM_000288.3:c.903+1G>C	Rhizomelic chondrodysplasia punctata type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PEX7 gene located on chromosomal region 6q23.3. The age of onset is early. This disease is characterized by proximal shortening of the humerus and to a lesser degree the femur (rhizomelia), punctate calcifications in cartilage with epiphyseal and metaphyseal abnormalities (chondrodysplasia punctata), coronal clefts of the vertebral bodies, cataracts, postnatal growth deficiency is profound, intellectual disability is severe, seizures. The prevalence is <1:100,000.	600,25
PHYH	Refsum disease	NM_001323082.1	NM_001323082.1:c.830G>A, NM_001323082.1:c.829C>T, NM_001323082.1:c.811A>C, NM_001323082.1:c.684+5G>T, NM_001323082.1:c.684+2T>G, NM_001323082.1:c.503-2A>G, NM_001323082.1:c.164delT, NM_001323082.1:c.135-1G>C, NM_001323082.1:c.135-2A>G	Refsum disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PHYH gene located on chromosomal region 10p13. The age of onset is variable. This disease is characterized by hemeralopia (loss of vision in the dark), followed by episods of chronic distal motor polyneuropathy. Other associated signs include perceptive deafness, anosmia, cerebellous ataxia and sometimes, severe intellectual deficiency. Over the course of time cutaneous signs appear (ichtyosis), along with polyepiphyseal dysplasia, myocardiopathy, elevated protein in cerebrospinal fluid, and pigmentary retinitis that may result in blindness. The prevalence is 1:1.000,000-9:1.000,000.	600,25

PKHD1	Polycystic kidney disease type 4	NM_138694.3	NM_138694.3:c.12027C>G, NM_138694.3:c.11363_11372delCTTCCCTGGA, NM_138694.3:c.10452dupT, NM_138694.3:c.10412T>G, NM_138694.3:c.10219C>T, NM_138694.3:c.9719G>A, NM_138694.3:c.9689delA, NM_138694.3:c.9530T>C, NM_138694.3:c.9370C>T, NM_138694.3:c.8870T>C, NM_138694.3:c.8824C>T, NM_138694.3:c.8408G>A, NM_138694.3:c.8407T>C, NM_138694.3:c.8317G>T, NM_138694.3:c.6499C>T, NM_138694.3:c.5895dupA, NM_138694.3:c.5325_5326delAG, NM_138694.3:c.4870C>T, NM_138694.3:c.3940delA, NM_138694.3:c.3766delC, NM_138694.3:c.3761_3762delCCinsG, NM_138694.3:c.3367G>A, NM_138694.3:c.3229-2A>C, NM_138694.3:c.2854G>A, NM_138694.3:c.2827_2828delGA, NM_138694.3:c.2452C>T, NM_138694.3:c.2414C>T, NM_138694.3:c.2341C>T, NM_138694.3:c.1486C>T, NM_138694.3:c.982C>T, NM_138694.3:c.930delC, NM_138694.3:c.682A>G, NM_138694.3:c.664A>G, NM_138694.3:c.370C>T, NM_138694.3:c.353delG, NM_138694.3:c.107C>T, NM_138694.3:c.85G>T	Polycystic kidney disease type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PKHD1 gene located on chromosomal region 6p12.3-p12.2. The age of onset is early. This disease is a severe form of polycystic kidney disease affecting the kidneys and, in some cases, the hepatic biliary tract. Up to 50% of the affected neonates die shortly after birth, as a result of severe pulmonary hypoplasia and secondary respiratory insufficiency. In the subset that survives the perinatal period, morbidity and mortality are mainly related to severe systemic hypertension, renal insufficiency, and portal hypertension due to portal-tract fibrosis.	600,25
PKLR	Pyruvate kinase deficiency	NM_000298.5	NM_000298.5:c.1675C>T, NM_000298.5:c.1529G>A, NM_000298.5:c.1528C>T, NM_000298.5:c.1456C>T, NM_000298.5:c.1436G>A, NM_000298.5:c.1261C>A, NM_000298.5:c.1151C>T, NM_000298.5:c.721G>T	Pyruvate kinase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PKLR gene located on chromosomal region 1q22. The age of onset is early. This disease is characterized by highly variable degree of chronic hemolysis, with severe neonatal jaundice and fatal anemia at birth, severe transfusion-dependent chronic hemolysis, and moderate hemolysis with exacerbation during infection. The prevalence is 1:20,000.	600,25
PLCE1	Nephrotic syndrome, type 3	NM_016341.3	NM_016341.3:c.961C>T, NM_016341.3:c.3346C>T, NM_016341.3:c.3736C>T, NM_016341.3:c.3846delG, NM_016341.3:c.4451C>T, NM_016341.3:c.4809delA, NM_016341.3:c.5560C>T	Nephrotic syndrome type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PLCE1 gene located on chromosomal region 10q23.33. The age of onset is variable. This disease is characterized by low blood protein levels, high cholesterol levels, high triglyceride levels, and presence of protein in the urine. The prevalence is 2:100,000-7:100,000 Children; 3:100,000 adults.	600,25
PLG	Plasminogen deficiency, type I	NM_000301.3	NM_000301.3:c.112A>G, NM_000301.3:c.693_695delGAA, NM_000301.3:c.704G>A, NM_000301.3:c.1120G>T, NM_000301.3:c.1435G>T, NM_000301.3:c.1848G>A	Plasminogen deficiency type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PLG gene located on chromosomal region 6q26. The age of onset is infantile.This disease is characterized by markedly impaired extracellular fibrinolysis leading to the formation of ligneous (fibrin-rich) pseudomembranes on mucosae during wound healing. The prevalence is 1:1,000,000-9:1,000,000.	600,25
PMM2	Congenital disorder of glycosylation, type 1a	NM_000303.2	NM_000303.2:c.26G>A, NM_000303.2:c.53C>G, NM_000303.2:c.95T>G, NM_000303.2:c.95_96delTAinsGC, NM_000303.2:c.97C>T, NM_000303.2:c.109C>T, NM_000303.2:c.131T>C, NM_000303.2:c.190delT, NM_000303.2:c.193G>T, NM_000303.2:c.255+2T>C, NM_000303.2:c.256-1G>C, NM_000303.2:c.323C>T, NM_000303.2:c.338C>T, NM_000303.2:c.349G>C, NM_000303.2:c.357C>A, NM_000303.2:c.368G>A, NM_000303.2:c.385G>A, NM_000303.2:c.395T>C, NM_000303.2:c.415G>A, NM_000303.2:c.422G>A, NM_000303.2:c.442G>A, NM_000303.2:c.470T>C, NM_000303.2:c.484C>T, NM_000303.2:c.563A>G, NM_000303.2:c.620T>C, NM_000303.2:c.623G>C, NM_000303.2:c.647A>T, NM_000303.2:c.652C>G, NM_000303.2:c.669C>G, NM_000303.2:c.677C>G, NM_000303.2:c.691G>A, NM_000303.2:c.710C>G, NM_000303.2:c.710C>T	Congenital disorder of glycosylation type 1a follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PMM2 gene located on chromosomal region 16p13.2. The age of onset is infantile. This disease is characterized by highly variable clinical manifestations that may include feeding problems, vomiting, and diarrhea with failure to thrive in infants, and severe encephalopathy with axial hypotonia, abnormal eye movement, marked psychomotor retardation, peripheral neuropathy, cerebellar hypoplasia, stroke-like episodes, and retinitis pigmentosa in late infancy, childhood or adulthood.	600,25
POLG	Mitochondrial DNA depletion syndrome 4A (Alpers type)	NM_001126131.1	NM_001126131.1:c.3644-1G>A, NM_001126131.1:c.3630dupC, NM_001126131.1:c.3286C>T, NM_001126131.1:c.3218C>T, NM_001126131.1:c.3151G>C, NM_001126131.1:c.2794C>T, NM_001126131.1:c.2617G>T, NM_001126131.1:c.2605C>T, NM_001126131.1:c.2591A>G, NM_001126131.1:c.2557C>T, NM_001126131.1:c.2542G>A, NM_001126131.1:c.2243G>C, NM_001126131.1:c.2209G>C, NM_001126131.1:c.1879C>T, NM_001126131.1:c.1760C>T, NM_001126131.1:c.1754G>A, NM_001126131.1:c.1437C>G, NM_001126131.1:c.1399G>A, NM_001126131.1:c.1120C>T, NM_001126131.1:c.911T>G, NM_001126131.1:c.752C>T	Mitochondrial DNA depletion syndrome, Alpers type follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the POLG gene located on chromosomal region 15q26.1. The age of onset is early. This disease is characterized by the clinical triad of psychomotor regression, seizures, and liver disease. The prevalence is 1:1,600 newborn.	600,25

POMGNT1	Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A, 3	NM_001243766.1	NM_001243766.1:c.1864delC, NM_001243766.1:c.1814G>C, NM_001243766.1:c.1545delC, NM_001243766.1:c.1539+1G>T, NM_001243766.1:c.1539+1G>A, NM_001243766.1:c.1469G>A, NM_001243766.1:c.1425G>A, NM_001243766.1:c.1411A>T, NM_001243766.1:c.1274G>C, NM_001243766.1:c.932G>A, NM_001243766.1:c.931C>T, NM_001243766.1:c.880-1G>A, NM_001243766.1:c.652+1G>A, NM_001243766.1:c.636C>T, NM_001243766.1:c.187C>T, NM_001243766.1:c.92dupA	Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies) type A3 which includes both the more severe Walker-Warburg syndrome (WWS) and the slightly less severe muscle-eye-brain disease (MEB), follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the POMGNT1 gene located on chromosomal region 1p34.1. The age of onset is infantile. This disease is characterized by generalized severe hypotonia, muscle weakness, absent psychomotor development, eye involvement and seizures. The prevalence is 1-9:100,000.	600,25
POMT1	Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A, 1	NM_007171.3	NM_007171.3:c.193G>A, NM_007171.3:c.226G>A, NM_007171.3:c.598G>C, NM_007171.3:c.793C>T, NM_007171.3:c.831C>G, NM_007171.3:c.907C>T, NM_007171.3:c.1153C>T, NM_007171.3:c.1242-2A>G, NM_007171.3:c.1261dupC, NM_007171.3:c.1280_1281delAGinsTC, NM_007171.3:c.1540C>T, NM_007171.3:c.1545C>G, NM_007171.3:c.1746G>C, NM_007171.3:c.1770G>C, NM_007171.3:c.2005G>A, NM_007171.3:c.2163C>A, NM_007171.3:c.2167dupG	Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the POMT1 gene located on chromosomal region 9q34.13. Congenital muscular dystrophy-dystroglycanopathy with brain and eye anomalies (type A), which includes both the more severe Walker-Warburg syndrome (WWS) and the slightly less severe muscle-eye-brain disease (MEB), is a genetically heterogeneous disorder with characteristic brain and eye malformations, profound mental retardation, congenital muscular dystrophy, and early death. The phenotype commonly includes cobblestone (type II) lissencephaly, cerebellar malformations, and retinal malformations.	600,25
POMT2	Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A, 2	NM_013382.5	NM_013382.5:c.2243G>C, NM_013382.5:c.2177G>A, NM_013382.5:c.1997A>G, NM_013382.5:c.1941G>A, NM_013382.5:c.1912C>T, NM_013382.5:c.1726-2A>G, NM_013382.5:c.1608_1609delCA, NM_013382.5:c.1445G>T, NM_013382.5:c.1417C>T, NM_013382.5:c.1057G>A, NM_013382.5:c.1045_1052delCGGATGGCinsG, NM_013382.5:c.551C>T	Muscular dystrophy-dystroglycanopathy (congenital with brain and eye anomalies), type A2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the POMT2 gene located on chromosomal region 14q24.3. Congenital muscular dystrophy-dystroglycanopathy with brain and eye anomalies (type A), which includes both the more severe Walker-Warburg syndrome (WWS) and the slightly less severe muscle-eye-brain disease (MEB), is a genetically heterogeneous disorder with characteristic brain and eye malformations, profound mental retardation, congenital muscular dystrophy, and early death. The phenotype commonly includes cobblestone (type II) lissencephaly, cerebellar malformations, and retinal malformations.	600,25
PPT1	Ceroid lipofuscinosis, neuronal, type 1	NM_000310.3	NM_000310.3:c.840dupA, NM_000310.3:c.627+1G>T, NM_000310.3:c.541G>T, NM_000310.3:c.451C>T, NM_000310.3:c.223A>C, NM_000310.3:c.169dupA, NM_000310.3:c.29T>A	Neuronal ceroid lipofuscinoses, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PPT1 gene located on chromosomal region 1p32. The age of onset is adult. This disease is characterized by dementia, seizures and loss of motor capacities, and sometimes associated with visual loss caused by retinal degeneration. The prevalence is 1.5:1,000,000-9:1,000,000.	600,25
PROM1	Retinitis pigmentosa, type 41	NM_006017.2	NM_006017.2:c.2490-2A>G, NM_006017.2:c.1841delG, NM_006017.2:c.1726C>T, NM_006017.2:c.1354dupT, NM_006017.2:c.1177_1178delAT, NM_006017.2:c.199C>T	Retinitis pigmentosa, type 41 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PROM1 gene located on chromosomal region 4p15.32. The age of onset is early. This disease is characterized by night blindness often in adolescence or earlier. They then develop peripheral visual field impairment, and overtime loss of central vision, usually at late stages, often around midlife. The prevalence is 19:100,000-27:100,000.	600,25
PYGM	McArdle disease	NM_005609.3	NM_005609.3:c.2392T>C, NM_005609.3:c.2262delA, NM_005609.3:c.2128_2130delTTC, NM_005609.3:c.1963G>A, NM_005609.3:c.1827G>A, NM_005609.3:c.1768+1G>A, NM_005609.3:c.1726C>T, NM_005609.3:c.1722T>G, NM_005609.3:c.1628A>C, NM_005609.3:c.1621G>T, NM_005609.3:c.1466C>G, NM_005609.3:c.613G>A, NM_005609.3:c.501dupT, NM_005609.3:c.393delG, NM_005609.3:c.280C>T, NM_005609.3:c.255C>A, NM_005609.3:c.148C>T, NM_005609.3:c.13_14delCT, NM_005609.3:c.1A>G	McArdle disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PYGM gene located on chromosomal region 11q13.1. The age of onset is infantile. This disease is characterized by muscular exercise intolerance with myalgia, cramps, fatigue, and muscle weakness.	600,25

RAG1	Omenn syndrome; Severe combined immunodeficiency, B cell-negative	NM_000448.2	NM_000448.2:c.256_257delAA, NM_000448.2:c.940C>T, NM_000448.2:c.983G>A, NM_000448.2:c.1681C>T, NM_000448.2:c.1682G>A, NM_000448.2:c.2164G>A, NM_000448.2:c.2320G>T, NM_000448.2:c.2326C>T, NM_000448.2:c.2333G>A, NM_000448.2:c.2814T>G, NM_000448.2:c.2923C>T	Omenn syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RAG1 and RAG2 genes located on chromosomal region 11p12. The age of onset is early. This disease is characterized by erythroderma, desquamation, alopecia, chronic diarrhea, failure to thrive, lymphadenopathy, and hepatosplenomegaly, associated with severe combined immunodeficiency. Severe combined immunodeficiency, autosomal recessive, T cell-negative (T-), B cell negative (B-), NK cell positive (NK+) is also caused by mutation in the RAG1 and RAG2 genes. This disease is characterized by impairment of both humoral and cell-mediated immunity, leukopenia, and low or absent antibody levels. Patients present in infancy recurrent, persistent infections by opportunistic organisms. The common characteristic of all types of SCID is absence of T-cell-mediated cellular immunity due to a defect in T-cell development. Without treatment, patients usually die within the first year of life.	600,25
RAPSN	Fetal akinesia deformation sequence	NM_005055.4	NM_005055.4:c.848T>C, NM_005055.4:c.807C>A, NM_005055.4:c.566C>T, NM_005055.4:c.490C>T, NM_005055.4:c.484G>A, NM_005055.4:c.416T>C, NM_005055.4:c.264C>A	Fetal akinesia deformation sequence follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RAPSN gene located on chromosomal region 11p11.2. The age of onset is early. This disease is characterized by multiple joint contractures, facial anomalies and pulmonary hypoplasia. The prevalence is 1:3,000.	600,25
RAX	Isolated microphthalmia, type 3	NM_013435.2	NM_013435.2:c.909C>G, NM_013435.2:c.439C>T, NM_013435.2:c.383_384delAG, NM_013435.2:c.18C>A	Isolated microphthalmia type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RAX gene located on chromosomal region 18q21.32. Microphthalmia designates a heterogeneous group of ocular malformations with a more or less evident reduction in the size of the eyeball. Additional features include high hypermetropia and a short axial length.	600,25
RDH12	Leber congenital amaurosis, type 13	NM_152443.2	NM_152443.2:c.146C>T, NM_152443.2:c.152T>A, NM_152443.2:c.184C>T, NM_152443.2:c.210dupC, NM_152443.2:c.295C>A, NM_152443.2:c.377C>T, NM_152443.2:c.379G>T, NM_152443.2:c.451C>A, NM_152443.2:c.451C>G, NM_152443.2:c.464C>T, NM_152443.2:c.523T>C, NM_152443.2:c.565C>T, NM_152443.2:c.677A>G, NM_152443.2:c.806_810delCCCTG	Leber congenital amaurosis type 13 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RDH12 gene located on chromosomal region 14q24.1. The age of onset is early. This disease is characterized by blindness, nystagmus, roving eye movement and lack of detectable signals on an electroretinogram, leading to severe visual impairment within the first year of life.	600,25
RGR	Retinitis pigmentosa, type 44	NM_002921.3	NM_002921.3:c.262_269dupGGCTCGGA, NM_002921.3:c.273_274insGGCTCGGA, NM_002921.3:c.877C>T	Retinitis pigmentosa type 44 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RGR gene located on chromosomal region 10q23.1. The age of onset is variable. This disease is characterized by night blindness (nyctalopia) due to loss of rod function, often in adolescence or earlier. They then develop peripheral visual field impairment, and overtime loss of central vision, usually at late stages, often around midlife. The prevalence is 1:10,000-5:10,000.	600,25
RHO	Retinitis pigmentosa, type 4, autosomal recessive	NM_000539.3	NM_000539.3:c.173C>T, NM_000539.3:c.448G>A, NM_000539.3:c.620T>G, NM_000539.3:c.745G>T	Retinitis pigmentosa type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RHO gene located on chromosomal region 3q22.1. The age of onset is variable. This disease is characterized by night blindness (nyctalopia) due to loss of rod function, often in adolescence or earlier. They then develop peripheral visual field impairment, and overtime loss of central vision, usually at late stages, often around midlife. The prevalence is 1:10,000-5:10,000.	600,25
RLBP1	Bothnia retinal dystrophy	NM_000326.4	NM_000326.4:c.700C>T, NM_000326.4:c.452G>A, NM_000326.4:c.333T>G	Bothnia retinal dystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RLBP1 gene located on chromosomal region 15q26.1. This disease is characterized by night blindness from early childhood with features consistent with retinitis punctata albescens and macular degeneration. The prevalence is unknown.	600,25

RPE65	Leber congenital amaurosis, type 2	NM_000329.2	NM_000329.2:c.1543C>T, NM_000329.2:c.1355T>G, NM_000329.2:c.1292A>G, NM_000329.2:c.1102T>C, NM_000329.2:c.1087C>A, NM_000329.2:c.1067delA, NM_000329.2:c.1022T>C, NM_000329.2:c.907A>T, NM_000329.2:c.514_515delGT, NM_000329.2:c.271C>T	Leber congenital amaurosis 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RPE65 gene located on chromosomal region 1p31.3-p31.2. The age of onset is variable. This disease is characterized by a severe dystrophy of the retina, typically becoming evident in the first years of life. Visual function is usually poor and often accompanied by nystagmus, sluggish or near-absent pupillary responses, photophobia, high hyperopia and keratoconus.	600,25
RPGRIP1L	Joubert syndrome, type 7; Meckel syndrome, type 5; COACH syndrome	NM_015272.4	NM_015272.4:c.3634_3637delGAAA, NM_015272.4:c.2794_2795delTT, NM_015272.4:c.2614C>T, NM_015272.4:c.2413C>T, NM_015272.4:c.2050C>T, NM_015272.4:c.1975T>C, NM_015272.4:c.1843A>C, NM_015272.4:c.1329dupA, NM_015272.4:c.1326_1329delAAAA, NM_015272.4:c.776+1G>A, NM_015272.4:c.757C>T, NM_015272.4:c.697A>T, NM_015272.4:c.394A>T	Joubert syndrome (JBTS) type 7 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RPGRIP1L gene located on chromosomal region 16q12.2. The age of onset is early. JBTS is characterized by congenital malformation of the brainstem and agenesis of the cerebellar vermis (molar tooth sign) leading to an abnormal respiratory pattern, nystagmus, hypotonia, mental retardation, ataxia, and delay in achieving motor milestones. Other variable features include retinal dystrophy (less common in JBTS7) and nephronophthisis (usually juvenile). The prevalence is 1:100,000. RPGRIP1L gene is also associated with Meckel syndrome type 5, a rare, autosomal recessive lethal condition characterized by central nervous system malformations, postaxial, polydactyly, multicystic kidney dysplasia, and ductal proliferation in the portal area of the liver. Other phenotype associated is COACH syndrome, an autosomal recessive disorder characterized by mental retardation, ataxia due to cerebellar hypoplasia, and hepatic fibrosis. Other features, such as coloboma and renal cysts, may be variable. COACH syndrome is considered by some to be a subtype of Joubert syndrome with congenital hepatic fibrosis.	600,25
RYR1	Minicore myopathy with external ophthalmoplegia	NM_000540.2	NM_000540.2:c.325C>T, NM_000540.2:c.487C>T, NM_000540.2:c.631+2T>C, NM_000540.2:c.738T>G, NM_000540.2:c.1021G>A, NM_000540.2:c.1186G>T, NM_000540.2:c.1205T>C, NM_000540.2:c.1739_1742dupATCA, NM_000540.2:c.1841G>T, NM_000540.2:c.4076delG, NM_000540.2:c.4405C>T, NM_000540.2:c.5333C>A, NM_000540.2:c.5726_5727delAG, NM_000540.2:c.6082C>T, NM_000540.2:c.6104A>T, NM_000540.2:c.6721C>T, NM_000540.2:c.7268T>A, NM_000540.2:c.7300G>A, NM_000540.2:c.7360C>T, NM_000540.2:c.7373G>A, NM_000540.2:c.7463_7475delCAAAGATGTCAGC, NM_000540.2:c.7781C>A, NM_000540.2:c.7836-1G>A, NM_000540.2:c.9000+1G>T, NM_000540.2:c.9905dupC, NM_000540.2:c.10343C>T, NM_000540.2:c.10579C>T, NM_000540.2:c.13480G>T, NM_000540.2:c.14126C>T, NM_000540.2:c.14365-2A>T, NM_000540.2:c.14545G>A	Multiminicore disease (MMD) is an inherited neuromuscular disorder defined pathologically by the presence of multiple areas of reduced mitochondrial oxidative activity running along a limited extent of the longitudinal axis of the muscle fiber, so-called 'minicores.' These regions show sarcomere disorganization and mitochondria depletion. Typically, no dystrophic signs, such as muscle fiber necrosis or regeneration or significant endomysial fibrosis, are present. MMD is a pathologic diagnosis and shows clinical and genetic heterogeneity. Affected individuals have clinical features of a congenital myopathy, including neonatal hypotonia, delayed motor development, and generalized muscle weakness and amyotrophy, which may progress slowly or remain stable (Ferreiro and Fardeau, 2002).Patients with recessive mutations in the RYR1 gene typically show severe congenital muscular dystrophy with ophthalmoplegia, although there is phenotypic variability. Some patients may present in utero with fetal akinesia, arthrogryposis, and lung hypoplasia resulting in fetal or perinatal death (McKie et al., 2014). Skeletal muscle biopsy of patients with recessive RYR1 mutations show variable features, including central cores (Jungbluth et al., 2007), congenital fiber-type disproportion (CFTD) (Monnier et al., 2009), and centronuclear myopathy (Wilmshurst et al., 2010).	600,25
SACS	Spastic ataxia, Charlevoix-Saguenay, type	NM_014363.5	NM_014363.5:c.13237C>T, NM_014363.5:c.12160C>T, NM_014363.5:c.8844delT, NM_014363.5:c.7504C>T, NM_014363.5:c.6563T>A, NM_014363.5:c.6355C>T, NM_014363.5:c.5618_5619delAT, NM_014363.5:c.4933C>T, NM_014363.5:c.3198T>A, NM_014363.5:c.994A>T, NM_014363.5:c.517C>T	Spastic ataxia, Charlevoix-Saguenay type follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SACS gene located on chromosomal region 13q11. The age of onset is early. This disease is characterized by early-onset cerebellar ataxia with spasticity, a pyramidal syndrome and peripheral neuropathy. The prevalence is 1:1,500-1:2,000.	600,25

SAG	Oguchi disease, type 1	NM_000541.4	NM_000541.4:c.298dupG, NM_000541.4:c.523C>T, NM_000541.4:c.577C>T, NM_000541.4:c.874C>T, NM_000541.4:c.916G>T, NM_000541.4:c.926delA, NM_000541.4:c.993C>G	Oguchi disease type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SAG gene located on chromosomal region 2q37. The age of onset is infantile. This disease is characterized by congenital stationary night blindness and the Mizuo-Nakamura phenomenon which is a unique morphological and functional abnormality of the retina that presents with a typical golden-yellow or silver-gray discoloration of the fundus in the presence of light that disappears after dark-adaptation and appears again after the onset of light.	600,25
SBDS	Shwachman-Diamond syndrome	NM_016038.2	NM_016038.2:c.377G>C, NM_016038.2:c.258+2T>C, NM_016038.2:c.184A>T, NM_016038.2:c.183_184delTAinsCT, NM_016038.2:c.120delG	Shwachman-Diamond syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SBDS gene located on chromosomal region 7q11.21. The age of onset is infantile. This disease is characterized by chronic and usually mild neutropenia, pancreatic exocrine insufficiency associated with steatorrhea and growth failure, skeletal dysplasia with short stature, and an increased risk of bone marrow aplasia or leukemic transformation, cutaneous (eczema or ichthyosis) and dental anomalies, and psychomotor retardation. The prevalence is 1:76,000 newborn.	600,25
SCNN1B	Pseudohypoaldosteronism, type 1	NM_000336.2	NM_000336.2:c.109G>A	Pseudohypoaldosteronism type 1, follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SCNN1A (12p13), SCNN1B (16p12.2-p12.1) and SCNN1G (16p12) genes. The age of onset is early. This disease is characterized by severe dehydration, vomiting and failure to thrive occurring in the first weeks of life, the clinical picture may be complicated by cardiac dysrhythmias, collapse, shock or cardiac arrest.	600,25
SCNN1G	Pseudohypoaldosteronism, type 1	NM_001039.3	NM_001039.3:c.600dupA, NM_001039.3:c.1373+2T>C, NM_001039.3:c.1570-1G>A, NM_001039.3:c.1627delG	Pseudohypoaldosteronism type 1, follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SCNN1A (12p13), SCNN1B (16p12.2-p12.1) and SCNN1G (16p12) genes. The age of onset is early. This disease is characterized by severe dehydration, vomiting and failure to thrive occurring in the first weeks of life, the clinical picture may be complicated by cardiac dysrhythmias, collapse, shock or cardiac arrest.	600,25
SETX	Spinocerebellar ataxia, autosomal recessive, type 1	NM_015046.5	NM_015046.5:c.6848_6851delCAGA, NM_015046.5:c.6834_6839delAACAAA, NM_015046.5:c.5927T>G, NM_015046.5:c.5630delG, NM_015046.5:c.5549-1G>T, NM_015046.5:c.5308_5311delGAGA, NM_015046.5:c.4087C>T, NM_015046.5:c.2602C>T, NM_015046.5:c.1166T>C, NM_015046.5:c.1027G>T, NM_015046.5:c.994C>T	Spinocerebellar ataxia with axonal neuropathy type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SETX gene located on chromosomal region 9q34.13. The age of onset is infantile. This disease is characterized by progressive cerebellar ataxia, axonal sensorimotor neuropathy with oculomotor apraxia, fixation instability, extrapyramidal features and an elevated serum alpha-fetoprotein level. The prevalence is 4:100,000-8:100,000.	600,25
SGCA	Muscular dystrophy, limb-girdle, type 2D	NM_000023.3	NM_000023.3:c.101G>A, NM_000023.3:c.229C>T, NM_000023.3:c.371T>C, NM_000023.3:c.518T>C, NM_000023.3:c.574C>T, NM_000023.3:c.739G>A, NM_000023.3:c.850C>T, NM_000023.3:c.903_904dupCC	Autosomal recessive limb-girdle muscular dystrophy type 2D follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SGCA gene located on chromosomal region 4q12. The age of onset is variable. This disease is characterized by limb-girdle weakness and calf pseudohypertrophy. The prevalence is 1:1,000,000-9:1,000,000.	600,25
SGCG	Muscular dystrophy, limb-girdle, type 2C	NM_000231.2	NM_000231.2:c.89delG, NM_000231.2:c.195+4_195+7delAGTA, NM_000231.2:c.505+1G>A, NM_000231.2:c.525delT, NM_000231.2:c.787G>A, NM_000231.2:c.848G>A	Autosomal recessive limb-girdle muscular dystrophy type 2C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SGCG gene located on chromosomal region 13q12.12. The age of onset is variable. This disease is characterized by limb-girdle weakness, calf hypertrophy, diaphragmatic weakness, and variable cardiac abnormalities.	600,25
SGSH	Mucopolysaccharidosis, type 3A (Sanfilippo A)	NM_000199.3	NM_000199.3:c.1380delT, NM_000199.3:c.1339G>A, NM_000199.3:c.1298G>A, NM_000199.3:c.1167C>A, NM_000199.3:c.892T>C, NM_000199.3:c.877C>T, NM_000199.3:c.757delG, NM_000199.3:c.617G>C, NM_000199.3:c.466A>T, NM_000199.3:c.449G>A, NM_000199.3:c.383C>T, NM_000199.3:c.364G>A, NM_000199.3:c.337_345delCAAGCTGGTinsGCACAGGTGAG, NM_000199.3:c.320delT, NM_000199.3:c.235A>C, NM_000199.3:c.220C>T, NM_000199.3:c.197C>G, NM_000199.3:c.130G>A	Mucopolysaccharidosis type 3A (Sanfilippo syndrome type A) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SGSH gene located on chromosomal region 17q25.3. The age of onset is infantile. This disease is characterized by behavioural disorders (hyperkinesia, aggressiveness) and intellectual deterioration, sleep disorders and very mild dysmorphism. The prevalence is >1:70,000 newborn.	600,25

SH3TC2	Charcot-Marie-Tooth disease, type 4C	NM_024577.3	NM_024577.3:c.3676-1G>A, NM_024577.3:c.3601C>T, NM_024577.3:c.3341delC, NM_024577.3:c.3326G>C, NM_024577.3:c.3325C>T, NM_024577.3:c.2993_2994insC, NM_024577.3:c.2860C>T, NM_024577.3:c.2829T>G, NM_024577.3:c.2710C>T, NM_024577.3:c.2491_2492delAG, NM_024577.3:c.2191delG, NM_024577.3:c.1982T>C, NM_024577.3:c.1972C>T, NM_024577.3:c.1969G>A, NM_024577.3:c.1747_1748delAG, NM_024577.3:c.1724T>A, NM_024577.3:c.1586G>A, NM_024577.3:c.920G>A, NM_024577.3:c.735G>A, NM_024577.3:c.530-2A>G, NM_024577.3:c.217_227delGCTGCTCGGAGinsCCAGTAA, NM_024577.3:c.53-1G>C, NM_024577.3:c.52+1delG, NM_024577.3:c.28delG	Charcot-Marie-Tooth disease, type 4C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SH3TC2 gene located on chromosomal region 5q32. The age of onset is infantile. This disease is characterized by scoliosis or kyphoscoliosis, neuropathy, foot deformities, respiratory insufficiency, hypoacousis and deafness.	600,25
SLC12A1	Bartter syndrome, type 1	NM_000338.2	NM_000338.2:c.223C>T, NM_000338.2:c.628+2T>C, NM_000338.2:c.814G>T, NM_000338.2:c.1875G>A, NM_000338.2:c.1942G>A, NM_000338.2:c.2805dupA, NM_000338.2:c.2952_2955delCAAA	Bartter syndrome type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC12A1 gene located on chromosomal region 15q15-21. The age of onset is infantile. This disease is characterized by polyhydramnios, premature delivery, polyuria, dehydration, hypercalciuria and nephrocalcinosis. The prevalence is 1:1,000,000.	600,25
SLC17A5	Salla disease	NM_012434.4	NM_012434.4:c.1259+1G>A, NM_012434.4:c.406A>G, NM_012434.4:c.115C>T, NM_012434.4:c.43G>T	Salla disease follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC17A5 gene located on chromosomal region 6q13. The age of onset is from infantile to adult forms. The main symptoms are hypotonia, cerebellar ataxia, and mental retardation; visceromegaly and coarse features are also present in the infantile cases.	600,25
SLC26A2	Achondrogenesis, type 1B (diastrophic dysplasia)	NM_000112.3	NM_000112.3:c.496G>A, NM_000112.3:c.532C>T, NM_000112.3:c.833delC, NM_000112.3:c.835C>T, NM_000112.3:c.1020_1022delTGT, NM_000112.3:c.1273A>G, NM_000112.3:c.1361A>C, NM_000112.3:c.1535C>A, NM_000112.3:c.1724delA, NM_000112.3:c.1878delG, NM_000112.3:c.1957T>A, NM_000112.3:c.2033G>T	Achondrogenesis type 1B (diastrophic dysplasia) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC26A2 gene located on chromosomal region 5q32. The age of onset is early. This disease is characterized by severe micromelia with very short fingers and toes, a flat face, a short neck, thickened soft tissue around the neck, hypoplasia of the thorax, protuberant abdomen, a hydropic fetal appearance and distinctive histological features of the cartilage. The prevalence is 1:20,000.	600,25
SLC26A4	Deafness, autosomal recessive, type 4	NM_000441.1	NM_000441.1:c.269C>T, NM_000441.1:c.281C>T, NM_000441.1:c.412G>T, NM_000441.1:c.554G>C, NM_000441.1:c.563T>C, NM_000441.1:c.626G>T, NM_000441.1:c.707T>C, NM_000441.1:c.916dupG, NM_000441.1:c.918+2T>C, NM_000441.1:c.919-2A>G, NM_000441.1:c.961A>T, NM_000441.1:c.1001G>T, NM_000441.1:c.1001+1G>T, NM_000441.1:c.1003T>C, NM_000441.1:c.1034T>A, NM_000441.1:c.1151A>G, NM_000441.1:c.1174A>T, NM_000441.1:c.1198delT, NM_000441.1:c.1226G>A, NM_000441.1:c.1229C>T, NM_000441.1:c.1246A>C, NM_000441.1:c.1263+1G>A, NM_000441.1:c.1334T>G, NM_000441.1:c.1489G>A, NM_000441.1:c.1707+5G>A, NM_000441.1:c.1975G>C, NM_000441.1:c.2048T>C, NM_000441.1:c.2162C>T, NM_000441.1:c.2168A>G	Autosomal recessive nonsyndromic sensorineural deafness type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC26A4 gene located on chromosomal region 7q22.3. The age of onset is early. This disease is characterized by hearing loss and deafness, no associated visible abnormalities of the external ear or any related medical problems.	600,25
SLC37A4	Glycogen storage disease, type 1b	NM_001164278.1	NM_001164278.1:c.1309C>T, NM_001164278.1:c.1190-2_1190-1delAG, NM_001164278.1:c.1129G>T, NM_001164278.1:c.1108_1109delCT, NM_001164278.1:c.1082G>A, NM_001164278.1:c.1081G>T, NM_001164278.1:c.706_708delGTG, NM_001164278.1:c.352T>C, NM_001164278.1:c.287G>A, NM_001164278.1:c.83G>A	Glycogen storage disease due to glucose-6-phosphatase deficiency type 1b follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC37A4 gene located on chromosomal region 11q23. The age of onset is early. This disease is characterized by impairment of terminal steps of glycogenolysis and gluconeogenesis. Patients manifest a wide range of clinical symptoms and biochemical abnormalities, including hypoglycemia, severe hepatomegaly due to excessive accumulation of glycogen, kidney enlargement, growth retardation, lactic acidemia, hyperlipidemia, and hyperuricemia. Glycogen storage disease type 1B patients also present a tendency towards infections associated with neutropenia, relapsing aphthous gingivostomatitis, and inflammatory bowel disease. The incidence is 1:100,000.	600,25

SLC4A11	Corneal endothelial dystrophy, autosomal recessive	NM_001174090.1	NM_001174090.1:c.2687G>A, NM_001174090.1:c.2686C>T, NM_001174090.1:c.2647A>G, NM_001174090.1:c.2609T>C, NM_001174090.1:c.2345G>A, NM_001174090.1:c.2314_2321dupTATGACAC, NM_001174090.1:c.2305G>A, NM_001174090.1:c.1894C>T, NM_001174090.1:c.1547C>T, NM_001174090.1:c.1544G>A, NM_001174090.1:c.1472G>A, NM_001174090.1:c.1119_1120insA, NM_001174090.1:c.718T>C, NM_001174090.1:c.554_561delGCTTCGCC	Congenital hereditary endothelial dystrophy type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC4A11 gene located on chromosomal region 20p13. The age of onset is early. This disease is characterized by a diffuse ground-glass appearance of the corneas and marked corneal thickening from birth with nystagmus, and blurred vision.	600,25
SMN1	Spinal muscular atrophy	0	del ex7, del ex7-8	Spinal muscular atrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SMN1 gene located on chromosomal region 5q13.2. The age of onset is variable. This disease comprise a group of neuromuscular disorders characterized by degeneration of the anterior horn cells of the spinal cord, leading to symmetrical muscle weakness and atrophy. Autosomal recessive forms are classified according to the age of onset, the maximum muscular activity achieved, and survivorship. The severity of the disease is mainly determined by the copy number of SMN2, a copy gene which predominantly produces exon 7-skipped transcripts and only low amount of full-length transcripts that encode for a protein identical to SMN1. Only about 4% of patients bear one SMN1 copy with an intragenic mutation. Type 1 is a severe form, with onset before 6 months of age. Patients never achieve the ability to sit. Type 2 has intermediate severity, with onset between 6 and 18 months. Patients do not reach the motor milestone of standing, and survive into adulthood. Type 3 onset is after 18 months. Patients develop ability to stand and walk and survive into adulthood. Type 4 onset is in adulthood, disease progression is slow, and patients can stand and walk. The incidence is 1:10,000 and the prevalence is 1:80,000.	600,25
SMPD1	Niemann-Pick disease, type A and type B	NM_000543.4	NM_000543.4:c.96G>A, NM_000543.4:c.103_107delCTGGT, NM_000543.4:c.106delG, NM_000543.4:c.354delC, NM_000543.4:c.475T>C, NM_000543.4:c.557C>T, NM_000543.4:c.564delC, NM_000543.4:c.564dupC, NM_000543.4:c.573delT, NM_000543.4:c.688C>T, NM_000543.4:c.730G>A, NM_000543.4:c.740delG, NM_000543.4:c.739G>A, NM_000543.4:c.742G>A, NM_000543.4:c.757G>C, NM_000543.4:c.788T>A, NM_000543.4:c.842_849dupTCCCCGCA, NM_000543.4:c.911T>C, NM_000543.4:c.996delC, NM_000543.4:c.1092-1G>C, NM_000543.4:c.1117C>T, NM_000543.4:c.1152G>A, NM_000543.4:c.1264-1G>T, NM_000543.4:c.1267C>T, NM_000543.4:c.1299T>G, NM_000543.4:c.1327C>T, NM_000543.4:c.1420_1421delCT, NM_000543.4:c.1426C>T, NM_000543.4:c.1624C>T, NM_000543.4:c.1630delA, NM_000543.4:c.1805G>A, NM_000543.4:c.1829_1831delGCC	Niemann-Pick disease, type A and type B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SMPD1 gene located on chromosomal region 11p15.4. The clinical phenotype ranges from a severe infantile form with neurologic degeneration resulting in death usually by 3 years of age (type A) to a later-onset nonneurologic form (type B) that is compatible with survival into adulthood. Since intermediate cases also have been reported, the disease is best regarded a single entity with a clinical spectrum.	600,25
SPG11	Amyotrophic lateral sclerosis, type 5, juvenile	NM_025137.3	NM_025137.3:c.7152-1G>C, NM_025137.3:c.6847_6848dupTC, NM_025137.3:c.6805_6806delCT, NM_025137.3:c.6100C>T, NM_025137.3:c.5623C>T, NM_025137.3:c.1736-1G>C, NM_025137.3:c.1339_1342dupGGCT, NM_025137.3:c.733_734delAT, NM_025137.3:c.529_533delATATT, NM_025137.3:c.342delT, NM_025137.3:c.118C>T	Amyotrophic lateral sclerosis, type 5, juvenile follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SPG11 gene located on chromosomal region 15q21.1. The age of onset is infancy/childhood. This disease is characterized by progressive upper and lower motor neuron degeneration causing facial spasticity, dysarthria, and gait disorders with onset before 25 years of age. The prevalence is <1/1,000,000.	600,25
SPG7	Spastic paraplegia, type 7, autosomal recessive	NM_003119.3	NM_003119.3:c.233T>A, NM_003119.3:c.286+1G>T, NM_003119.3:c.679C>T, NM_003119.3:c.758+2T>C, NM_003119.3:c.773_774delTG, NM_003119.3:c.1045G>A, NM_003119.3:c.1124delG, NM_003119.3:c.1529C>T, NM_003119.3:c.1676delA, NM_003119.3:c.1749G>C, NM_003119.3:c.2075G>C	Spastic paraplegia type 7 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SPG7 gene located on chromosomal region 16q24.3. The age of onset is adult. This disease is characterized by by progressive muscle stiffness (spasticity) and the development of paralysis of the lower limbs (paraplegia) due to degeneration of corticospinal axons. The prevalence is 1:100,000-9:100,000.	600,25
STRC	Deafness, autosomal recessive, type 16	NM_153700.2	NM_153700.2:c.5188C>T, NM_153700.2:c.5185C>T, NM_153700.2:c.5168_5171delTTCT, NM_153700.2:c.4560dupC, NM_153700.2:c.4545+1G>C, NM_153700.2:c.3556C>T	Autosomal recessive nonsyndromic sensorineural deafness type DFNB16 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the STRC gene located on chromosomal region 15q15.3. The age of onset is early. This disease is characterized by hearing loss and deafness, no associated visible abnormalities of the external ear or any related medical problems.	600,25

TCAP	Muscular dystrophy, limb-girdle, type 2G	NM_003673.3	NM_003673.3:c.157C>T	Autosomal recessive limb-girdle muscular dystrophy type 2G follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TCAP gene located on chromosomal region 17q12. The age of onset is variable. This disease is characterized by muscle weakness in the four limbs, mild scapular winging, severe atrophy of the quadriceps and anterior tibialis muscles, calf hypertrophy, and lack of respiratory and cardiac involvement.	600,25
TCIRG1	Osteopetrosis, autosomal recessive, type 1	NM_006019.3	NM_006019.3:c.115_116delGA, NM_006019.3:c.1213G>A, NM_006019.3:c.1331G>T, NM_006019.3:c.1674-1G>A, NM_006019.3:c.2236+1G>A	Autosomal recessive osteopetrosis type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TCIRG1 gene located on chromosomal region 11q13.2. The age of onset is early. This disease is characterized by bone marrow failure, fractures and visual impairment. The incidence is 1:200.000 live births and the prevalence is 1:250,000.	600,25
TERT	Dyskeratosis congenita, autosomal recessive, type 4	NM_198253.2	NM_198253.2:c.2701C>T, NM_198253.2:c.2431C>T	Dyskeratosis congenita, autosomal recessive follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TERT gene located on chromosomal region 5p15.33. The age of onset is early. This disease has a wide phenotypic spectrum and age onset. It usually manifests during childhood with the triad of dysplastic nails, lacy reticular pigmentation and atrophy of the skin at the level of the neck and upper chest, and oral leukoplakia. Patients show an increased risk for progressive bone marrow failure and may develop myelodysplastic syndrome or acute myelogenous leukemia at any age (the risk increasing with age). There is also an increased risk for solid tumors, typically squamous cell carcinoma of head and neck (see this term) or anogenital cancer. Various additional clinical findings have been reported and may include: developmental delay, short stature, microcephaly, blepharitis, epiphora, periodontal disease, taurodontism, decreased teeth/root ratio, esophageal stenosis, liver disease, urethral stenosis, osteoporosis, avascular necrosis of femur and/or humerus, premature hair greying/alopecia, or abnormal eyelashes. Individuals with DC are at high risk of pulmonary fibrosis. The prevalence is 1:1,000,000.	600,25
TFR2	Hemochromatosis, type 3	NM_001206855.1	NM_001206855.1:c.2T>A	Hemochromatosis type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TFR2 gene located on chromosomal region 7q22.1. The age of onset is adult. This disease is characterized by excessive tissue iron deposition of genetic origin, liver disease, hypogonadism, arthritis, diabetes and skin pigmentation. The prevalence is <1:1,000,000.	600,25
TFR2	Hemochromatosis, type 3	NM_003227.3	NM_003227.3:c.2374G>A, NM_003227.3:c.2343G>A, NM_003227.3:c.2014C>T, NM_003227.3:c.1861_1872delGCCGTGGCCCAG, NM_003227.3:c.1665delC, NM_003227.3:c.1632_1633delGA, NM_003227.3:c.1473+1G>A, NM_003227.3:c.1469T>G, NM_003227.3:c.1330G>A, NM_003227.3:c.1235_1237delACA, NM_003227.3:c.1186C>T, NM_003227.3:c.949C>T, NM_003227.3:c.750C>G, NM_003227.3:c.313C>T	Hemochromatosis type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TFR2 gene located on chromosomal region 7q22.1. The age of onset is adult. This disease is characterized by excessive tissue iron deposition of genetic origin, liver disease, hypogonadism, arthritis, diabetes and skin pigmentation. The prevalence is <1:1,000,000.	600,25
TK2	Mitochondrial DNA depletion syndrome , type 2 (myopathic type)	NM_004614.4	NM_004614.4:c.635T>A, NM_004614.4:c.604_606delAAG, NM_004614.4:c.500G>A, NM_004614.4:c.373C>T, NM_004614.4:c.361C>A, NM_004614.4:c.323C>T, NM_004614.4:c.268C>T, NM_004614.4:c.159C>G	Mitochondrial DNA depletion syndrome type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TK2 gene located on chromosomal region 16q21. The age of onset is infantile. This disease is characterized by generalized hypotonia, proximal muscle weakness, loss of previously acquired motor skills, poor feeding, and respiratory difficulties leading to respiratory failure and death within a few years after diagnosis. The prevalence is 1.2:100,000.	600,25

TMEM67	Joubert syndrome, type 6; Meckel syndrome, type 3; COACH syndrome	NM_153704.5	NM_153704.5:c.130C>T, NM_153704.5:c.148_149insTAAT, NM_153704.5:c.622A>T, NM_153704.5:c.755T>C, NM_153704.5:c.1046T>C, NM_153704.5:c.1538A>G, NM_153704.5:c.1769T>C, NM_153704.5:c.2498T>C	Joubert syndrome (JBTS) type 6 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TMEM67 gene located on chromosomal region 8q22.1. The age of onset is early. JBTS is characterized by congenital malformation of the brainstem and agenesis of the cerebellar vermis (molar tooth sign) leading to an abnormal respiratory pattern, nystagmus, hypotonia, mental retardation, ataxia, and delay in achieving motor milestones. Other variable features include retinal dystrophy (manifesting with either Leber congenital amaurosis or progressive retinal dystrophy) and nephronophthisis (usually juvenile). The prevalence is 1:100,000. The TMEM67 gene is also associated with Meckel syndrome type 3, a rare, autosomal recessive lethal condition characterized by central nervous system malformations, postaxial, polydactyly, multicystic kidney dysplasia, and ductal proliferation in the portal area of the liver. Other phenotype associated with mutations in the TMEM67 gene is COACH syndrome, an autosomal recessive disorder characterized by mental retardation, ataxia due to cerebellar hypoplasia, and hepatic fibrosis. Other features, such as coloboma and renal cysts, may be variable. COACH syndrome is considered by some to be a subtype of Joubert syndrome with congenital hepatic fibrosis.	600,25
TMPRSS3	Deafness, autosomal recessive, type 8/10	NM_024022.2	NM_024022.2:c.1276G>A, NM_024022.2:c.1211C>T, NM_024022.2:c.753G>C, NM_024022.2:c.647G>T, NM_024022.2:c.446+1G>T, NM_024022.2:c.413C>A, NM_024022.2:c.242C>G, NM_024022.2:c.208delC	Autosomal recessive nonsyndromic sensorineural deafness type DFNB10 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TMPRSS3 gene located on chromosomal region 21q22.3. The age of onset is early. This disease is characterized by hearing loss and deafness.	600,25
TPP1	Ceroid lipofuscinosis, neuronal, type 2	NM_000391.3	NM_000391.3:c.1340G>A, NM_000391.3:c.1093T>C, NM_000391.3:c.851G>T, NM_000391.3:c.827A>T, NM_000391.3:c.622C>T, NM_000391.3:c.616C>T, NM_000391.3:c.509-1G>C, NM_000391.3:c.141_144delGAGT	Neuronal ceroid lipofuscinosis type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TPP1 gene located on chromosomal region 11p15.4. Age of onset is infantile. This disease is characterized by epilepsy, followed by regression of developmental milestones, myoclonic ataxia, and pyramidal signs. Visual impairment typically appears at age four to six years and rapidly progresses to light/dark awareness only. Life expectancy ranges from age six years to early teenage. The prevalence is 1.5:1,000,000-9:1,000,000.	600,25
TRIOBP	Deafness, autosomal recessive, type 28	NM_001039141.2	NM_001039141.2:c.1039C>T, NM_001039141.2:c.1741C>T, NM_001039141.2:c.2362C>T, NM_001039141.2:c.2639_2640insTCAC, NM_001039141.2:c.3195delT, NM_001039141.2:c.3202C>T, NM_001039141.2:c.4436dupG, NM_001039141.2:c.4577C>G, NM_001039141.2:c.5316G>A	Deafness autosomal recessive type 28 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TRIOBP gene located on chromosomal region 22q13.1. The age of onset is early. This disease is characterized by hearing loss and deafness, no associated visible abnormalities of the external ear or any related medical problems.	600,25
TSEN54	Pontocerebellar hypoplasia, type 2A	NM_207346.2	NM_207346.2:c.670_671delAA, NM_207346.2:c.736C>T, NM_207346.2:c.887G>A, NM_207346.2:c.919G>T, NM_207346.2:c.1027C>T, NM_207346.2:c.1039A>T	Pontocerebellar hypoplasia type 2A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TSEN54 gene located on chromosomal region 17q25.1. Pontocerebellar hypoplasia (PCH) refers to a group of severe neurodegenerative disorders affecting growth and function of the brainstem and cerebellum, resulting in little or no development. Different types were classified based on the clinical picture and the spectrum of pathologic changes.ï¾	600,25
TSFM	Combined oxidative phosphorylation deficiency, type 3	NM_001172696.1	NM_001172696.1:c.1_2delAT, NM_001172696.1:c.24_25delCG, NM_001172696.1:c.581delC, NM_001172696.1:c.919C>T	Combined oxidative phosphorylation deficiency type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TSFM gene located on chromosomal region 12q14.1. The age of onset is early. This disease is characterized by hypotonia, lactic acidosis, and hepatic insufficiency, with progressive encephalomyopathy or hypertrophic cardiomyopathy.	600,25
TSHR	Hypothyroidism, congenital, nongoitrous, type 1	NM_000369.2	NM_000369.2:c.122G>C, NM_000369.2:c.202C>T, NM_000369.2:c.326G>A, NM_000369.2:c.484C>G, NM_000369.2:c.500T>A, NM_000369.2:c.1170T>G, NM_000369.2:c.1742dupC	Hypothyroidism, congenital, nongoitrous, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TSHR gene located on chromosomal region 14q31.1. This disease is characterized by increased levels of plasma TSH and low levels of thyroid hormone. Only a subset of patients develop frank hypothyroidism; the remainder are euthyroid and asymptomatic.	600,25

TTN	Limb-girdle muscular dystrophy type 10 (LGMDR10; formerly LGMD2J); Early-onset myopathy with fatal cardiomyopathy	NM_001267550.2	NM_001267550.2:c.107889delA, NM_001267550.2:c.106070_106071delAT, NM_001267550.2:c.104092delC, NM_001267550.2:c.104092C>T, NM_001267550.2:c.98818_98821delTCCA, NM_001267550.2:c.92373_92379delTGAATTC, NM_001267550.2:c.69344C>G, NM_001267550.2:c.60681dupT, NM_001267550.2:c.56648-1G>A, NM_001267550.2:c.52372delG, NM_001267550.2:c.48253delA, NM_001267550.2:c.47915dupT, NM_001267550.2:c.32471-1G>A, NM_001267550.2:c.28300_28303delAGCA, NM_001267550.2:c.16881C>A, NM_001267550.2:c.15796C>T, NM_001267550.2:c.3165-1G>T	LGMDR10 is a severe recessive form of LGMD phenotype with onset in the first to third decades involving weakness of all proximal muscles. Severe disability with loss of ambulation may occur within 20 years (third to sixth decades). Most of the cases are without facial muscle involvement or cardiomyopathy. Some patients later developed distal muscle involvement. Early-onset myopathy with fatal cardiomyopathy (EOMFC), known as Salih myopathy, also follows an autosomal recessive pattern of inheritance. This disease is characterized by skeletal muscle weakness and a form of heart disease called dilated cardiomyopathy. Affected individuals have delayed development of motor skills, such as sitting, standing, and walking. The age of onset is neonatal/infancy. LGMDR10 and EOMFC are caused by pathogenic variants in the TTN gene located on chromosomal region 2q31.2.	600,25
TTPA	Ataxia with isolated vitamin E deficiency	NM_000370.3	NM_000370.3:c.744delA, NM_000370.3:c.661C>T, NM_000370.3:c.575G>A	Ataxia with vitamin E deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TTPA gene located on chromosomal region 8q13. The age of onset is variable. This disease is characterized by progressive spino-cerebellar ataxia, loss of proprioception, areflexia, and is associated with a marked deficiency in vitamin E. The prevalence is 0.56:1,000,000-3.5:1,000,000.	600,25
TYR	Albinism, oculocutaneous, type 1A	NM_000372.4	NM_000372.4:c.1A>G, NM_000372.4:c.140G>A, NM_000372.4:c.164G>A, NM_000372.4:c.230G>A, NM_000372.4:c.242C>T, NM_000372.4:c.265T>C, NM_000372.4:c.272G>A, NM_000372.4:c.286dupA, NM_000372.4:c.325G>A, NM_000372.4:c.533G>A, NM_000372.4:c.572delG, NM_000372.4:c.616G>A, NM_000372.4:c.646T>A, NM_000372.4:c.650G>A, NM_000372.4:c.823G>T, NM_000372.4:c.896G>A, NM_000372.4:c.1012_1013insC, NM_000372.4:c.1111A>G, NM_000372.4:c.1118C>A, NM_000372.4:c.1146C>A, NM_000372.4:c.1147G>A, NM_000372.4:c.1164delT, NM_000372.4:c.1177delG, NM_000372.4:c.1209G>T, NM_000372.4:c.1217C>T, NM_000372.4:c.1255G>A, NM_000372.4:c.1265G>A, NM_000372.4:c.1336G>A, NM_000372.4:c.1342G>A, NM_000372.4:c.1467dupT, NM_000372.4:c.1501dupC	Oculocutaneous albinism type 1A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TYR gene located on chromosomal region 11q14.2. The age of onset is early. This disease is characterized by white hair and skin, blue, fully translucent irises, nystagmus and misrouting of the optic nerves.	600,25
TYRP1	Albinism, oculocutaneous, type 3	NM_000550.2	NM_000550.2:c.107delT, NM_000550.2:c.176C>G, NM_000550.2:c.497C>G, NM_000550.2:c.1057_1060delAACA, NM_000550.2:c.1067G>A, NM_000550.2:c.1103delA, NM_000550.2:c.1120C>T, NM_000550.2:c.1372_1375dupGACA	Type 3 oculocutaneous albinism follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TYRP1 gene located on chromosomal region 9p23. The age of onset is early. This disease is characterized by rufous or brown albinism and occurring mainly in the African population. The prevalence is of 1/8,500 individuals in Africa.	600,25
UGT1A1	Crigler-Najjar syndrome, type 2	NM_000463.2	NM_000463.2:c.44T>G, NM_000463.2:c.1021C>T, NM_000463.2:c.1070A>G, NM_000463.2:c.1456T>G	Crigler-Najjar syndrome type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the UGT1A1 gene located on chromosomal region 2q37. The age of onset is early. This disease is characterized by unconjugated hyperbilirubinemia due to reduced and inducible activity of hepatic bilirubin glucuronosyltransferase with pigmented bile that contains bilirubin glucuronides, and generally do not present neurologic or intellectual impairment. Bilirubin encephalopathy may develop in later life when patients experience a superimposed infection or stress.	600,25
USH1C	Usher syndrome, type 1C; Deafness, autosomal recessive, type 18A	NM_153676.3	NM_153676.3:c.2688_2695dupAATTCACC, NM_153676.3:c.2622_2623delCA, NM_153676.3:c.2547-1G>T, NM_153676.3:c.238dupC, NM_153676.3:c.238delC, NM_153676.3:c.216G>A	Usher syndrome type 1C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the USH1C gene located on chromosomal region 11p15.1. This disease is characterized by the association of sensorineural deafness (usually congenital, severe and stable), progressive vision loss caused by retinitis pigmentosa apparent in childhood and balance problems. The prevalence is 4.4:100,000. The USH1C gene is also associated with autosomal recessive nonsyndromic sensorineural deafness type 18A. This phenotype is characterized by profound, prelingual, nonsyndromic sensorineural deafness with normal vestibular and visual function.	600,25

USH2A	Usher syndrome, type 2A	NM_206933.2	NM_206933.2:c.15520-1G>A, NM_206933.2:c.15371delT, NM_206933.2:c.15089C>A, NM_206933.2:c.14803C>T, NM_206933.2:c.14442C>A, NM_206933.2:c.13709delG, NM_206933.2:c.12574C>T, NM_206933.2:c.12234_12235delGA, NM_206933.2:c.11864G>A, NM_206933.2:c.10636G>A, NM_206933.2:c.10561T>C, NM_206933.2:c.10073G>A, NM_206933.2:c.9799T>C, NM_206933.2:c.8981G>A, NM_206933.2:c.7364G>A, NM_206933.2:c.6862G>T, NM_206933.2:c.5743_5744delAG, NM_206933.2:c.5573-2A>G, NM_206933.2:c.4338_4339delCT, NM_206933.2:c.3491_3492delCT, NM_206933.2:c.2898delG, NM_206933.2:c.2299delG, NM_206933.2:c.2276G>T, NM_206933.2:c.2167+5G>A, NM_206933.2:c.2135delC, NM_206933.2:c.920_923dupGCCA, NM_206933.2:c.820C>T, NM_206933.2:c.779T>G	Usher syndrome type 2A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the USH2A gene located on chromosomal region 1q41. This disease is characterized by the association of sensorineural deafness (usually congenital, moderate/severe and stable) and progressive vision loss that begins in adolescence or adulthood caused by retinitis pigmentosa. Unlike the other forms of Usher syndrome, type 2 is not associated with vestibular abnormalities that cause difficulties with balance. USH2A accounts for more than half of all cases of Usher syndrome type 2. The estimated prevalence is 3:100,000-4:100,000.	600,25
WFS1	Wolfram syndrome, type 1	NM_001145853.1	NM_001145853.1:c.616C>T, NM_001145853.1:c.676C>T, NM_001145853.1:c.1060_1062delTTC, NM_001145853.1:c.1230_1233delCTCT, NM_001145853.1:c.1234_1237delGTCT, NM_001145853.1:c.1511C>T, NM_001145853.1:c.1943G>A, NM_001145853.1:c.1944G>A, NM_001145853.1:c.2084G>T, NM_001145853.1:c.2643_2644delCT	Wolfram syndrome, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the WFS1 gene located on chromosomal region 4p16.1. The age of onset is infantile. This disease is characterized by diabetes mellitus type I, diabetes insipidus, optical atrophy and neurological signs. The prevalence is 1:1,000,000-9:1,000,000.	600,25
WHRN	Usher syndrome, type 2D; Deafness, autosomal recessive, type 31	NM_015404.3	NM_015404.3:c.817C>T	Usher syndrome type 2D follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the WHRN gene located on chromosomal region 9q32. This disease is characterized by the association of sensorineural deafness (usually congenital, moderate/severe and stable) and progressive vision loss that begins in adolescence or adulthood caused by retinitis pigmentosa. Unlike the other forms of Usher syndrome, type 2 is not associated with vestibular abnormalities that cause difficulties with balance. The WHRN gene is also associated with autosomal recessive nonsyndromic sensorineural deafness type 31. This phenotype is characterized by congenital, non-progressive, mild-to-profound sensorineural hearing impairment.ï¾	600,25
WNT10A	Odontoonychodermal dysplasia	NM_025216.2	NM_025216.2:c.321C>A, NM_025216.2:c.383G>A, NM_025216.2:c.697G>T	Odonto-onycho-dermal dysplasia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the WNT10A gene located on chromosomal region 2q35. The age of onset is infantile. This disease is characterized by hyperkeratosis and hyperhidrosis of the palms and soles, atrophic malar patches, hypodontia, conical teeth, onychodysplasia, and dry and sparse hair. The prevalence is <1:1,000,000.	600,25
ZFYVE26	Spastic paraplegia, type 15, autosomal recessive	NM_015346.3	NM_015346.3:c.5485-1G>A, NM_015346.3:c.5422C>T, NM_015346.3:c.4936C>T, NM_015346.3:c.4312C>T, NM_015346.3:c.3642_3643insCCACACTTAG, NM_015346.3:c.3206G>A, NM_015346.3:c.3182delT, NM_015346.3:c.2114dupC, NM_015346.3:c.1477C>T	Spastic paraplegia type 15 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ZFYVE26 gene located on chromosomal region 14q24.1. The age of onset is infancy. This disease is characterized by progressive spasticity primarily affecting the lower limbs. It is a complex form of spastic paraplegia, associated with other neurologic dysfunction, including variable mental retardation, hearing and visual defects, and thin corpus callosum. The prevalence is <1 / 1,000,000.	600,25