CGT 600 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
ABCB7	X-linked sideroblastic anemia and ataxia (XLSA/A)	NM_004299.4	NM_004299.4:c.1300G>A, NM_004299.4:c.1234G>C, NM_004299.4:c.1203T>G	XLSA/A is caused by pathogenic variants in the ABCB7 gene located on chromosomal region Xq13.3. The age of onset is neonatal/infantile. XLSA/A is a rare condition characterized by a blood disorder called sideroblastic anemia and movement problems known as ataxia. This condition occurs only in males. People with X-linked sideroblastic anemia and ataxia have mature red blood cells that are smaller than normal (microcytic) and appear pale (hypochromic) because of the shortage of hemoglobin. This disorder also leads to an abnormal accumulation of iron in red blood cells but does not cause a potentially dangerous buildup of iron in the body. The anemia is typically mild and usually does not cause any symptoms. The prevalence is very rare, estimated at <1:1,000,000.	600
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
ACAT1	Alpha-methylacetoacetic aciduria	NM_000019.3	NM_000019.3:c.2T>A, NM_000019.3:c.412_419delCAAAGTCT, NM_000019.3:c.547G>A, NM_000019.3:c.622C>T, NM_000019.3:c.905delA, NM_000019.3:c.1035_1037delAGA, NM_000019.3:c.1083dupA, NM_000019.3:c.1136G>T, NM_000019.3:c.1138G>A	Alpha-methylacetoacetic aciduria, also known as 3-ketothiolase deficiency, is an inborn error of isoleucine catabolism characterized by urinary excretion of 2-methyl-3-hydroxybutyric acid, 2-methylacetoacetic acid, tiglylglycine, and 2-butanone. This deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ACAT1 gene located on chromosomal region 11q22.3. The age of onset is neonatal/infantile. This disease is characterized by normal early development followed by a progressive loss of mental and motor skills. The prevalence is < 1:1,000,000.	600
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
ACOX1	Peroxisomal acyl-CoA oxidase deficiency	NM_004035.6	NM_004035.6:c.832A>G, NM_004035.6:c.591delG, NM_004035.6:c.532G>T	Peroxisomal acyl-CoA oxidase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ACOX1 gene located on chromosomal region 17q25.1. The age of onset is neonatal/infantile. This disease is characterized by hypotonia and seizures in the neonatal period and neurological regression in early infancy. The prevalence is < 1:1,000,000.	600
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
ADAMTS2	Ehlers-Danlos syndrome, dermatosparaxis type	NM_014244.4	NM_014244.4:c.2384G>A	Ehlers-Danlos syndrome dermatosparaxis type follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ADAMTS2 gene located on chromosomal region 5q35.3. The age of onset is neonatal/infantile. This disease is characterized by extremely fragile tissues, hyperextensible skin and easy bruising. The prevalence is <1:1,000,000.	600
ADAMTSL2	Geleophysic dysplasia type 1	NM_001145320.1	NM_001145320.1:c.338G>A, NM_001145320.1:c.340G>A, NM_001145320.1:c.440C>T, NM_001145320.1:c.661C>T	Geleophysic dysplasia type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ADAMTSL2 gene located on chromosomal region 9q34.2. The age of onset is infantile. This disease is characterized by extremely by short stature, prominent abnormalities in hands and feet, and a characteristic facial appearance. The prevalence is <1:1,000,000.	600

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
AGA	Aspartylglucosaminuria	NM_000027.3	NM_000027.3:c.904G>A, NM_000027.3:c.800dupT, NM_000027.3:c.755G>A, NM_000027.3:c.488G>C, NM_000027.3:c.302C>T, NM_000027.3:c.214T>C	Aspartylglucosaminuria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the AGA gene located on chromosomal region 4q34.3. The age of onset is infantile. This disease is characterized by slowly developping mental retardation, beginning with clumsiness, late speech, and hyperkinesia, mild facial dysmorphism, and slight kyphoscoliosis.	600
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
AGPS	Rhizomelic chondrodysplasia punctata, type 3	NM_003659.3	NM_003659.3:c.926C>T, NM_003659.3:c.1256G>A, NM_003659.3:c.1406T>C, NM_003659.3:c.1703C>T	Rhizomelic chondrodysplasia punctata type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the AGPS gene located on chromosomal region 2q31.2. The age of onset is neonatal/infantile. This disease is characterized by shortness of the femur and humerus, vertebral disorders, cataract, cutaneous lesions and severe intellectual deficit. The prevalence is 1:100,000-9:100,000.	600
AGT	Renal tubular dysgenesis	NM_000029.3	NM_000029.3:c.1290dupT, NM_000029.3:c.1290delT, NM_000029.3:c.1124G>A, NM_000029.3:c.604C>T	Renal tubular dysgenesis deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ACE (chromosomal region 17q23.3), AGT (1q42.2) AGTR1 (3q24) and REN (1q32.1) genes. 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
AGTR1	Renal tubular dysgenesis	NM_004835.4	NM_004835.4:c.215dupT, NM_004835.4:c.259dupG, NM_004835.4:c.481delC, NM_004835.4:c.481C>T	Renal tubular dysgenesis deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ACE (chromosomal region 17q23.3), AGT (1q42.2) AGTR1 (3q24) and REN (1q32.1) genes. 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
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
ALAS2	X-linked sideroblastic anemia, type 1 (XLSA or SIDBA1)	NM_000032.4	NM_000032.4:c.1706_1709delAGTG, NM_000032.4:c.1699_1700delAT, NM_000032.4:c.1354C>T	X-linked sideroblastic anemia type 1 is caused by pathogenic variants in the ALAS2 gene, located on chromosomal region Xp11.21. This disease is characterized by clinical features of anemia and/or iron overload such as pallor, fatigue, weakness, and more rarely breathlessness, mild splenomegaly, cardiac problems, abnormal liver function, hyperglycemia, glucose intolerance and skin hyperpigmentation. The age of clinical onset of the disorder can vary from in utero to the ninth decade. Whereas males are preferentially affected, females may present with clinically severe anemia. More commonly, female carriers of the disease have an increased red blood cell distribution width and sometimes erythrocyte dimorphism.	600
ALDH4A1	Hyperprolinemia, type 2	NM_003748.3	NM_003748.3:c.1055C>T	Hyperprolinemia type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ALDH4A1 gene located on chromosomal region 1p36. The age of onset is variable. This disease is characterized by seizures, intellectual deficit and mild developmental delay.	600
ALDH5A1	Succinic semialdehyde dehydrogenase deficiency	NM_170740.1	NM_170740.1:c.612G>A, NM_170740.1:c.842G>A, NM_170740.1:c.1265G>A, NM_170740.1:c.1273C>T, NM_170740.1:c.1579C>T	Succinic semialdehyde dehydrogenase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ALDH451 gene located on chromosomal region 6p22. The age of onset is infantile. This disease is characterized by psychomotor retardation, delayed speech development, hypotonia and ataxia. It is a rare disease with around 350 cases reported.	600
ALDOA	Glycogen storage disease type 12	NM_001243177.1	NM_001243177.1:c.548A>G, NM_001243177.1:c.781G>A	Glycogen storage disease type 12 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ALDOA gene located on chromosomal region 16p11.2. The age of onset is neonatal/infantile. This disease is characterized by myopathy with exercise intolerance and rhabdomyolysis associated with hemolytic anaemia.ï¾	600
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
ALG1	Congenital disorder of glycosylation, type 1k	NM_019109.4	NM_019109.4:c.434G>A, NM_019109.4:c.450C>G, NM_019109.4:c.773C>T, NM_019109.4:c.1079C>T, NM_019109.4:c.1129A>G, NM_019109.4:c.1187+1G>A	Congenital disorder of glycosylation type 1k follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ALG1 gene located on chromosomal region 16p13.3. The age of onset is neonatal/infantile. This disease is characterized by psychomotor delay, seizures, microcephaly and coagulation anomalies. The prevalence is <1:1,000,000.	600

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
ALPL	Hypophosphatasia, childhood/infantile	NM_000478.5	NM_000478.5:c.98C>T, NM_000478.5:c.211C>T, NM_000478.5:c.212G>C, NM_000478.5:c.323C>T, NM_000478.5:c.346G>A, NM_000478.5:c.407G>A, NM_000478.5:c.526G>A, NM_000478.5:c.535G>A, NM_000478.5:c.571G>A, NM_000478.5:c.620A>C, NM_000478.5:c.814C>T, NM_000478.5:c.881A>C, NM_000478.5:c.892G>A, NM_000478.5:c.1001G>A, NM_000478.5:c.1133A>T, NM_000478.5:c.1250A>G, NM_000478.5:c.1306T>C, NM_000478.5:c.1366G>A	Childhood-onset hypophosphatasia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ALPL gene located on chromosomal region 1p36.12. The age of onset is infantile. This inborn error of metabolism is characterized clinically by defective bone mineralization ranging from stillbirth without mineralized bone to pathologic fractures of the lower extremities in later adulthood; biochemically is characterized by deficient activity of the tissue-nonspecific isoenzyme of alkaline phosphatase.	600
AMT	Glycine encephalopathy	NM_000481.3	NM_000481.3:c.959G>A, NM_000481.3:c.826G>C, NM_000481.3:c.806G>A, NM_000481.3:c.574C>T, NM_000481.3:c.259-1G>C, NM_000481.3:c.125A>G	Glycine encephalopathy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the AMT and GLDC genes located on chromosomal regions 3p21.31 and 9p24.1 respectively. 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
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
ARG1	Argininemia	NM_001244438.1	NM_001244438.1:c.32T>C, NM_001244438.1:c.61C>T, NM_001244438.1:c.389G>A, NM_001244438.1:c.437G>T, NM_001244438.1:c.727G>C, NM_001244438.1:c.895C>T	Argininemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ARG1 gene located on chromosomal region 6q23. The age of onset is neonatal/infantile. This disease is characterized by variable degrees of hyperammonemia, developing from about 3 years of age, and leading to progressive loss of developmental milestones and spasticity in the absence of treatment. The prevalence is 1:350,000-1:1,000,000.	600
ARL13B	Joubert syndrome type 8	NM_001174150.1	NM_001174150.1:c.246G>A, NM_001174150.1:c.598C>T, NM_001174150.1:c.1252C>T	Joubert syndrome type 8 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ARL13B gene located on chromosomal region 3q11.1. The age of onset is neonatal/infantile. This disease is characterized by congenital malformation of the brainstem and agenesis or hypoplasia of the cerebellar vermis leading to an abnormal respiratory pattern, nystagmus, hypotonia, ataxia and delay in achieving motor milestones. The prevalence is 1/80,000 to 1/100,000.	600
ARL6	Bardet-Biedl syndrome type 3	NM_001323513.1	NM_001323513.1:c.4G>T, NM_001323513.1:c.92C>G, NM_001323513.1:c.92C>T, NM_001323513.1:c.266C>T, NM_001323513.1:c.281T>C, NM_001323513.1:c.364C>T	Bardet-Biedl syndrome type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ARL6 gene located on chromosomal region 3q11.2. The age of onset is early. A syndrome characterized by usually severe pigmentary retinopathy, early-onset obesity, polydactyly, hypogenitalism, renal malformation and mental retardation. Secondary features include diabetes mellitus, hypertension and congenital heart disease.	600
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
ARX	Epileptic encephalopathy, early infantile, type 1; ARX-related developmental disorders	NM_139058.2	NM_139058.2:c.1058C>T, NM_139058.2:c.980_983delAACA	Early infantile epileptic encephalopathy type 1 (EIEE1) follows an X-linked recessive pattern of inheritance and is caused by pathogenic variants in the ARX gene located on chromosomal region Xp21.3. The age of onset is early. This severe disease is characterized by the onset of tonic spasms within the first 3 months of life leading to psychomotor impairment and death. Particularly,it is characterized by frequent tonic seizures or spasms beginning in infancy with a specific EEG finding of suppression-burst patterns, with high-voltage bursts alternating with almost flat suppression phases. Approximately 75% of EIEE patients progress to 'West syndrome,' which is characterized by tonic spasms with clustering, arrest of psychomotor development, and hypsarrhythmia on EEG (Kato et al., 2007). EIEE1 is part of a phenotypic spectrum of disorders caused by mutation in the ARX gene comprising a nearly continuous series of developmental disorders ranging from lissencephaly (LISX2; 300215) to Proud syndrome (300004) to infantile spasms without brain malformations (EIEE1) to syndromic (Partington syndrome; 309510) and nonsyndromic (Mental retardation, X-linked type 29; 300419) mental retardation. Although males with ARX mutations are often more severely affected, female mutation carriers may also be affected (Kato et al., 2004; Wallerstein et al., 2008). The prevalence is <1:1,000,000.	600
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.ï¾ 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
ATP7A	Menkes disease	NM_000052.6	NM_000052.6:c.1639C>T, NM_000052.6:c.1974_1977dupGTTT, NM_000052.6:c.2938C>T, NM_000052.6:c.2981C>T, NM_000052.6:c.3257_3258delAC, NM_000052.6:c.3294+2T>G, NM_000052.6:c.3911A>G, NM_000052.6:c.3915_3921delCTCCCCA	Menkes disease follows an X-linked pattern of inheritance and is caused by pathogenic variants in the ATP7A gene located on chromosomal region Xq21.1. The age of onset is neonatal/infantile. This disease is characterized by progressive neurodegeneration and marked connective tissue anomalies as well as typical sparse abnormal steely hair. The birth incidence is 1:300,000 in Europe, 1:360,000 in Japan and 1:50,000-1:100,000 in Australia, and the prevalence is 1:100,000 newborns. Mutations in the ATP7A can also cause Occipital horn syndrome, which is considered a mild form of Menkes syndrome.	600

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
AUH	3-methylglutaconic aciduria, type 1	NM_001698.2	NM_001698.2:c.991A>T, NM_001698.2:c.943-2A>G, NM_001698.2:c.895-1G>A, NM_001698.2:c.656-2A>G, NM_001698.2:c.650G>A, NM_001698.2:c.589C>T, NM_001698.2:c.559G>A, NM_001698.2:c.471delT	3-Methylglutaconic aciduria type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the AUH gene located on chromosomal region 9q22.31. The age of onset is neonatal/infantile. This disease is characterized by a variable clinical phenotype ranging from mildly delayed speech to psychomotor retardation, coma, failure to thrive, metabolic acidosis and dystonia.ï¾ The prevalence is <1:1,000,000.	600
B4GALT1	Congenital disorder of glycosylation, type 2d	NM_001497.3	NM_001497.3:c.1031dupC	Congenital disorder of glycosylation type 2d follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the B4GALT1 gene located on chromosomal region 9p13. The age of onset is neonatal/infantile. This disease is characterized by macrocephaly, hydrocephaly, hypotonia, myopathy and coagulation anomalies. The prevalence is <1:1,000,000.	600
B9D2	Joubert syndrome type 34; Meckel syndrome type 10	NM_030578.3	NM_030578.3:c.301A>C	Joubert syndrome (JBTS) 34 is an autosomal recessive disorder presenting with cerebellar ataxia, oculomotor apraxia, hypotonia, neonatal breathing abnormalities and psychomotor delay. Neuroradiologically, it is characterized by cerebellar vermian hypoplasia/aplasia, thickened and reoriented superior cerebellar peduncles, and an abnormally large interpeduncular fossa, giving the appearance of a molar tooth on transaxial slices (molar tooth sign). Additional variable features include retinal dystrophy, renal disease, liver fibrosis, and polydactyly. On the other side, Meckel syndrome (MKS) type 10 (MKS10) is a very rare autosomal-recessive disorder resulting in perinatal lethality and characterized by renal cysts, hepatic ductal plate malformation, and central nervous system defects, such as occipital encephalocele. JBST34 and MKS10 are caused by pathogenic variants in the B9D2 gene located on chromosomal region 19q13.2.	600
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

BCKDHB	Maple syrup urine disease, type 1b	NM_000056.4	NM_000056.4:c.302G>A, NM_000056.4:c.342T>G, NM_000056.4:c.344-1G>A, NM_000056.4:c.356T>G, NM_000056.4:c.479T>G, NM_000056.4:c.488A>T, NM_000056.4:c.508C>A, NM_000056.4:c.508C>G, NM_000056.4:c.508C>T, NM_000056.4:c.509G>A, NM_000056.4:c.526A>T, NM_000056.4:c.547C>T, NM_000056.4:c.548G>C, NM_000056.4:c.748G>T, NM_000056.4:c.752T>C, NM_000056.4:c.799C>T, NM_000056.4:c.832G>A, NM_000056.4:c.853C>T, NM_000056.4:c.885delT, NM_000056.4:c.902T>G, NM_000056.4:c.952-1G>A, NM_000056.4:c.970C>T, NM_000056.4:c.1046G>A, NM_000056.4:c.1114G>T	Maple syrup urine disease type 1B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the BCKDHB gene located on chromosomal region 6q14.1. 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 1:10,000-5:10,000.	600
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
BSCL2	Congenital generalized lipodystrophy, type 2; Encephalopathy, progressive, with or without lipodystrophy	NM_001122955.3	NM_001122955.3:c.1166_1167insG, NM_001122955.3:c.1015C>T, NM_001122955.3:c.985C>T, NM_001122955.3:c.974dupG, NM_001122955.3:c.864-3C>G, NM_001122955.3:c.863+5G>A, NM_001122955.3:c.826G>C, NM_001122955.3:c.604C>T	Congenital generalized lipodystrophy (also called Berardinelli-Seip congenital lipodystrophy) type 2 is a rare condition caused by pathogenic variants in the BSCL2 gene located on chromosomal region 11q12.3. Its characterized by an almost total absence of adipose tissue and a very muscular appearance. A shortage of adipose tissue leads to multiple health problems, including high levels of fats called triglycerides circulating in the bloodstream (hypertriglyceridemia) and diabetes mellitus. In some cases, this form of the condition is also associated with intellectual disability, which is usually mild to moderate. Progressive encephalopathy follows an autosomal recessive pattern of inheritance and is also caused by pathogenic variants in the BSCL2 gene. This is a severe neurodegenerative disorder characterized by developmental regression of motor and cognitive skills in the first years of life, often leading to death in the first decade. Patients may show a mild or typical lipodystrophic appearance.	600

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
BTK	Agammaglobulinemia X-linked, type 1	NM_001287344.1	NM_001287344.1:c.2008G>T, NM_001287344.1:c.1991T>A, NM_001287344.1:c.1940G>A, NM_001287344.1:c.1922C>A, NM_001287344.1:c.1875C>A, NM_001287344.1:c.1868A>G, NM_001287344.1:c.1661G>A, NM_001287344.1:c.1660C>T, NM_001287344.1:c.1618T>C, NM_001287344.1:c.1608C>A, NM_001287344.1:c.1390A>G, NM_001287344.1:c.1377C>A, NM_001287344.1:c.1325T>C, NM_001287344.1:c.1227T>G, NM_001287344.1:c.1184A>G, NM_001287344.1:c.1103A>C, NM_001287344.1:c.1021A>G, NM_001287344.1:c.964C>T, NM_001287344.1:c.865C>T, NM_001287344.1:c.857G>A, NM_001287344.1:c.820G>T, NM_001287344.1:c.440T>A	Agammaglobulinemia X-linked (XLA), type 1 follows an X-linked pattern of inheritance and is caused by pathogenic variants in the BTK gene located on chromosomal region Xq21.33-q22. The age of onset is neonatal. Individuals with XLA are more susceptible to infections because their body makes very few antibodies. In children with XLA, infections generally take longer to get better and then they come back again, even with antibiotic medications. The most common bacterial infections that occur in people with XLA are lung infections (pneumonia and bronchitis), ear infections (otitis), pink eye (conjunctivitis), and sinus infections (sinusitis). Infections that cause chronic diarrhea are also common. Recurrent infections can lead to organ damage. The X-linked form accounts for approximately 85 to 90% of cases of agammaglobulinemia. The prevalence is 3:1,000,000-6:1,000,000 men.	600
C3	Complement C3 deficiency	NM_000064.3	NM_000064.3:c.4851-1G>A, NM_000064.3:c.3627_3628insGGGGCCC, NM_000064.3:c.3116dupT, NM_000064.3:c.2562C>G, NM_000064.3:c.2354+1G>A, NM_000064.3:c.1119+1G>T, NM_000064.3:c.1004-2A>T	C3 deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the C3 gene located on chromosomal region 19p13.3-p13.2. The age of onset is infantile. It is a rare defect of the complement classical pathway. The main clinical manifestation of primary C3 deficiency is childhood-onset of recurrent bacterial infections, mainly caused by gram-negative bacteria, such as Neisseria meningitidis, Enterobacter aerogenes, Haemophilus influenzae, and Escherichia coli; infections with gram-positive bacteria also occur. Infections in the upper and lower respiratory tract, including pneumonia, episodes of sinusitis, tonsillitis, and otitis, are the most frequent consequence of the C3 deficiency. Approximately 26% of patients with C3 deficiency develop immune complex-mediated autoimmune diseases resembling systemic lupus erythematosus, and about 26% of patients develop mesangiocapillary or membranoproliferative glomerulonephritis, resulting in renal failure (summary by Reis et al., 2006). The prevalence is <1:1.000.000.	600
CA2	Osteopetrosis, autosomal recessive type 3	NM_000067.2	NM_000067.2:c.120T>G, NM_000067.2:c.319C>T, NM_000067.2:c.663+2T>C	Osteopetrosis, autosomal recessive, type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CA2 gene located on chromosomal region 8q22. The age of onset is neonatal/infantile. This disease is characterized by osteopetrosis, renal tubular acidosis, and neurological disorders related to cerebral calcifications. The prevalence is <1:1.000.000.	600

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
CD40LG	Immunodeficiency, X-linked, with hyper-IgM	NM_000074.2	NM_000074.2:c.107T>G, NM_000074.2:c.368C>A	Immunodeficiency, X-linked, with hyper-IgM follows an X-linked pattern of inheritance and is caused by pathogenic variants in the CD40LG gene located on chromosomal region Xq26. The age of onset is neonatal/infantile. This disease is characterized by lower-respiratory tract bacterial infections, opportunistic infections, recurrent or protracted diarrhea associated with failure to thrive, neutropenia, thrombocytopenia and anemia. The prevalence is 2:1,000,000 male newborns.	600
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
CDH3	Ectodermal dysplasia, ectrodactyly, and macular dystrophy	NM_001793.5	NM_001793.5:c.461dupC, NM_001793.5:c.830delG, NM_001793.5:c.965A>T, NM_001793.5:c.981delG, NM_001793.5:c.1508G>A	Ectodermal dysplasia, ectrodactyly, and macular dystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CDH3 gene located on chromosomal region 16q22.1. The age of onset is neonatal/infantile. This disease is characterized by the association of ectodermal dysplasia, ectrodactyly, and macular dystrophy. The prevalence is <1:1,000,000.	600
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

CDK5RAP2	Primary microcephaly type 3, autosomal recessive	NM_018249.5	NM_018249.5:c.4672C>T, NM_018249.5:c.4658_4661dupTATT, NM_018249.5:c.4546G>T, NM_018249.5:c.700G>T, NM_018249.5:c.524_528delAGGCA, NM_018249.5:c.246T>A, NM_018249.5:c.127+1G>C	Primary autosomal recessive microcephaly type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CDK5RAP2 gene located on chromosomal region 9q33.2. 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
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
CEP152	Primary microcephaly type 9, autosomal recessive	NM_001194998.1	NM_001194998.1:c.2034T>G, NM_001194998.1:c.1578-1G>A, NM_001194998.1:c.794A>C, NM_001194998.1:c.749_750delGA	Primary autosomal recessive microcephaly type 9 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CEP152 gene located on chromosomal region 15q21.1. 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
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.1096_1097insG, NM_000492.3:c.1097T>A	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
CLCN7	Osteopetrosis, autosomal recessive type 4	NM_001287.5	NM_001287.5:c.781A>T, NM_001287.5:c.622C>T	Osteopetrosis type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CLCN7 gene located on chromosomal region 16p13. The age of onset is neonatal/infantile. This disease is characterized bone marrow failure, fractures and visual impairment. The incidence is 1:200,000 live births and the prevalence is 1:100,000.	600
CLDN14	Deafness type 29, autosomal recessive	NM_001146077.1	NM_001146077.1:c.398delT, NM_001146077.1:c.301G>A, NM_001146077.1:c.254T>A	Deafness type 29, autosomal recessive follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CLDN14 gene located on chromosomal region 21q22.3. The age of onset is neonatal/infantile. This disease is characterized by congenital, non-progressive, mild-to-profound sensorineural hearing impairment.	600
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

CLN3	Ceroid lipofuscinosis, neuronal, type 3	NM_000086.2	NM_000086.2:c.1272delG, NM_000086.2:c.883G>A, NM_000086.2:c.622dupT, NM_000086.2:c.597C>A	Juvenile neuronal ceroid lipofuscinosis 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CLN3 gene located on chromosomal region 16p12.1. The age of onset is infantile. This disease is characterized by onset at early school age with vision loss due to retinopathy, seizures and the decline of mental and motor capacities. The annual birth incidence is 1:217,000-1:450,000 in Sweden and 1:143,000 in Germany, and the prevalence is 1.5:1,000,000-9:1,000,000.	600
CLN5	Ceroid lipofuscinosis, neuronal, type 5	NM_006493.2	NM_006493.2:c.335G>C, NM_006493.2:c.377G>A, NM_006493.2:c.433C>T, NM_006493.2:c.524T>G, NM_006493.2:c.526dupA, NM_006493.2:c.565C>T, NM_006493.2:c.575A>G, NM_006493.2:c.593T>C, NM_006493.2:c.595C>T, NM_006493.2:c.613C>T, NM_006493.2:c.620G>C, NM_006493.2:c.669dupC, NM_006493.2:c.835G>A, NM_006493.2:c.919delA, NM_006493.2:c.924_925delAT, NM_006493.2:c.1026C>A	Neuronal ceroid lipofuscinosis type 5 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CLN5 gene located on chromosomal region 3q21.1-q32. The age of onset is infantile. This disease is characterized by onset during infancy or early childhood with decline of mental and motor capacities, epilepsy and vision loss through retinal degeneration. The prevalence is <1:1,000,000.	600
CLN6	Ceroid lipofuscinosis, neuronal, type 6	NM_017882.2	NM_017882.2:c.663C>G, NM_017882.2:c.214G>T, NM_017882.2:c.200T>C	Neuronal ceroid lipofuscinosis 6 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CLN6 gene located on chromosomal region 15q23. The age of onset is infantile. This disease is characterized by onset during infancy or early childhood with decline of mental and motor capacities, epilepsy and vision loss through retinal degeneration. The prevalence is <1:1,000,000.	600
CLN8	Ceroid lipofuscinosis, neuronal, type 8	NM_018941.3	NM_018941.3:c.88delG, NM_018941.3:c.88G>C, NM_018941.3:c.610C>T, NM_018941.3:c.789G>C	Neuronal ceroid lipofuscinosis 8 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CLN8 gene located on chromosomal region 8p23.3. The age of onset is infantile. This disease is characterized by onset during infancy or early childhood with decline of mental and motor capacities, epilepsy, and vision loss through retinal degeneration. The prevalence is <1:1,000,000.	600
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

COL11A1	Fibrochondrogenesis type 1	NM_080629.2	NM_080629.2:c.3745-1G>A, NM_080629.2:c.2386G>C, NM_080629.2:c.1786dupG	Fibrochondrogenesis type 1 (FBCG1) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COL11A1 gene located on chromosomal region 1p21. The age of onset is neonatal. Fibrochondrogenesis is a severe short-limbed skeletal dysplasia clinically characterized by a flat midface with a small nose and anteverted nares, significant shortening of all limb segments but relatively normal hands and feet, and a small bell-shaped thorax with a protuberant abdomen. Radiographically, the long bones are short and have broad metaphyseal ends, giving them a dumb-bell shape. The vertebral bodies are flat and, on lateral view, have a distinctive pinched appearance, with a hypoplastic posterior end and a rounded anterior end. The ribs are typically short and wide and have metaphyseal cupping at both ends (Tompson et al., 2010). Genetic heterogeneity: Fibrochondrogenesis type 2 (FBCG2; OMIM 614524) is caused by mutations in the COL11A2 gene on chromosome 6p21.3.	600
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
COL1A2	Ehlers-Danlos syndrome, cardiac valvular type	NM_000089.3	NM_000089.3:c.133-1G>A, NM_000089.3:c.241_248delTATGATGG, NM_000089.3:c.293dupC, NM_000089.3:c.1404+1G>A, NM_000089.3:c.1404+1G>C, NM_000089.3:c.3601G>T	Ehlers-Danlos syndrome, cardiac valvular type follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COL1A2 gene located on chromosomal region 7q22.1. The age of onset is neonatal/infantile. This disease is characterized by joint hypermobility, skin hyperextensibility and cardiac valvular defects.ï¾ The prevalence is 6/100,000 to 7/100,000.	600
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
COL9A1	Stickler syndrome, type 4	NM_001851.4	NM_001851.4:c.883C>T, NM_001851.4:c.706C>T	Stickler syndrome type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the COL9A1 gene located on chromosomal region 6q13. The age of onset is infantile. This disease is characterized by opthalmological (myopia, retinal detachment and cataracts), orofacial (micrognathia, midface hypoplasia and cleft palate) auditory (sensorineural hearing loss) and articular (epiphyseal dysplasia) symptoms. The prevalence is <1:1,000,000.	600
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
CPS1	Carbamoylphosphate synthetase 1 deficiency	NM_001122633.2	NM_001122633.2:c.1649C>T, NM_001122633.2:c.1930C>T, NM_001122633.2:c.3574delA	Carbamoylphosphate synthetase deficiency type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CPS1 gene located on chromosomal region 2q35. The age of onset is infantile. This disease is characterized by congenital hyperammonemia and defective citrulline synthesis. The prevalence is 1:800,000 newborn in Japan.	600
CPT1A	Carnitine palmitoyltransferase type 1A deficiency, hepatic	NM_001876.3	NM_001876.3:c.1436C>T, NM_001876.3:c.1393G>T, NM_001876.3:c.1361A>G, NM_001876.3:c.1241C>T, NM_001876.3:c.1216C>T, NM_001876.3:c.1079A>G, NM_001876.3:c.335_336delCC, NM_001876.3:c.298C>T, NM_001876.3:c.281+1G>A, NM_001876.3:c.222C>A	Carnitine palmitoyl transferase 1A deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CPT1A gene located on chromosomal region 11q13.2. The age of onset is neonatal/infantile. This disease is characterized by recurrent attacks of fasting-induced hypoketotic hypoglycemia and risk of liver failure. The prevalence is 1.3:1,000 newborn.	600
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
CRLF1	Cold-induced sweating syndrome type 1	NM_004750.4	NM_004750.4:c.1137C>G, NM_004750.4:c.1125delG, NM_004750.4:c.935G>A, NM_004750.4:c.856-1G>A, NM_004750.4:c.852G>T, NM_004750.4:c.845_846delTG, NM_004750.4:c.829C>T, NM_004750.4:c.713dupC, NM_004750.4:c.708_709delCCinsT, NM_004750.4:c.676dupA, NM_004750.4:c.538C>T, NM_004750.4:c.527+5G>A, NM_004750.4:c.413C>T, NM_004750.4:c.397+1G>A, NM_004750.4:c.303delC, NM_004750.4:c.226T>G	Cold-induced sweating syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CRLF1 gene located on chromosomal region 19p12. The age of onset is infantile. This disease is characterized by profuse sweating (involving the chest, face, arms and trunk) induced by cold ambient temperature kyphoscoliosis, a high-arched palate, depressed nasal bridge and impaired peripheral sensitivity to pain and temperature. The prevalence is <1:1,000,000.	600
CRTAP	Osteogenesis imperfecta, type 7	NM_006371.4	NM_006371.4:c.180G>A, NM_006371.4:c.561T>G, NM_006371.4:c.634C>T, NM_006371.4:c.826C>T	Osteogenesis imperfecta type 7 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CRTAP gene located on chromosomal region 3p22.3. The age of onset is variable. This disease is characterized by increased bone fragility, low bone mass, and susceptibility to bone fractures with variable severity. The prevalence is 6:100,000-7:100,000.	600
CSTB	Epilepsy, progressive myoclonic type 1A (Unverricht and Lundborg)	NM_000100.3	NM_000100.3:c.212A>C, NM_000100.3:c.202C>T	Progressive myoclonic epilepsy type 1A (Unverricht and Lundborg) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CSTB gene located on chromosomal region 21q22.3. The age of onset is infantile. This disease is characterized by severe, stimulus-sensitive myoclonus and tonic-clonic seizures. The onset, occurring between 6 and 13 years of age, is characterized by convulsions. Myoclonus begins 1 to 5 years later. The twitchings occur predominantly in the proximal muscles of the extremities and are bilaterally symmetrical, although asynchronous. At first small, they become late in the clinical course so violent that the victim is thrown to the floor. Mental deterioration and eventually dementia develop. The prevalence is 1:20,000 newborn.	600
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
CTSD	Ceroid lipofuscinosis, neuronal, type 10	NM_001909.4	NM_001909.4:c.1149G>C, NM_001909.4:c.685T>A	Neuronal ceroid lipofuscinosis type 10 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CTSD gene located on chromosomal region 11p15.5. 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 2:100,000-4:100,000 newborn.	600
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

CYP21A2	Congenital adrenal hyperplasia due to 21-hydroxylase deficiency	0	NM_000500.7:c.92C>T, NM_000500.7:c.293-13A/C>G, NM_000500.7:c.332_339del, NM_000500.7:c.518T>A, NM_000500.7:c.[710T>A;713T>A;719T>A], NM_000500.7:c.710T>A, NM_000500.7:c.713T>A, NM_000500.7:c.844G>T, NM_000500.7:c.923_924insT, NM_000500.7:c.955C>T, NM_000500.7:c.1069C>T, NM_000500.7:c.1360C>T, NM_000500.7:c.[710T>A;713T>A], NM_000500.7:c.[710T>A;719T>A], NM_000500.7:c.[713T>A;719T>A], Abnormal CNV, Large gene conversion, NM_000500.7:c.955C>T+CYP21A2dup	Classic congenital adrenal hyperplasia due to 21-hydroxylase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the CYP21A2 gene located on chromosomal region 6p21.3. The age of onset is neonatal/infantile. This disease is characterized by simple virilizing or salt wasting forms that can manifest with genital ambiguity in females, and in both sexes with adrenal insufficiency with dehydration during the neonatal period, life threatening hypoglycemia and hyperandrogenia. The prevalence is 1/100,000 to 9/100,000. There is a common milder form of congenital adrenal hyperplasia (Nonclassic) characterized by a later onset of androgen excess symptoms seen in females and precocious pseudopuberty in both sexes. Cortisol and aldosterone levels are normal but there is an increased amount of androgens. Nonclassic form onset occurs in adolescence with variable degrees of postnatal androgen excess (precocious pubarche, hirsutism, acne, alopecia, anovulation and menstrual irregularities and in the post-pubertal period it can mimic polycystic ovary syndrome. It is also sometimes asymptomatic. The prevalence ranges from 1/1,000-1/500 in the general Caucasian population, but up to 1-2% among inbred populations, such as Eastern European (Ashkenazi) Jews.	600
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
DDB2	Xeroderma pigmentosum, group E	NM_000107.2	NM_000107.2:c.730A>G, NM_000107.2:c.818G>A, NM_000107.2:c.919G>T, NM_000107.2:c.937C>T	Xeroderma pigmentosum complementation group E follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DDB2 gene located on chromosomal region 11p12-p11. The age of onset is variable. This disease is characterized by mild xeroderma pigmentosum symptoms and no neurological abnormalities. The prevalence is 1/1,000,000.	600
DDC	Aromatic L-amino acid decarboxylase deficiency	NM_000790.3	NM_000790.3:c.1040G>A, NM_000790.3:c.823G>A, NM_000790.3:c.749C>T, NM_000790.3:c.304G>A, NM_000790.3:c.272C>T, NM_000790.3:c.100delG	Aromatic L-amino acid decarboxylase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DDC gene located on chromosomal region 7p12.2. The age of onset is neonatal/infantile. This disease is characterized by severe developmental delay, weak muscle tone (hypotonia), muscle stiffness, difficulty moving, and involuntary writhing movements of the limbs (athetosis). The prevalence is below 1,000,000.	600
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
DHDDS	Retinitis pigmentosa type 59	NM_024887.3	NM_024887.3:c.124A>G, NM_024887.3:c.330delA, NM_024887.3:c.998C>G	Retinitis pigmentosa type 59 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DHDDS gene located on chromosomal region 1p36.11. 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
DKC1	Dyskeratosis congenita, X-linked	NM_001363.4	NM_001363.4:c.91C>A, NM_001363.4:c.91C>G, NM_001363.4:c.194G>C, NM_001363.4:c.196A>G, NM_001363.4:c.200C>T, NM_001363.4:c.204C>A, NM_001363.4:c.214_215delCTinsTA	X-linked dyskeratosis congenita follows an X-linked pattern of inheritance and is caused by pathogenic variants in the DKC1 gene located on chromosomal region Xq28. Tha age of onset is infantile. This disease is classically defined by the triad of abnormal skin pigmentation, nail dystrophy, and leukoplakia of the oral mucosa. Progressive bone marrow failure occurs in over 80% of cases and is the main cause of early mortality. The phenotype is highly variable, and affected individuals may have multiple additional features.	600

DLD	Dihydrolipoamide dehydrogenase deficiency	NM_000108.4	NM_000108.4:c.105_106insA, NM_000108.4:c.916_926delTGTGATGTACT, NM_000108.4:c.1483A>G	Dihydrolipoamide dehydrogenase deficiency E3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DLD gene located on chromosomal region 7q31-q32. The age of onset is neonatal/infantile. This disease is characterized by poor feeding, lethargy, vomiting and a maple syrup odor in the cerumen (and later in urine) noted soon after birth, followed by progressive encephalopathy and central respiratory failure if untreated. The prevalence is 1/1,000,000 to 9/1,000,000.	600
DLL3	Spondylocostal dysostosis type 1	NM_016941.3	NM_016941.3:c.231C>A, NM_016941.3:c.712C>T	Spondylocostal dysostosis type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DLL3 gene located on chromosomal region 19q13. The age of onset is neonatal/infantile. This disease is associated with vertebral and rib segmentation defects and characterised by a short neck with limited mobility, winged scapulae, a short trunk, and short stature with multiple vertebral anomalies at all levels of the spine. The prevalence is below 1/1,000,000.	600
DMD	Duchenne/Becker muscular dystrophy	0	NM_004006.2:c.10774delA, NM_004006.2:c.10454delT, NM_004006.2:c.10453_10454delCT, NM_004006.2:c.10447_10448delTC, NM_004006.2:c.10141C>T, NM_004006.2:c.10086+1G>A, NM_004006.2:c.10033C>T, NM_004006.2:c.9854_9863delTGAGACTGGA, NM_004006.2:c.9862G>T, NM_004006.2:c.9851G>A, NM_004006.2:c.9767dupG, NM_004006.2:c.9650-2A>G, NM_004006.2:c.9568C>T, NM_004006.2:c.9564-1G>A, NM_004006.2:c.9380C>G, NM_004006.2:c.9361+1G>C, NM_004006.2:c.9361+1G>A, NM_004006.2:c.9346C>T, NM_004006.2:c.9337C>T, NM_004006.2:c.9164-1G>T, NM_004006.2:c.9164-1G>C, NM_004006.2:c.8944C>T, NM_004006.2:c.8713C>T, NM_004006.2:c.8656C>T, NM_004006.2:c.8652_8653delCT, NM_004006.2:c.8608C>T, NM_004006.2:c.8464C>T, NM_004006.2:c.8443C>T, NM_004006.2:c.8374_8375delAA, NM_004006.2:c.8358G>A, NM_004006.2:c.8086delC, NM_004006.2:c.8069T>G, NM_004006.2:c.8064_8065delTA, NM_004006.2:c.7922delA, NM_004006.2:c.7894C>T, NM_004006.2:c.7771G>T, NM_004006.2:c.7764dupT, NM_004006.2:c.7683G>A, NM_004006.2:c.7682G>A, NM_004006.2:c.6986dupA, NM_004006.2:c.6982A>T, NM_004006.2:c.6964delG, NM_004006.2:c.6943G>T, NM_004006.2:c.6936delA, NM_004006.2:c.6906G>A, NM_004006.2:c.6834delT, NM_004006.2:c.6763-2A>G, NM_004006.2:c.6391_6392dupCA, NM_004006.2:c.6391_6392delCA, NM_004006.2:c.6373C>T, NM_004006.2:c.6340A>T, NM_004006.2:c.6292C>T, NM_004006.2:c.6238delC, NM_004006.2:c.6226G>T, NM_004006.2:c.6182delC, NM_004006.2:c.6014_6017delCTCA, NM_004006.2:c.6000T>A, NM_004006.2:c.5899C>T, NM_004006.2:c.5807T>A, NM_004006.2:c.5773G>T, NM_004006.2:c.5697delA, NM_004006.2:c.5671A>T, NM_004006.2:c.5640T>A, NM_004006.2:c.5570_5571dupAA, NM_004006.2:c.5554C>T, NM_004006.2:c.5530C>T, NM_004006.2:c.5363C>G, NM_004006.2:c.5353C>T, NM_004006.2:c.5313dupT, NM_004006.2:c.5287C>T, NM_004006.2:c.4843A>T, NM_004006.2:c.4735G>T, NM_004006.2:c.4518+5G>A, NM_004006.2:c.4500delA, NM_004006.2:c.4486delG, NM_004006.2:c.4471_4472delAA, NM_004006.2:c.4409_4412dupGTCT, NM_004006.2:c.4405C>T, NM_004006.2:c.4375C>T, NM_004006.2:c.4117C>T, NM_004006.2:c.3779_3785delCTTTGGAinsGG, NM_004006.2:c.3747delG, NM_004006.2:c.3697delG, NM_004006.2:c.3629dupA	Duchenne muscular dystrophy follows an X-linked pattern of inheritance and is caused by pathogenic variants in the DMD gene located on chromosomal region Xp21.2. The age of onset is infantile. This disease is characterized by progressive muscle wasting and weakness due to degeneration of skeletal, smooth and cardiac muscle. The incidence is 1/3,300 male newborns and the prevalence is 1/16,000 to 1/125,000. Becker muscular dystrophy is characterized by progressive muscle wasting and weakness due to degeneration of skeletal, smooth and cardiac muscle. The incidence is 1/18,000 to 1/31,000 male newborns and the prevalence is 1/10,000 to 5/10,000.	600
DMP1	Hypophosphatemic rickets, autosomal recessive	NM_004407.3	NM_004407.3:c.1A>G, NM_004407.3:c.31delT, NM_004407.3:c.55-1G>C, NM_004407.3:c.362delC	Hypophosphatemic rickets follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DMP1 gene located on chromosomal region 4q21. The age of onset is variable. This disease is associated with vertebral and rib segmentation defects and characterised by hypophosphatemia, rickets and/or osteomalacia and slow growth. The prevalence is below 1/20,000 newborns.	600
DNAJC19	3-methylglutaconic aciduria, type 5	NM_145261.3	NM_145261.3:c.300delA	3-methylglutaconic aciduria, type 5 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DNAJC19 gene located on chromosomal region 3q26.33. The age of onset is infantile. This disease is characterized by severe early onset (before the age of three years) dilated cardiomyopathy with conduction defects (long QT syndrome), non-progressive cerebellar ataxia, testicular dysgenesis, and 3-methylglutaconic aciduria.	600

DPAGT1	Congenital disorder of glycosylation, type 1j	NM_001382.3	NM_001382.3:c.980_981delCT, NM_001382.3:c.791T>G, NM_001382.3:c.643+1G>A, NM_001382.3:c.358C>A, NM_001382.3:c.349G>A	Congenital disorder of glycosylation, type 1j follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DPAGT1 gene located on chromosomal region 11q23.3. The age of onset is neonatal/infantile. This disease is characterized by severe psychomotor delay, seizures, hypotonia and dysmorphism (microcephaly, ocular exotropia, micrognathia and clinodactyly). The prevalence is below 1,000,000.	600
DPM1	Congenital disorder of glycosylation, type 1e	NM_001317034.1	NM_001317034.1:c.847T>C, NM_001317034.1:c.784-1G>T, NM_001317034.1:c.733delC, NM_001317034.1:c.669-1G>A, NM_001317034.1:c.274C>G	Congenital disorder of glycosylation, type 1e follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the DPM1 gene located on chromosomal region 20q13.13. The age of onset is neonatal/infantile. This disease is characterized by psychomotor delay, seizures, hypotonia, facial dysmorphism and microcephaly. The prevalence is below 1,000,000.	600
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
EDN3	Waardenburg syndrome, type 4B	NM_207034.2	NM_207034.2:c.262_263delGCinsT, NM_207034.2:c.277C>G, NM_207034.2:c.476G>T, NM_207034.2:c.568_569delGA	Waardenburg-Shah syndrome, type 4B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the EDN3 gene located on chromosomal region 20q13.2-q13.3. The age of onset is neonatal/infantile. This disease is characterized by the association of Waardenburg syndrome (sensorineural hearing loss and pigmentary abnormalities) and Hirschsprung disease (signs of intestinal obstruction). The prevalence is below 1/40,000.	600
EDNRB	ABCD syndrome	NM_001201397.1	NM_001201397.1:c.1098G>T, NM_001201397.1:c.818C>G, NM_001201397.1:c.46delC	ABCD syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the EDNRB gene located on chromosomal region 13q22.3. This disease is characterized by albinism, black lock at temporal occipital region, bilateral deafness, aganglionosis of the large intestine and total absence of neurocytes and nerve fibers in the small intestine. ABCD syndrome is not a separate entity, but rather an expression of Shah-Waardenburg syndrome (WS4)	600
EIF2AK3	Wolcott-Rallison syndrome	NM_004836.6	NM_004836.6:c.1763G>A, NM_004836.6:c.994G>T	Wolcott-Rallison syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the EIF2AK3 gene located on chromosomal region 2p12. The age of onset is neonatal/infantile. This disease is characterized by permanent neonatal diabetes mellitus with multiple epiphyseal dysplasia and other clinical manifestations, including recurrent episodes of acute liver failure. The prevalence is above 1/10,000 newborns.	600
ELP1	Dysautonomia, familial	NM_003640.4	NM_003640.4:c.3332delC, NM_003640.4:c.2741C>T, NM_003640.4:c.2328delT, NM_003640.4:c.2204+6T>C, NM_003640.4:c.2087G>C, NM_003640.4:c.1460+2T>C	Familial dysautonomia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ELP1 gene located on chromosomal region 9q31.3. The age of onset is infantile. This disease is characterized by sensory dysfunction and severe impairment of the autonomic nervous system activity, resulting in multisystem dysfunction. The prevalence is <1:1,000,000	600

EMD	Emery-Dreifuss muscular dystrophy, type 1, X-linked	NM_000117.2	NM_000117.2:c.547C>A, NM_000117.2:c.631_635delCGTGC	Emery-Dreifuss muscular dystrophy, type 1, X-linked follows an X-linked pattern of inheritance and is caused by pathogenic variants in the EMD gene located on chromosomal region Xq28. ï¾ This is a condition that primarily affects muscles used for movement (skeletalï¾ muscles) and the heart (cardiac muscle). Among the earliest features of this disorder are joint deformities called contractures. Contractures restrict the movement of certain joints, most often the elbows, ankles, and neck, and usually become noticeable in early childhood. Most affected individuals also experience muscle weakness andï¾ wastingï¾ that worsen slowly over time, beginning in muscles of the upper arms and lower legs and later also affecting muscles in the shoulders and hips. Almost all people with Emery-Dreifuss muscular dystrophy develop heart problems by adulthood. The X-linked type of this disorder affects an estimated 1 in 100,000 people.	600
ENPP1	Arterial calcification, generalized, of infancy, type 1	NM_006208.2	NM_006208.2:c.783C>G, NM_006208.2:c.797G>T, NM_006208.2:c.900G>A, NM_006208.2:c.913C>A, NM_006208.2:c.1025G>T, NM_006208.2:c.1112A>T, NM_006208.2:c.1612G>C, NM_006208.2:c.2230C>T, NM_006208.2:c.2677G>T, NM_006208.2:c.2702A>C	Arterial calcification, generalized, of infancy, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ENPP1 gene located on chromosomal region 6q22-q23. The age of onset is neonatal/infancy. A severe autosomal recessive disorder characterized by calcification of the internal elastic lamina of muscular arteries and stenosis due to myointimal proliferation. The disorder is often fatal within the first 6 months of life because of myocardial ischemia resulting in refractory heart failure.	600
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
ERCC3	Trichothiodystrophy, type 2	NM_000122.1	NM_000122.1:c.1858delG, NM_000122.1:c.1757_1758delAG, NM_000122.1:c.1757delA, NM_000122.1:c.1633C>T, NM_000122.1:c.1273C>T, NM_000122.1:c.296T>C	Trichothiodystrophy (TTD), type 2 is a heterogeneous group of disorders that follows an autosomal recessive pattern of inheritance. It is caused by pathogenic variants in the ERCC3 gene located on chromosomal region 2q14.3. 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
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
ERCC8	Cockayne syndrome, type A	NM_000082.3	NM_000082.3:c.966C>A, NM_000082.3:c.618-1G>A, NM_000082.3:c.593_594dupAT, NM_000082.3:c.37G>T	Cockayne syndrome, type A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ERCC8 gene located on chromosomal region 5q12.1. 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. The prevalence is 2.7/1,000,000 newborns in Western Europe.	600
ESCO2	Roberts syndrome	NM_001017420.2	NM_001017420.2:c.296_297dupGA, NM_001017420.2:c.308_309delAA, NM_001017420.2:c.505C>T, NM_001017420.2:c.604C>T, NM_001017420.2:c.876_879delCAGA, NM_001017420.2:c.879_880delAG, NM_001017420.2:c.1269G>A, NM_001017420.2:c.1597dupT, NM_001017420.2:c.1615T>G	Roberts syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ESCO2 gene located on chromosomal region 8p21.1. The age of onset is neonatal/infantile. This disease is characterized by pre- and postnatal growth retardation, severe symmetric limb reduction defects, craniofacial anomalies and severe intellectual deficit.	600
ESPN	Deafness, autosomal recessive, type 36	NM_031475.2	NM_031475.2:c.1988_1991delAGAG, NM_031475.2:c.2470_2473delTCAG	Autosomal recessive nonsyndromic sensorineural deafness type 36 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ESPN gene located on chromosomal region 1p36.31. The age of onset is neonatal/infantile. This disease is characterized by congenital, non-progressive, mild-to-profound sensorineural hearing impairment.	600
ESRRB	Deafness, autosomal recessive, type 35	NM_004452.3	NM_004452.3:c.329C>T	Autosomal recessive nonsyndromic sensorineural deafness type 35 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ESRRB gene located on chromosomal region 14q24.3. The age of onset is neonatal/infantile. This disease is characterized by congenital, non-progressive, mild-to-profound sensorineural hearing impairment.	600
ETFA	Glutaric acidemia, type 2A	NM_000126.3	NM_000126.3:c.797C>T, NM_000126.3:c.470T>G	Glutaric acidemia, type 2A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ETFA gene located on chromosomal region 15q23-q25. The age of onset is variable. This disease is characterized by clinically heterogeneous symptoms ranging from a severe neonatal presentation with metabolic acidosis, cardiomyopathy and liver disease, to a mild childhood/adult disease with episodic metabolic decompensation, muscle weakness, and respiratory failure.	600
ETFB	Glutaric acidemia, type 2B	NM_001014763.1	NM_001014763.1:c.887_889delAGA, NM_001014763.1:c.764G>A, NM_001014763.1:c.655G>A, NM_001014763.1:c.551_552insG, NM_001014763.1:c.334C>T, NM_001014763.1:c.278_279insG	Glutaric acidemia, type 2B follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ETFB gene located on chromosomal region 19q13.3. The age of onset is variable. This disease is characterized by clinically heterogeneous symptoms ranging from a severe neonatal presentation with metabolic acidosis, cardiomyopathy and liver disease, to a mild childhood/adult disease with episodic metabolic decompensation, muscle weakness, and respiratory failure.	600
ETFDH	Glutaric acidemia, type 2C	NM_004453.3	NM_004453.3:c.2T>C, NM_004453.3:c.250G>A, NM_004453.3:c.413T>G, NM_004453.3:c.524G>T, NM_004453.3:c.1001T>C, NM_004453.3:c.1234G>T, NM_004453.3:c.1367C>T, NM_004453.3:c.1570_1571delCT, NM_004453.3:c.1823delG, NM_004453.3:c.1832G>A	Glutaric acidemia, type 2C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ETFDH gene located on chromosomal region 4q32-q35. The age of onset is variable. This disease is characterized by clinically heterogeneous symptoms disease, to a mild childhood/adult disease with episodic metabolic decompensation, muscle weakness, and respiratory failure.	600

ETHE1	Ethylmalonic encephalopathy	NM_014297.4	NM_014297.4:c.604dupG, NM_014297.4:c.554T>G, NM_014297.4:c.488G>A, NM_014297.4:c.487C>T, NM_014297.4:c.440_450delACAGCATGGCC, NM_014297.4:c.221dupA	Ethylmalonic encephalopathy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ETHE1 gene located on chromosomal region 19q13.31. The age of onset is neonatal/infantile. This disease is characterized by elevated excretion of ethylmalonic acid with recurrent petechiae, orthostatic acrocyanosis and chronic diarrhoea associated with neurodevelopmental delay, psychomotor regression and hypotonia with brain magnetic resonance imaging abnormalities. The prevalence is below 1/1,000,000, with total of 30 cases of patients reported worldwide, mainly for Mediterranean and Arab populations.	600
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
F8	Hemophilia A	0	Inv22	Hemophilia A follows an X-linked pattern of inheritance and is caused by pathogenic variants in the F8 gene located on chromosomal region Xq28. The age of onset is neonatal/infantile. This disease is characterized by spontaneous or prolonged hemorrhages due to factor VIII deficiency. The prevalence is 1/4,000 to 1/ 5,000 male newborns.	600
F8	Hemophilia A	NM_000132.3	NM_000132.3:c.7033_7040delTGCGAGGC, NM_000132.3:c.7034G>A, NM_000132.3:c.7031G>A, NM_000132.3:c.7030G>T, NM_000132.3:c.7030G>A, NM_000132.3:c.7021G>T, NM_000132.3:c.7016G>T, NM_000132.3:c.7012delC, NM_000132.3:c.6997delG, NM_000132.3:c.6996G>A, NM_000132.3:c.6995G>C, NM_000132.3:c.6988delC, NM_000132.3:c.6986C>T, NM_000132.3:c.6976C>G, NM_000132.3:c.6914_6918delATCAA, NM_000132.3:c.6915delT, NM_000132.3:c.6905T>C, NM_000132.3:c.6904T>G, NM_000132.3:c.6901-2A>G, NM_000132.3:c.6900+1G>A, NM_000132.3:c.6887delA, NM_000132.3:c.6870G>A, NM_000132.3:c.6869G>T, NM_000132.3:c.6857_6867delATGGCCATCAG, NM_000132.3:c.6865C>T, NM_000132.3:c.6842T>C, NM_000132.3:c.6839T>C, NM_000132.3:c.6836T>G, NM_000132.3:c.6836T>C, NM_000132.3:c.6825T>A, NM_000132.3:c.6804delA, NM_000132.3:c.6797delG, NM_000132.3:c.6797G>A, NM_000132.3:c.6796G>A, NM_000132.3:c.6780_6788delAGGAGTAAC, NM_000132.3:c.6786_6787insCAA, NM_000132.3:c.6760delC, NM_000132.3:c.6760C>T, NM_000132.3:c.6752T>A, NM_000132.3:c.6746T>G, NM_000132.3:c.6743G>C, NM_000132.3:c.6740_6741delAG, NM_000132.3:c.6739G>T, NM_000132.3:c.6738delA, NM_000132.3:c.6574+5G>C, NM_000132.3:c.6574+3A>C, NM_000132.3:c.6574+1G>T, NM_000132.3:c.6574+1G>A, NM_000132.3:c.6565_6566delGA, NM_000132.3:c.6551A>T, NM_000132.3:c.6548T>G, NM_000132.3:c.6544C>G, NM_000132.3:c.6537C>G, NM_000132.3:c.6533G>A, NM_000132.3:c.6520C>G, NM_000132.3:c.6515C>G, NM_000132.3:c.6501delC, NM_000132.3:c.6497delG, NM_000132.3:c.6494delC, NM_000132.3:c.6489delT, NM_000132.3:c.6488T>G, NM_000132.3:c.6482C>T, NM_000132.3:c.6482C>A, NM_000132.3:c.6477delT, NM_000132.3:c.6469_6470delAA, NM_000132.3:c.6465delA, NM_000132.3:c.6464_6465delAA, NM_000132.3:c.6449A>T, NM_000132.3:c.6430-3C>G, NM_000132.3:c.6273+1G>A, NM_000132.3:c.6269T>A, NM_000132.3:c.6263C>T, NM_000132.3:c.6253G>T, NM_000132.3:c.6250A>T, NM_000132.3:c.6243G>C, NM_000132.3:c.6242G>C, NM_000132.3:c.6239C>T, NM_000132.3:c.6213A>T, NM_000132.3:c.6194G>A, NM_000132.3:c.6136dupA, NM_000132.3:c.6124G>T, NM_000132.3:c.6120delC, NM_000132.3:c.6120T>A	Hemophilia A follows an X-linked pattern of inheritance and is caused by pathogenic variants in the F8 gene located on chromosomal region Xq28. The age of onset is neonatal/infantile. This disease is characterized by spontaneous or prolonged hemorrhages due to factor VIII deficiency. The prevalence is 1/4,000 to 1/ 5,000 male newborns.	600

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
FAM126A	Hypomyelinating leukodystrophy, type 5	NM_032581.3	NM_032581.3:c.158T>C	Hypomyelinating leukodystrophy, type 5 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FAM126A gene located on chromosomal region 7p15.3. The age of onset is neonatal/infantile. This disease is characterized by the onset of cataract either at birth or in the first two months of life, delayed psychomotor development by the end of the first year of life and moderate intellectual deficit. The prevalence is below 1/1,000,000.	600
FAM20C	Raine syndrome	NM_020223.3	NM_020223.3:c.1093G>C, NM_020223.3:c.1163T>G	Raine syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FAM20C gene located on chromosomal region 7p22.3. The age of onset is neonatal/infantile. This disease is characterized by generalized osteosclerosis with periosteal bone formation, characteristic facial dysmorphism, brain abnormalities including intracerebral calcifications, and neonatal lethal course. The prevalence is below 1/1,000,000.	600
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
FGA	Afibrinogenemia, congenital	NM_000508.4	NM_000508.4:c.1441delG, NM_000508.4:c.1359dupC, NM_000508.4:c.1039C>T	Congenital afibrinogenemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FGA 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

FGA	Afibrinogenemia, congenital	NM_021871.3	NM_021871.3:c.1906dupC	Congenital afibrinogenemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FGA 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
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
FGD4	Charcot-Marie-Tooth disease, type 4H	NM_001304480.1	NM_001304480.1:c.1006C>T, NM_001304480.1:c.1229T>C, NM_001304480.1:c.1229T>G, NM_001304480.1:c.1661G>A	Charcot-Marie-Tooth disease, type 4H follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FGD4 gene located on chromosomal region 12p11.21. The age of onset is neonatal/infantile. This disease is characterized by slowly progressive muscle weakness in the distal extremities, and other common features include delayed walking, an abnormal gait, scoliosis and pes equines with toe retraction. The prevalence is 1/3,300.	600
FH	Fumarase deficiency	NM_000143.3	NM_000143.3:c.1446_1449delAAAG, NM_000143.3:c.1431_1433dupAAA, NM_000143.3:c.1394A>G, NM_000143.3:c.1293delA, NM_000143.3:c.1255T>C, NM_000143.3:c.1236+1G>C, NM_000143.3:c.1200delT, NM_000143.3:c.1189G>A, NM_000143.3:c.1093A>G, NM_000143.3:c.1067T>A, NM_000143.3:c.901dupA, NM_000143.3:c.793G>A, NM_000143.3:c.760C>T, NM_000143.3:c.698G>A, NM_000143.3:c.697C>T, NM_000143.3:c.521C>G, NM_000143.3:c.320A>C, NM_000143.3:c.40dupC	Fumarase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FH gene located on chromosomal region 1q42.1. The age of onset is neonatal/infantile. This disease is characterized byï¾ hypotonia, severe psychomotor impairment, convulsions, respiratory distress, feeding difficulties and frequent cerebral malformations, along with a distinctive facies, although some patients present with only moderate intellectual impairment. The prevalence is below 1,000,000.	600
FHL1	Emery-Dreifuss muscular dystrophy, type 6, X-linked	NM_001159702.2	NM_001159702.2:c.310T>C, NM_001159702.2:c.625T>C, NM_001159702.2:c.838G>A	Emery-Dreifuss muscular dystrophy, type 6, X-linked follows an X-linked pattern of inheritance and is caused by pathogenic variants in the FHL1 gene located on chromosomal region Xq26. ï¾ This is a condition that primarily affects muscles used for movement (skeletalï¾ muscles) and the heart (cardiac muscle). Among the earliest features of this disorder are joint deformities called contractures. Contractures restrict the movement of certain joints, most often the elbows, ankles, and neck, and usually become noticeable in early childhood. Most affected individuals also experience muscle weakness andï¾ wastingï¾ that worsen slowly over time, beginning in muscles of the upper arms and lower legs and later also affecting muscles in the shoulders and hips. Almost all people with Emery-Dreifuss muscular dystrophy develop heart problems by adulthood. The X-linked type of this disorder affects an estimated 1 in 100,000 people.	600
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
FKTN	Muscular dystrophy-dystroglycanopathy, type 4A, 4B and 4C	NM_001079802.1	NM_001079802.1:c.411C>A, NM_001079802.1:c.509C>A, NM_001079802.1:c.527T>C, NM_001079802.1:c.766C>T, NM_001079802.1:c.1112A>G, NM_001079802.1:c.1167dupA, NM_001079802.1:c.1380dupA	Muscular dystrophy-dystroglycanopathy type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FKTN gene located on chromosomal region 9q31.2. The age of onset is neonatal or early infancy. There are three subtypes of dystroglycanopathies related to FKTN gene: subtype 4A, 4B and 4C. Subtype 4A is the most severe phenotype and is associated with congenital brain and eye anomalies, seizures, 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 4B represents an intermediate phenotype and congenital mental retardation is not a feature. Finally, subtype 4C is the less severe phenotype characterized by limb-girdle muscular dystrophy, onset in early childhood and cognition and brain structure are usually normal.	600
FLNA	FLNA-related disorders	NM_001110556.1	NM_001110556.1:c.7757-1G>C, NM_001110556.1:c.7551_7552+6delAGGTGAGC, NM_001110556.1:c.7153C>T, NM_001110556.1:c.5132_5133delTCinsAA, NM_001110556.1:c.4777_4778dupAA, NM_001110556.1:c.4543C>T, NM_001110556.1:c.4446_4447dupAT, NM_001110556.1:c.3557C>T, NM_001110556.1:c.3476A>C, NM_001110556.1:c.2761C>T, NM_001110556.1:c.760G>A	Mutation in FLNA causes a wide spectrum of disease including skeletal dysplasia, neuronal migration abnormality, cardiovascular malformation, intellectual disability and intestinal obstruction. FLNA-related disorders can be X-linked recessive (XLR) or X-linked dominant (XLD). Frontometaphyseal dysplasia-1 (FMD1;XLR) is 1 of 4 otopalatodigital syndromes caused by mutations in the FLNA gene. The disorders, which include otopalatodigital syndrome-1 (OPD1; XLD; OMIMï¾ 311300), otopalatodigital syndrome-2 (OPD2; XLD;ï¾ 304120), and Melnick-Needles syndrome (MNS; XLD;ï¾ 309350), constitute a phenotypic spectrum. At the mild end of the spectrum, males with OPD1 have cleft palate and mild skeletal anomalies with conductive deafness caused by ossicular anomalies. FMD1 is characterized by a generalized skeletal dysplasia, deafness, and urogenital defects. Males with OPD2 have disabling skeletal anomalies in addition to variable malformations in the hindbrain, heart, intestines, and kidneys that frequently lead to perinatal death. The most severe phenotype, MNS, is characterized by a skeletal dysplasia in the heterozygote. Affected males exhibit severe malformations similar to those observed in individuals with OPD2, resulting in prenatal lethality or death in the first few months of life (review byï¾ Robertson, 2005).ï¾ Verloes et al. (2000)ï¾ suggested that these disorders constitute a single entity, which they termed 'frontootopalatodigital osteodysplasia.' Other studies confirm an association between FLNA gene mutation and lung disease, seen in more than 80% of patients with cerebral periventricular nodular heterotopia (PVNH; XLD; 300049); FLNA mutation also cause cardiac valvular dysplasia (XLR; 314400). De novo mutations and mosaic cases have been described.	600

FLVCR1	Posterior column ataxia-retinitis pigmentosa syndrome	NM_014053.3	NM_014053.3:c.361A>G, NM_014053.3:c.574T>C, NM_014053.3:c.739-2delA	Posterior column ataxia-retinitis pigmentosa follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FLVCR1 gene located on chromosomal region 1q32.3. The age of onset is childhood. This disease is characterized by sensory ataxia, proprioceptive loss and blindness. The prevalence is <1 / 1.000.000.	600
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
FOXN1	T-cell immunodeficiency, congenital alopecia and nail dystrophy	NM_003593.2	NM_003593.2:c.763C>T	T-cell immunodeficiency, congenital alopecia and nail dystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FOXN1 gene located on chromosomal region 17q11.2. The age of onset is infantile. This disease is characterized by T-cell immunodeficiency, the skin disorder congenital alopecia, and nail dystrophy. The prevalence is <1:1,000,000.	600
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
FREM2	Fraser syndrome, type 2	NM_207361.5	NM_207361.5:c.2366dupC, NM_207361.5:c.3792_3795delTTAT, NM_207361.5:c.5920G>A, NM_207361.5:c.8409+1G>A	Fraser syndrome, type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the gene FREM2 located on chromosomal region 13q13.3. 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
FUCA1	Fucosidosis	NM_000147.4	NM_000147.4:c.1279C>T, NM_000147.4:c.1229T>G, NM_000147.4:c.856C>T, NM_000147.4:c.648C>A, NM_000147.4:c.244C>T	Fucosidosis follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the FUCA1 gene located on chromosomal region 1p36.11. The age of onset is infantile. This disease is characterized by facial dysmorphism, dysostosis multiplex, moderate hepatomegaly, severe intellectual deficit, deafness, and according to age, angiokeratomas. The prevalence is <1:1,000,000.	600
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
G6PC3	Dursun syndrome	NM_138387.3	NM_138387.3:c.141C>G, NM_138387.3:c.346A>G, NM_138387.3:c.758G>A, NM_138387.3:c.778G>C, NM_138387.3:c.784G>C, NM_138387.3:c.935dupT	Dursun syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the G6PC3 gene located on chromosomal region 17q21.31. This disease is characterized by familial pulmonary arterial hypertension, cardiac abnormalities including atrial septal defect, leukopenia including intermittent neutropenia, lymphopenia, monocytosis, and anemia. The prevalence is 1:100,000.	600

GAA	Glycogen storage disease 2	NM_000152.4	NM_000152.4:c.118C>T, NM_000152.4:c.236_246delCCACACAGTGC, NM_000152.4:c.307T>G, NM_000152.4:c.525delT, NM_000152.4:c.546+2_546+5delTGGG, NM_000152.4:c.546G>A, NM_000152.4:c.546G>C, NM_000152.4:c.655G>A, NM_000152.4:c.698delA, NM_000152.4:c.768dupT, NM_000152.4:c.853C>T, NM_000152.4:c.877G>A, NM_000152.4:c.925G>A, NM_000152.4:c.1064T>C, NM_000152.4:c.1115A>T, NM_000152.4:c.1316T>A, NM_000152.4:c.1327-2A>G, NM_000152.4:c.1431delT, NM_000152.4:c.1465G>A, NM_000152.4:c.1548G>A, NM_000152.4:c.1552-3C>G, NM_000152.4:c.1561G>A, NM_000152.4:c.1585_1586delTCinsGT, NM_000152.4:c.1634C>T, NM_000152.4:c.1650dupG, NM_000152.4:c.1799G>A, NM_000152.4:c.1827_1828insA, NM_000152.4:c.1847dupA, NM_000152.4:c.1912G>T, NM_000152.4:c.1927G>A, NM_000152.4:c.1933G>T, NM_000152.4:c.1935C>A, NM_000152.4:c.2012T>G, NM_000152.4:c.2015G>A, NM_000152.4:c.2041-1G>A, NM_000152.4:c.2066_2070dupAGCCG, NM_000152.4:c.2105G>T, NM_000152.4:c.2237G>A, NM_000152.4:c.2238G>A, NM_000152.4:c.2238G>C, NM_000152.4:c.2512C>T, NM_000152.4:c.2544delC, NM_000152.4:c.2560C>T	Glycogen storage disease, type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GAA gene located on chromosomal region 17q25.3. There are two forms: adult and infantile.The age of onset in this last form is before the age of three months. This disease is characterized by severe hypotonia, hypertrophic cardiomyopathy and progressive hepatomegaly. The incidence is 1/57,000 for the adult form and 1/138,000 for infantile form.	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
GAMT	Cerebral creatine deficiency syndrome type 2	NM_138924.2	NM_138924.2:c.506G>A	Cerebral creatine deficiency syndrome type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GAMT gene located on chromosomal region 19p13.3. The age of onset is infantile. This disease is characterized by intellectual disability, seizures and behavioral problems, often in conjunction with pyramidal and/or extrapyramidal manifestations with muscular hypotony. Biochemical symptoms are also included with high urinary excretion of guanidinoacetate, low urinary excretion of creatinine and creatine depletion in brain and muscles.	600

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
GDAP1	Charcot-Marie-Tooth disease, recessive intermediate, type A	NM_018972.2	NM_018972.2:c.92G>A, NM_018972.2:c.311-1G>A, NM_018972.2:c.358C>T, NM_018972.2:c.487C>T, NM_018972.2:c.715C>T, NM_018972.2:c.844C>T	Autosomal recessive intermediate Charcot-Marie-Tooth disease type A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GDAP1 gene located on chromosomal region 8q21.11. The age of onset is usually in early childhood. This disease is characterized by by distal sensory impairment predominantly affecting the lower limbs and resulting in walking difficulties due to muscle weakness and atrophy. The upper limbs may also be affected. The prevalence is below 1/1,000,000.	600
GFM1	Combined oxidative phosphorylation deficiency, type 1	NM_001308164.1	NM_001308164.1:c.139C>T, NM_001308164.1:c.521A>G, NM_001308164.1:c.805C>T, NM_001308164.1:c.1354_1357delGACA, NM_001308164.1:c.1589_1590delAG	Combined oxidative phosphorylation deficiency, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GFM1 gene located on chromosomal region 3q25.32. The age of onset is from early infancy until adult. This disease is characterized by ptosis, external ophthalmoplegia, proximal myopathy and exercise intolerance, cardiomyopathy, sensorineural deafness, optic atrophy, pigmentary retinopathy, and diabetes mellitus.	600

GJA1	Craniometaphyseal dysplasia, autosomal recessive	NM_000165.4	NM_000165.4:c.97C>T, NM_000165.4:c.227G>A	Craniometaphyseal dysplasia, autosomal recessive follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GJA1 gene located on chromosomal region 6q22.31. The age of onset is infantile. This disease is characterized by hyperostosis and sclerosis of the craniofacial bones associated with abnormal modeling of the metaphyses. Sclerosis of the skull may lead to asymmetry of the mandible, as well as to cranial nerve compression, that may finally result in hearing loss and facial pals. The prevalence is below 1/1,000,000.	600
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
GJC2	Spastic paraplegia, type 44, autosomal recessive	NM_020435.3	NM_020435.3:c.268C>T, NM_020435.3:c.613C>T, NM_020435.3:c.718C>T, NM_020435.3:c.787G>A, NM_020435.3:c.814T>G, NM_020435.3:c.857T>C	Autosomal recessive spastic paraplegia type 44 (SPG44) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GJC2 gene located on chromosomal region 1q42.13. This disease is characterized by a late-onset, slowly progressive spastic paraplegia associated with mild ataxia and dysarthria, upper extremity involvement (i.e. loss of finger dexterity, dysmetria), and mild cognitive impairment, without the presence of nystagmus. A hypomyelinating leukodystrophy and thin corpus callosum is observed in all cases and psychomotor development is normal or near normal. The prevalence is below 1/1,000,000.	600
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
GM2A	GM2-gangliosidosis, AB variant	NM_000405.4	NM_000405.4:c.160G>T, NM_000405.4:c.285delC, NM_000405.4:c.506G>C	GM2-gangliosidosis, AB variant follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GM2A gene located on chromosomal region 5q33.1. The age of onset is infantile. This disease is characterized by a group of neurodegenerative disorders: seizures, blindness, spasticity, eventual total incapacitation, and death. The prevalence is <1:100.000.	600
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
GNS	Mucopolysaccharidosis, type 3D (Sanfilippo D)	NM_002076.3	NM_002076.3:c.1226dupG, NM_002076.3:c.1169delA, NM_002076.3:c.1168C>T, NM_002076.3:c.1063C>T, NM_002076.3:c.413C>G	Mucolipidosis type 3D (Sanfilippo disease) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GNS gene located on chromosomal region 12q14.3. The age of onset is infantile. This disease is characterized by joint stiffness and pain initially in the shoulders, hips, and fingers; and gradual mild coarsening of facial features, cardiorespiratory complications and mild cognitive impairment. The incidence is 1:70,000 newborn.	600
GPR143	Ocular albinism, type 1 (Nettleship-Falls type)	NM_000273.2	NM_000273.2:c.992_993insCG, NM_000273.2:c.695C>A	X-linked recessive ocular albinism follows an X-linked pattern of inheritance and is caused by pathogenic variants in the GPR143 gene located on chromosomal region Xp22.2. The age of onset is infantile. This condition reduces the coloring (pigmentation) of the iris, which is the colored part of the eye, and the retina, which is the light-sensitive tissue at the back of the eye. Pigmentation in the eye is essential for normal vision. Ocular albinism type I (OA1) is the most common form of ocular albinism. Clinical presentation of OA1 in Caucasians is characterized by nystagmus, impaired visual acuity, iris hypopigmentation with translucency, albinotic fundus, macular hypoplasia, and normally pigmented skin and hair. Carrier females usually have punctate iris translucency and a mottled pattern of fundus pigmentation. In contrast to Caucasian patients, black or Japanese patients with OA1 often have brown irides with little or no translucency and varying degrees of fundus hypopigmentation, the so-called 'nonalbinotic fundus' (summary by Xiao and Zhang, 2009). The prevalence is 1/60,000 to 1/150,000 live male births.	600

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
GRHPR	Hyperoxaluria, primary, type 2	NM_012203.1	NM_012203.1:c.103delG, NM_012203.1:c.295C>T, NM_012203.1:c.435G>A, NM_012203.1:c.622C>T, NM_012203.1:c.755dupA	Primary hyperoxaluria, type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GRHPR gene located on chromosomal region 9p13.2. The age of onset is infantile. This disease is characterized by recurrent nephrolithiasis, nephrocalcinosis and end-stage renal disease with subsequent systemic oxalosis.	600
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
GRXCR1	Deafness, autosomal recessive, type 25	NM_001080476.2	NM_001080476.2:c.229C>T, NM_001080476.2:c.710_711delAT	Autosomal recessive nonsyndromic sensorineural deafness type 25 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GRXCR1 gene located on chromosomal region 4p13. The age of onset is infantile. This disease is characterized by hearing loss which is not associated visible abnormalities of the external ear or any related medical problems.	600
GSS	Glutathione synthetase deficiency	NM_000178.3	NM_000178.3:c.847C>T, NM_000178.3:c.832C>T, NM_000178.3:c.799C>T, NM_000178.3:c.754C>T, NM_000178.3:c.656A>G, NM_000178.3:c.656A>C, NM_000178.3:c.491G>A	Glutathione synthetase deficiency with 5-oxoprolinuria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GSS gene located on chromosomal region 20q11.22. The severity and age of onset are variable. This disease is characterized by affectation of the neutrophil respiratory burst and can increase host susceptibility to infections, is associated with hemolytic anemia and intellectual disability. The prevalence is <1:1,000,000.	600
GUCY2D	Leber congenital amaurosis, type 1	NM_000180.3	NM_000180.3:c.456C>A, NM_000180.3:c.622delC, NM_000180.3:c.1694T>C, NM_000180.3:c.2735_2736delTT, NM_000180.3:c.2945delG	Leber congenital amaurosis type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GUCY2D gene located on chromosomal region 17p13.1. The age of onset is infantile. This disease is characterized by blindness, nystagmus, roving eye movement and severe visual impairment.	600
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

HADHB	Trifunctional protein deficiency	NM_000183.2	NM_000183.2:c.788A>G, NM_000183.2:c.1331G>A, NM_000183.2:c.1364T>G	Mitochondrial trifunctional protein deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in HADHB gene located on chromosomal region 2p23.3. The age of onset is neonatal/infancy. It is characterized by a wide clinical spectrum ranging from severe neonatal manifestations including cardiomyopathy, hypoglycemia, metabolic acidosis, skeletal myopathy and neuropathy, liver disease and death to a mild phenotype with peripheral polyneuropathy, episodic rhabdomyolysis and pigmentary retinopathy. The prevalence is <1 / 1,000,000.	600
HBA1/HBA2	Thalassemia, alpha-	0	-?3.7, -?4.2, -(?)20.5, --SEA, --MED, --FIL, --THAI	Alpha-thalassemia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HBA1 gene located on chromosomal region 16p13.3. The age of onset is infantile. It is characterized by impaired synthesis of alpha-globin chains leading to a variable clinical picture depending on the number of affected alleles. The disease can be classified into clinical subtypes of increasing severity: silent alpha thalassemia, alpha thalassemia trait (or alpha thalassemia minor), hemoglobin H disease (HbH), and Hb Bart's hydrops fetalis (see these terms). A rare form called alpha-thalassemia-intellectual deficit syndrome has also been identified (see these terms). Alpha thalassemia trait causes microcytosis and hypochromia with absent or mild anemia (often detected on routine blood tests), generally with no other symptoms. HbH patients develop moderate hemolytic anemia with variable amounts of HbH along with occasionally severe splenomegaly, sometimes complicated by hypersplenism. Hb Bart's hydrops fetalis involves a severe deficiency in alpha-globin with serious developmental implications. Alpha-thalassemia-intellectual deficit syndrome is characterized by very mild to severe anemia associated with developmental abnormalities. The prevalence is 1:10,000-5:10,000.	600
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>C, NM_000518.4:c.127T>G, NM_000518.4:c.114_129delCAGGCAC	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
HGF	Deafness, autosomal recessive, type 39	NM_000601.5	NM_000601.5:c.2028delA, NM_000601.5:c.1597C>T	Autosomal recessive nonsyndromic sensorineural deafness type 39 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HGF gene located on chromosomal region 7q21.11. 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
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

HIBCH	3-hydroxyisobutryl-CoA hydrolase deficiency	NM_014362.3	NM_014362.3:c.1012A>T, NM_014362.3:c.494_495delTT, NM_014362.3:c.365A>G, NM_014362.3:c.220-9T>G, NM_014362.3:c.79-3C>G	3-Hydroxyisobutryl-CoA hydrolase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HIBCH gene located on chromosomal region 2q32.2. The age of onset is infantile. This disease is characterized by delayed motor development, hypotonia and progressive neurodegeneration. The prevalence is <1:1,000,000.	600
HMGCL	HMG-CoA lyase deficiency	NM_000191.2	NM_000191.2:c.835G>A, NM_000191.2:c.698A>G, NM_000191.2:c.505_506delTC, NM_000191.2:c.230delT, NM_000191.2:c.206_207delCT, NM_000191.2:c.122G>A	3-hydroxy-3-methylglutaric aciduria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HMGCL gene located on chromosomal region 1p36.11. The age of onset is infantile. This disease is is an organic aciduria, due to deficiency of 3-hydroxy-3-methylglutaryl-CoA-lyase (a key enzyme in ketogenesis and leucine metabolism) usually presenting in infancy with episodes of metabolic decompensation triggered by periods of fasting or infections, which when left untreated are life-threatening and may lead to neurological sequelae.	600
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
HPRT1	Lesch-Nyhan syndrome	NM_000194.2	NM_000194.2:c.486-1G>A, NM_000194.2:c.508C>T, NM_000194.2:c.532+2T>G, NM_000194.2:c.610-2A>G	Lesch-Nyhan syndrome follows an X-linked pattern of inheritance and is caused by pathogenic variants in the HPRT1 gene located on chromosomal region Xq26.2-q26.3. The age of onset is infantile. This disease is characterized by acid overproduction, neurological troubles, and behavioral problems. The prevalence is 1:380,000.	600
HPS1	Hermansky-Pudlak syndrome, type 1	NM_000195.4	NM_000195.4:c.1996G>T, NM_000195.4:c.972dupC, NM_000195.4:c.972delC, NM_000195.4:c.398+5G>A, NM_000195.4:c.397G>T	Hermansky-Pudlak syndrome, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HPS1 gene located on chromosomal region 10q24.2. The age of onset is early childhood. This disease is characterized by oculocutaneous albinism, bleeding diathesis and, in some cases, neutropenia, pulmonary fibrosis, or granulomatous colitis. The prevalence is 1/500,000 - 1/1,000,000.	600
HSD17B4	D-bifunctional protein deficiency	NM_000414.3	NM_000414.3:c.46G>A	Bifunctional enzyme deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HSD17B4 gene located on chromosomal region 5q23. The age of onset is juvenile. This disease is characterized by slowly progressive cerebellar atrophy and ataxia, intellectual decline, hearing loss, hypogonadism, hyperreflexia, a demyelinating sensorimotor neuropathy.	600
HSD17B4	D-bifunctional protein deficiency	NM_001199291.2	NM_001199291.2:c.392G>C, NM_001199291.2:c.725A>G, NM_001199291.2:c.1047+1G>T, NM_001199291.2:c.1444A>T	Bifunctional enzyme deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HSD17B4 gene located on chromosomal region 5q23. The age of onset is juvenile. This disease is characterized by slowly progressive cerebellar atrophy and ataxia, intellectual decline, hearing loss, hypogonadism, hyperreflexia, a demyelinating sensorimotor neuropathy.	600
HSPD1	Leukodystrophy, hypomyelinating, type 4	NM_002156.4	NM_002156.4:c.292G>A	Leukodystrophy hypomyelinating, type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HSPD1 gene located on chromosomal region 2q33.1. The age of onset is infantile. A severe autosomal recessive hypomyelinating leukodystrophy. Clinically characterized by infantile-onset rotary nystagmus, progressive spastic paraplegia, neurologic regression, motor impairment, profound mental retardation. Death usually occurs within the first two decades of life.	600

HSPG2	Dyssegmental dysplasia, Silverman-Handmaker type	NM_001291860.1	NM_001291860.1:c.13078delC, NM_001291860.1:c.9329delA, NM_001291860.1:c.8467+4A>G, NM_001291860.1:c.1656_1657insT, NM_001291860.1:c.1125C>A	Dyssegmental dysplasia, Silverman-Handmaker type follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HSPG2 gene located on chromosomal region 1p36.12. The age of onset is prenatal/neonatal. This disease is characterized by anisospondyly, severe short stature and limb shortening, metaphyseal flaring and distinct dysmorphic features (i.e. flat facial appearance, abnormal ears, short neck, narrow thorax). Additional features may include other skeletal findings (e.g. joint contractures, bowed limbs, talipes equinovarus) and urogenital and cardiovascular abnormalities. The prevalence is below 1/1,000,000.	600
HTRA1	CARASIL syndrome	NM_002775.4	NM_002775.4:c.754G>A, NM_002775.4:c.883G>A, NM_002775.4:c.889G>A, NM_002775.4:c.904C>T, NM_002775.4:c.1108C>T	Cerebral autosomal recessive arteriopathy with subcortical infarcts and leukoencephalopathy (CARASIL syndrome) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HTRA1 gene located on chromosomal region 10q26.13. The age of onset is adult. This disease is characterized by early-onset gait disturbances, premature scalp alopecia, ischemic stroke, acute mid to lower back pain and progressive cognitive disturbances leading to severe dementia. About 50 people diagnosed, mainly in Japan and China.	600
HYLS1	Hydrolethalus syndrome	NM_001134793.1	NM_001134793.1:c.632A>G, NM_001134793.1:c.669G>A, NM_001134793.1:c.724C>T	Hydrolethalus syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the HYLS1 gene located on chromosomal region 11q24.2. The age of onset is fetal. This disease is characterized by craniofacial dysmorphic features, central nervous system, cardiac, respiratory tract and limb abnormalities. The incidence is 1/20,000 in Finland and the prevalence is <1:1,000,000.	600
IDH3B	Retinitis pigmentosa, type 46	NM_006899.4	NM_006899.4:c.589delA, NM_006899.4:c.490C>T, NM_006899.4:c.395T>C	Retinitis pigmentosa, type 46 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the IDH3B gene located on chromosomal region 20p13. The age of onset is variable. This disease is characterized by night blindness, followed by a progressive loss of peripheral vision in the daylight period and leading to blindness. The prevalence is 1/3,000 to 1/5,000.	600
IDS	Mucopolysaccharidosis, type 2	NM_000202.7	NM_000202.7:c.1508T>A, NM_000202.7:c.1505G>C, NM_000202.7:c.1148delC, NM_000202.7:c.1122C>T, NM_000202.7:c.998C>T, NM_000202.7:c.880-8A>G, NM_000202.7:c.690_691insT, NM_000202.7:c.683C>T, NM_000202.7:c.596_599delAACA, NM_000202.7:c.597delA, NM_000202.7:c.587T>C, NM_000202.7:c.514C>T, NM_000202.7:c.404A>G, NM_000202.7:c.388_389insG, NM_000202.7:c.314_317dupTCAA, NM_000202.7:c.278delC, NM_000202.7:c.240+1G>A, NM_000202.7:c.208dupC	Mucopolysaccharidosis, type 2 follows an X-linked pattern of inheritance and is caused by pathogenic variants in the IDS gene located on chromosomal region Xq28. The age of onset is infantile. This disease is characterized by distinctive coarse facial features, short stature, cardio-respiratory involvement and skeletal abnormalities. The prevalence is 1:100,000-1:170,000 mannewborn.	600
IDS	Mucopolysaccharidosis, type 2	NM_001166550.3	NM_001166550.3:c.15-2A>G	Mucopolysaccharidosis, type 2 follows an X-linked pattern of inheritance and is caused by pathogenic variants in the IDS gene located on chromosomal region Xq28. The age of onset is infantile. This disease is characterized by distinctive coarse facial features, short stature, cardio-respiratory involvement and skeletal abnormalities. The prevalence is 1:100,000-1:170,000 mannewborn.	600
IFT80	Short-rib thoracic dysplasia, type 2, with or without polydactyly	NM_020800.2	NM_020800.2:c.701C>G, NM_020800.2:c.315C>G	Short-rib thoracic dysplasia type 2 with or without polydactyly an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the IFT80 gene located on chromosomal region 3q25.33. The age of onset is antenatal/neonatal. This is, a group of autosomal recessive ciliopathies that are characterized by a constricted thoracic cage, short ribs, shortened tubular bones, and a trident appearance of the acetabular roof. Polydactyly is variably present. Non-skeletal involvement can include cleft lip/palate as well as anomalies of major organs such as the brain, eye, heart, kidneys, liver, pancreas, intestines, and genitalia. Some forms of the disease are lethal in the neonatal period due to respiratory insufficiency secondary to a severely restricted thoracic cage, whereas others are compatible with life. Disease spectrum encompasses Ellis-van Creveld syndrome, asphyxiating thoracic dystrophy (Jeune syndrome), Mainzer-Saldino syndrome, and short rib-polydactyly syndrome. The incidence is 1-5/500,000.	600

IGF1	Growth retardation with deafness and mental retardation due to IGF1 deficiency	NM_001111285.2	NM_001111285.2:c.274G>A	Growth retardation with deafness and mental retardation due to IGF1 deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the IGF1 gene located on chromosomal region 12q23.2. The age of onset is infantile. This disease is characterized by the association of intrauterine and postnatal growth retardation with sensorineural deafness and intellectual deficit, addition clinical features include microcephaly, adiposity, and insulin resistance. The prevalence is <1:1,000,000.	600
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
IL2RG	Severe combined immunodeficiency, X-linked	NM_000206.2	NM_000206.2:c.854G>A, NM_000206.2:c.664C>T, NM_000206.2:c.454+1G>A, NM_000206.2:c.452T>C, NM_000206.2:c.355A>T, NM_000206.2:c.343T>C, NM_000206.2:c.341G>A, NM_000206.2:c.186T>A	Severe combined immunodeficiency, X-linked follows an X-linked pattern of inheritance and is caused by pathogenic variants in the IL2RG gene located on chromosomal region Xq13.1. The age of onset is infantile. This disease is characterized by absent or markedly reduced numbers of T cells, leading to recurrent infections. The prevalence is 1:50,000-1:100,000.	600
IMPG2	Retinitis pigmentosa, type 56	NM_016247.3	NM_016247.3:c.3262C>T, NM_016247.3:c.2890C>T, NM_016247.3:c.635C>G, NM_016247.3:c.502-1G>C	Retinitis pigmentosa type 56 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the IMPG2 gene located on chromosomal region 3q12.3. The age of onset is infantile. This disease is characterized by progressive loss of the photoreceptors and retinal pigment epithelium and resulting in blindness usually after several decades. The prevalence is 1/4.000.	600
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

IQCB1	Senior-Loken syndrome, type 5	NM_001023570.3	NM_001023570.3:c.1518_1519delCA, NM_001023570.3:c.1465C>T, NM_001023570.3:c.1381C>T, NM_001023570.3:c.1090C>T, NM_001023570.3:c.1069C>T, NM_001023570.3:c.1036G>T, NM_001023570.3:c.817G>T	Senior-Loken syndrome, type 5 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the IQCB1 gene located on chromosomal region 3q13.33. The age of onset is infantile. This disease is characterized by the association of nephronophthisis (NPHP), a chronic kidney disease, with retinal dystrophy. The prevalence is 1/1.000.000.	600
ISCU	Myopathy with lactic acidosis, hereditary	NM_213595.3	NM_213595.3:c.149G>A, NM_213595.3:c.338_339+2delCGGT	Hereditary myopathy with lactic acidosis due to ISCU deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ISCU gene located on chromosomal region 12q23.3. The age of onset is infantile. This disease is characterized by myopathy with severe exercise intolerance.	600
ITGA6	Epidermolysis bullosa, junctional, with pyloric stenosis	NM_001079818.2	NM_001079818.2:c.791delC, NM_001079818.2:c.1255dupA	Junctional epidermolysis bullosa with pyloric atresia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ITGA6 gene located on chromosomal region 2q31.1 . 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.	600
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
KCNJ13	Leber congenital amaurosis, type 16	NM_002242.4	NM_002242.4:c.722T>C	Leber congenital amaurosis, type 16 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the KCNJ13 gene located on chromosomal region 2q37.1. The age of onset is early infantile. This disease is characterized by retinal dystrophy defined by blindness, nystagmus, roving eye movement, leading to severe visual impairment within the first year of life.	600

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
KIF7	Acrocallosal syndrome; Joubert syndrome, type 12	NM_198525.2	NM_198525.2:c.3772_3773insC, NM_198525.2:c.3001C>T, NM_198525.2:c.2896_2897delGC, NM_198525.2:c.2473G>T, NM_198525.2:c.687delG, NM_198525.2:c.460C>T, NM_198525.2:c.61C>T	Acrocallosal syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the KIF7 gene located on chromosomal region 15q26.1. The age of onset is infantile. This disease is considered a ciliopathy and is characterized by mental retardation, brain abnormalities such as corpus callosum agenesis and/or Dandy-Walker malformation as well as dysmorphic features, postaxial polydactyly of the hands, and preaxial polydactyly of the feet. The prevalence is below 1/1,000,000. Mutations in KIF7 gene are also associated with Joubert syndrome type 12, a disorder with an acrocallosal syndrome overlapping phenotype characterized by the hallmark finding of the molar tooth sign (MTS) on brain MRI.	600
L1CAM	L1 Syndrome	NM_000425.4	NM_000425.4:c.3581C>T, NM_000425.4:c.3489_3490delTG, NM_000425.4:c.3201T>G, NM_000425.4:c.2879delA, NM_000425.4:c.2254G>A, NM_000425.4:c.2092G>A, NM_000425.4:c.1792G>A, NM_000425.4:c.1354G>A, NM_000425.4:c.1108G>A, NM_000425.4:c.924C>T, NM_000425.4:c.800dupA, NM_000425.4:c.791G>A, NM_000425.4:c.772C>T, NM_000425.4:c.719C>T, NM_000425.4:c.551G>A, NM_000425.4:c.536T>G, NM_000425.4:c.23delT	L1 syndromeï¾ describes a group of conditions that primarily affect the nervous system and occur almost exclusively in males. These conditions vary in severity and include, from most severe to least, X-linked hydrocephalus with stenosis of the aqueduct of Sylvius (HSAS), MASA syndrome, spastic paraplegia type 1, and X-linked complicated corpus callosum agenesis. HSAS is an acronym for the characteristic features of the condition: fluid in the brain (hydrocephalus), muscle stiffness (spasticity), thumbs that are permanently bent toward the palms (adducted thumbs), and narrowing (stenosis) of the aqueduct of Sylvius in the brain. Individuals with HSAS often have severe intellectual disability and may have seizures. MASA syndrome include intellectual disability (mental retardation), mild to moderate, delayed speech (aphasia), spasticity, and adducted thumbs. Individuals with MASA syndrome may have mild enlargement of the ventricles. Spastic paraplegia type 1 is characterized by progressive muscle stiffness (spasticity) and the development of paralysis of the limbs (paraplegia). Affected individuals also have mild to moderate intellectual disability. X-linked complicated corpus callosum agenesis is defined by underdevelopment (hypoplasia) or absence (agenesis) of the tissue that connects the left and right halves of the brain (the corpus callosum). The life expectancy of individuals with L1 syndrome varies depending on the severity of the signs and symptoms.	600

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
LAMA3	Junctional epidermolysis bullosa, Herlitz and non-Herlitz type	NM_198129.2	NM_198129.2:c.5162delG, NM_198129.2:c.6009delG, NM_198129.2:c.6808C>T, NM_198129.2:c.6943A>T, NM_198129.2:c.7489C>T, NM_198129.2:c.8177+2T>G, NM_198129.2:c.8962C>T, NM_198129.2:c.9162dupA, NM_198129.2:c.9705dupT	Junctional epidermolysis bullosa follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LAMA3 gene located on chromosomal region 18q11.2. 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 30 mutations in the LAMA3 gene have been identified in people with Herlitz JEB. Other LAMA3 gene mutations cause the milder form non-Herlitz JEB, phenotype characterized by generalized skin blistering, atrophic scarring, nail dystrophy or nail absence, and enamel hypoplasia, with extracutaneous involvement.	600
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

LAMC2	Junctional epidermolysis bullosa, Herlitz and non-Herlitz type	NM_005562.2	NM_005562.2:c.283C>T, NM_005562.2:c.343C>T, NM_005562.2:c.405-1G>A, NM_005562.2:c.1659C>A, NM_005562.2:c.1782_1783delGC, NM_005562.2:c.2137_2143delCAGAACC, NM_005562.2:c.3069+1G>A, NM_005562.2:c.3120_3121insA, NM_005562.2:c.3512dupA	Junctional epidermolysis bullosa follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LAMC2 gene located on chromosomal region 1q25.3. 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 30 mutations in the LAMC2 gene have been identified in people with Herlitz JEB. Other LAMC2 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
LARGE1	Muscular dystrophy-dystroglycanopathy, type 6A and 6B	NM_004737.4	NM_004737.4:c.1525G>A, NM_004737.4:c.1483T>C, NM_004737.4:c.1102C>T, NM_004737.4:c.992C>T	Muscular dystrophy-dystroglycanopathy, type 6 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LARGE1 gene located on chromosomal region 22q12.3. The age of onset is infantile. There are two subtypes of dystroglycanopathies related to LARGE1 gene: subtype 6A and 6B. Subtype 6A 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 6B represents an intermediate phenotype with or without congenital mental retardation, white matter changes and structural brain abnormalities. The prevalence is 1:100,000-9:100,000.	600
LBR	Greenberg skeletal dysplasia	NM_002296.3	NM_002296.3:c.1748G>A, NM_002296.3:c.1402delT, NM_002296.3:c.1114C>T, NM_002296.3:c.32_35delTGGT	Greenberg dysplasia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LBR gene located on chromosomal region 1q42.12. The age of onset is fetal. This disease is characterized by fetal hydrops, short limbs and abnormal chondro-osseous calcification. The prevalence is <1:1,000,000.	600
LDHA	Glycogen storage disease type 11	NM_001165414.1	NM_001165414.1:c.213+1G>A, NM_001165414.1:c.727_728delCT	Glycogen storage disease type 11 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LDHA gene located on chromosomal region 11p15.1. The age of onset is infantile. This disease is characterized by hepatic glycogenosis and renal Fanconi syndrome.	600
LHFPL5	Deafness, autosomal recessive type 67	NM_182548.3	NM_182548.3:c.250delC, NM_182548.3:c.380A>G, NM_182548.3:c.494C>T, NM_182548.3:c.649+1delG	Autosomal recessive nonsyndromic sensorineural deafness type 67 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LHFPL5 gene located on chromosomal region 6p21.31. 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
LHX3	Pituitary hormone deficiency, combined, type 3	NM_014564.4	NM_014564.4:c.687G>A, NM_014564.4:c.347A>G	Combined pituitary hormone deficiency type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LHX3 gene located on chromosomal region 9q34.3. The age of onset is infantile, etc/. This disease is characterized by somatolactotroph, thyrotroph and gonadotroph deficiencies, limited head and neck rotation associated with spinal abnormalities. The prevalence is <1 /1,000,000.	600
LIFR	Stuve-Wiedemann syndrome / Schwartz-Jampel type 2 syndrome	NM_001127671.1	NM_001127671.1:c.2503G>T, NM_001127671.1:c.2013dupT, NM_001127671.1:c.1789C>T, NM_001127671.1:c.1018_1022delAATTG, NM_001127671.1:c.653dupT, NM_001127671.1:c.171_174delTAAC	Stï¿½ve-Wiedemann syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LIFR gene located on chromosomal region 5p13.1. The age of onset is neonatal. This disease is characterized by small stature, congenital bowing of the long bones and campodactyly.	600

LIG4	LIG4 syndrome	NM_001098268.1	NM_001098268.1:c.2440C>T, NM_001098268.1:c.1738C>T, NM_001098268.1:c.1512_1513delTC, NM_001098268.1:c.1455_1456delTG, NM_001098268.1:c.1406G>A, NM_001098268.1:c.1369_1372delGGAC, NM_001098268.1:c.1271_1275delAAAGA, NM_001098268.1:c.833G>A	LIG4 syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LIG4 gene located on chromosomal region 10p13. The age of onset is infantile. It is associated with impaired DNA double-strand break repair mechanisms and characterized by microcephaly, unusual facial features (''bird-like''), growth and developmental delay, skin anomalies including photosensitivity and psoriatic-like lesions, and pancytopenia. The disease is associated with immunodeficiency. Some patients have been reported as having telangiectasias, leukemia, lymphoma, bone marrow abnormalities, and type 2 diabetes. The prevalence 1-9/1.000.000.	600
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
LOXHD1	Deafness, autosomal recessive type 77	NM_144612.6	NM_144612.6:c.4714C>T, NM_144612.6:c.4524_4525delAG, NM_144612.6:c.3924C>A, NM_144612.6:c.2008C>T, NM_144612.6:c.512-1G>A, NM_144612.6:c.457_461dupCGCCA	Autosomal recessive nonsyndromic sensorineural deafness type 77 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LOXHD1 gene located on chromosomal region 18q21.1. 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
LRAT	Leber congenital amaurosis type 14	NM_001301645.1	NM_001301645.1:c.217_218delAT, NM_001301645.1:c.525T>A, NM_001301645.1:c.588dupT	Leber congenital amaurosis type 14 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LRAT gene located on chromosomal region 4q32.1. The age of onset is infantile. This disease is characterized by blindness, nystagmus, roving eye movement. The prevalence is 2:100,000-3:100,000 newborn.	600

LRP2	Donnai-Barrow syndrome	NM_004525.2	NM_004525.2:c.13388+2T>C, NM_004525.2:c.13139dupC, NM_004525.2:c.11636-1G>T, NM_004525.2:c.11469_11472delTTTG, NM_004525.2:c.10769-2A>G, NM_004525.2:c.9484_9485delGT, NM_004525.2:c.8519_8522delATTT, NM_004525.2:c.7564T>C, NM_004525.2:c.2640-1G>A, NM_004525.2:c.1341+2T>G, NM_004525.2:c.1093C>T	Donnai-Barrow syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LRP2 gene located on chromosomal region 2q31.1. The age of onset is infantile. This disease is characterized by diaphragmatic hernia, ocular findings, hipertelorism, agenesis of the corpus callosum, hearing loss and facial dimorphism. The prevalence is <1:1,000,000.	600
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
LRPPRC	Leigh syndrome, French-Canadian type	NM_133259.3	NM_133259.3:c.3830_3839delGTGGTGCAATinsAG, NM_133259.3:c.1061C>T	French-Canadian type Leigh syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LRPPRC gene located on chromosomal region 2p21. The age of onset is infantile. This disease is characterized by chronic metabolic acidosis, hypotonia, facial dysmorphism and delayed development. The prevalence is 1:2,000 newborn.	600
LRTOMT	Deafness, autosomal recessive type 63	NM_001145308.4	NM_001145308.4:c.242G>A	Autosomal recessive nonsyndromic sensorineural deafness type 63 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the LRTOMT gene located on chromosomal region 11q13.4. 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
MAK	Retinitis pigmentosa type 62	NM_001242957.2	NM_001242957.2:c.1087_1088delAG, NM_001242957.2:c.719_720dupAG, NM_001242957.2:c.718C>T, NM_001242957.2:c.388A>C, NM_001242957.2:c.37G>A	Retinitis pigmentosa type 62 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MAK gene located on chromosomal region 6p24.2. The age of onset is infantile. This disease is characterized by progressive loss of the photoreceptors and retinal pigment epithelium and resulting in blindness usually after several decades.	600
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
MARVELD2	Deafness, autosomal recessive type 49	NM_001038603.2	NM_001038603.2:c.1183-1G>A, NM_001038603.2:c.1363C>T	Autosomal recessive nonsyndromic sensorineural deafness type 49 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MARVELD2 gene located on chromosomal region 5q13.2. 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
MAT1A	Methionine adenosyltransferase deficiency, autosomal recessive	NM_000429.2	NM_000429.2:c.1070C>T, NM_000429.2:c.1043_1044delTG, NM_000429.2:c.1006G>A, NM_000429.2:c.966T>G, NM_000429.2:c.914T>C, NM_000429.2:c.827_828insG, NM_000429.2:c.791G>A, NM_000429.2:c.790C>T, NM_000429.2:c.538_539insTG	Methionine adenosyltransferase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MAT1A gene located on chromosomal region 10q23.1. This disease is characterized by brain demyelination (rarely leading to neurological disorders) and isolated hepatic hypermethioninemia. The prevalence is <1:1,000,000.	600

MBTPS2	IFAP/BRESHECK syndrome; Osteogenesis imperfecta, type 19	NM_015884.3	NM_015884.3:c.261G>A, NM_015884.3:c.677G>T, NM_015884.3:c.1286G>A, NM_015884.3:c.1424T>C	IFAP/BRESHECK syndrome and Osteogenesis imperfecta, type 19 follow an X-linked pattern of inheritance and are caused by pathogenic variants in the MBTPS2 gene located on chromosomal region Xp22.12-p22.11. IFAP/ BRESHECK syndrome's age of onset is infantile and it is characterized by the triad of ichthyosis follicularis, alopecia, and photophobia. Some patients have additional features, including mental retardation, brain anomalies, Hirschsprung disease, corneal opacifications, kidney dysplasia, cryptorchidism, cleft palate, and skeletal malformations, which constitutes BRESHECK syndrom . The prevalence of this syndrome is 1:200,000. Osteogenesis imperfecta type 19 is characterized by prenatal fractures and generalized osteopenia, with severe short stature in adulthood, as well as variable scoliosis and pectal deformity, and marked anterior angulation of the tibia.	600
MCCC1	3-Methylcrotonyl-CoA carboxylase type 1 deficiency	NM_020166.4	NM_020166.4:c.2079delA, NM_020166.4:c.1930G>T, NM_020166.4:c.1905delA, NM_020166.4:c.1526delG, NM_020166.4:c.1380T>G, NM_020166.4:c.1310T>C, NM_020166.4:c.1277T>C, NM_020166.4:c.1155A>C, NM_020166.4:c.1114C>T, NM_020166.4:c.1074delG, NM_020166.4:c.640-1G>A, NM_020166.4:c.640-2A>G, NM_020166.4:c.558delA, NM_020166.4:c.343C>T, NM_020166.4:c.310C>T	3-methylcrotonyl-CoA carboxylase deficiency type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MCCC1 gene located on chromosomal region 3q27.1. 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
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
MCEE	Methylmalonyl-CoA epimerase deficiency	NM_032601.3	NM_032601.3:c.139C>T, NM_032601.3:c.2T>C	Methylmalonic acidemia due to methylmalonyl-CoA epimerase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MCEE gene located on chromosomal region 2p13.3. The age of onset is neonatal. This disease is characterized by lethargy, vomiting, hypotonia, hypothermia, respiratory distress, severe ketoacidosis, hyperammonemia, neutropenia, and thrombocytopenia. The prevalence is 1:50,000-1:80,000.	600
MCOLN1	Mucolipidosis type 4	NM_020533.2	NM_020533.2:c.304C>T, NM_020533.2:c.964C>T, NM_020533.2:c.1084G>T, NM_020533.2:c.1207C>T	Mucolipidosis type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MCOLN1 gene located on chromosomal region 19p13.2. The age of onset is infantile. This disease is characterized by psychomotor retardation and visual abnormalities including corneal clouding, retinal degeneration, or strabismus. The prevalence is 1:40,000.	600
MCPH1	Microcephaly type 1, primary, autosomal recessive	NM_001322042.1	NM_001322042.1:c.215C>T, NM_001322042.1:c.427dupA, NM_001322042.1:c.1249dupT, NM_001322042.1:c.1935+1G>T, NM_001322042.1:c.1973+1G>A, NM_001322042.1:c.2221C>T	Autosomal recessive primary microcephaly type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MCPH1 gene located on chromosomal region 8p23.1. The age of onset is neonatal. This disease is characterized by reduced head circumference at birth with no gross anomalies of brain architecture and variable degrees of intellectual impairment. The incidence is 1/1,000,000.	600

MECP2	Encephalopathy, neonatal severe	NM_001110792.1	NM_001110792.1:c.1001C>T, NM_001110792.1:c.1000C>T, NM_001110792.1:c.952C>T, NM_001110792.1:c.916C>T, NM_001110792.1:c.844C>T, NM_001110792.1:c.842delG, NM_001110792.1:c.799C>T, NM_001110792.1:c.789delC, NM_001110792.1:c.766C>T, NM_001110792.1:c.710C>T, NM_001110792.1:c.647C>G, NM_001110792.1:c.538C>T, NM_001110792.1:c.251dupC	Encephalopathy, neonatal severe follows an X -linked pattern of inheritance and is caused by pathogenic variants in the MECP2 gene located on chromosomal region Xq28. The age of onset is neonatal. This neurological disorder primarily affects males and causes brain dysfunction (encephalopathy). Affected males have microcephaly, poor muscle tone (hypotonia), movement disorders, rigidity, and seizures. Individuals with MECP2-related severe neonatal encephalopathy have severe to profound intellectual disability. Genetic heterogeneity: Many of the mutations causing male's phenotype also cause Rett syndrome, a severe neurodevelopmental disorder that almost always occurs in females. Most severe neonatal encephalopathy cases are surviving male sibs of patients with Rett syndrome. Males with non-Rett syndrome mutations in the MECP2 gene can demonstrate a wide variety of phenotypes. Note: other conditions are also associated to the MECP2 gene, like MECP2 duplication syndrome, a condition characterized by intellectual disability, delayed development, and seizures. It is caused by a duplication of the MECP2 gene and surrounding DNA; this duplication is not tested in the CGT analysis.	600
MED12	Lujan-Fryns syndrome	NM_005120.2	NM_005120.2:c.3443G>A, NM_005120.2:c.3493T>C, NM_005120.2:c.5185C>A	Lujan-Fryns syndrome follows an X-linked pattern of inheritance and is caused by pathogenic variants in the MED12 gene located on chromosomal region Xq13.1. The age of onset is neonatal. It is characterized by mild to moderate intellectual disability, behavioral problems (such as hyperactivity, aggressiveness, extreme shyness, and excessive attention-seeking), and certain physical features such as tall, thin body and an unusually large head (macrocephaly). Almost all people with this condition have weak muscle tone (hypotonia).	600
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
MFSD8	Ceroid lipofuscinosis, neuronal, type 7	NM_152778.2	NM_152778.2:c.1525_1526delCT, NM_152778.2:c.1286G>A, NM_152778.2:c.1235C>T, NM_152778.2:c.1090delA, NM_152778.2:c.999-2A>G, NM_152778.2:c.929G>A, NM_152778.2:c.894T>G, NM_152778.2:c.881C>A, NM_152778.2:c.362A>G	Neuronal ceroid lipofuscinosis type 7 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MFSD8 gene located on chromosomal region 4q28.2. The age of onset is late infantile. This disease is characterized by decline of mental and motor capacities, epilepsy, and vision loss through retinal degeneration. The prevalence is 0.56:100,000-3.9:100,000.	600

MGAT2	Congenital disorder of glycosylation, type 2a	NM_002408.3	NM_002408.3:c.785A>G, NM_002408.3:c.869C>T, NM_002408.3:c.1017T>A	Congenital disorder of glycosylation type 2a follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MGAT2 gene located on chromosomal region 14q21.3. The age of onset is infantile. This disease is characterized by severe psychomotor delay, postnatal growth retardation, facial dysmorphology and bleeding tendency. It has been described in four children.	600
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
MLC1	Megalencephalic leukoencephalopathy with subcortical cysts	NM_015166.3	NM_015166.3:c.424-2A>C, NM_015166.3:c.423C>A, NM_015166.3:c.422A>G, NM_015166.3:c.278C>T, NM_015166.3:c.274C>T, NM_015166.3:c.206C>T, NM_015166.3:c.135dupC, NM_015166.3:c.33dupC	Megalencephalic leukoencephalopathy with subcortical cysts follows an autosomal recessive patternof inheritance and is caused by pathogenic variants in the MLC1 gene located on chromosomal region 22q13.33. The age of onset is infantile. This disease is characterized by ataxia followed by progressive signs of pyramidal tract involvement and mental deterioration.	600
MLYCD	Malonyl-CoA decarboxylase deficiency	NM_012213.2	NM_012213.2:c.560C>G, NM_012213.2:c.680_685dupTGAAGC, NM_012213.2:c.758delT	Malonyl-CoA decarboxylase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MLYCD gene located on chromosomal region 16q23.3. 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
MMAA	Methylmalonic aciduria, vitamin B12-responsive	NM_172250.2	NM_172250.2:c.283C>T, NM_172250.2:c.387C>A, NM_172250.2:c.450dupG, NM_172250.2:c.455delC, NM_172250.2:c.503delC, NM_172250.2:c.586C>T, NM_172250.2:c.620A>G, NM_172250.2:c.811G>T, NM_172250.2:c.1034delT	Vitamin B12-responsive methylmalonic acidemia type cblA follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MMAA gene located on chromosomal region 4q31.21. 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
MMAB	Methylmalonic aciduria, vitamin B12-responsive, type cblB	NM_052845.3	NM_052845.3:c.700C>T, NM_052845.3:c.569G>A, NM_052845.3:c.568C>T, NM_052845.3:c.556C>T, NM_052845.3:c.220G>T, NM_052845.3:c.197-1G>T, NM_052845.3:c.197-1G>A	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
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

MMADHC	Homocystinuria, cblD type, variant 1	NM_015702.2	NM_015702.2:c.795dupT, NM_015702.2:c.776T>C, NM_015702.2:c.748C>T, NM_015702.2:c.746A>G, NM_015702.2:c.545C>A, NM_015702.2:c.478+1G>T, NM_015702.2:c.419dupA, NM_015702.2:c.57_64delCTCTTTAG	Homocystinuria, cblD type, variant 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MMADHC gene located on chromosomal region 2q23.2. The age of onset is variable (infantile to adult). This disease is characterized by developmental delay, severe learning difficulties, seizures, movement and gait abnormalities, behavioral problems and signs of megaloblastic anemia (pallor, fatigue, anorexia). The prevalence is 1:50,000-1:80,000.	600
MOCS1	Molybdenum cofactor deficiency A	NM_001075098.3	NM_001075098.3:c.1027C>T, NM_001075098.3:c.956G>A, NM_001075098.3:c.397_406delCCGGACGTGG, NM_001075098.3:c.217C>T	Molybdenum cofactor deficiency type A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MOCS1 gene located on chromosomal region 6p21.2. The age of onset is infantile. This disease is characterized by severe neurological abnormalities, dislocated ocular early death.	600
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
MPI	Congenital disorder of glycosylation, type 1b	NM_002435.2	NM_002435.2:c.305C>T, NM_002435.2:c.413T>C, NM_002435.2:c.656G>A, NM_002435.2:c.884G>A, NM_002435.2:c.1016_1019delACCC	Congenital disorder of glycosylation type 1b follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MPI gene located on chromosomal region 15q24.1. The age of onset is infantile. This disease is characterized by hepatic-intestinal manifestations (diarrhoea, vomiting, and hepatomegaly associated with hepatic fibrosis).	600
MPV17	Mitochondrial DNA depletion syndrome type 6 (hepatocerebral)	NM_002437.4	NM_002437.4:c.498C>A, NM_002437.4:c.462-2A>C, NM_002437.4:c.359G>A, NM_002437.4:c.284dupG, NM_002437.4:c.263_265delAGA, NM_002437.4:c.149G>A, NM_002437.4:c.148C>T, NM_002437.4:c.70G>T	Mitochondrial DNA depletion syndrome type 6 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MPV17 gene located on chromosomal region 2p23.3. The age of onset is infantile. It is a disease due to mitochondrial dysfunction. It is characterized by infantile onset of progressive liver failure, often leading to death in the first year of life, peripheral neuropathy, corneal scarring, acral ulceration and osteomyelitis leading to autoamputation, cerebral leukoencephalopathy, failure to thrive, and recurrent metabolic acidosis with intercurrent infections.	600
MRPS16	Combined oxidative phosphorylation deficiency 2	NM_016065.3	NM_016065.3:c.331C>T, NM_016065.3:c.2T>C	Combined oxidative phosphorylation defect type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MRPS16 gene located on chromosomal region 10q22.2. The age of onset is infantile. This disease is characterized by agenesis of corpus callosum, dismorphism and fatal lactic acidosis.	600
MRPS22	Combined oxidative phosphorylation deficiency type 5	NM_020191.2	NM_020191.2:c.40_41insA, NM_020191.2:c.509G>A, NM_020191.2:c.644T>C	Combined oxidative phosphorylation defect type 5 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MRPS22 gene located on chromosomal region 3q23. The age of onset is infantile. This disease is characterized by evere hypotonia, lactic academia and congenital hyperammonaemia.	600
MTM1	Myotubular myopathy, X-linked	NM_000252.2	NM_000252.2:c.70C>T, NM_000252.2:c.420C>G, NM_000252.2:c.461T>G, NM_000252.2:c.595_599delCCTGC, NM_000252.2:c.670C>T, NM_000252.2:c.721C>T, NM_000252.2:c.780T>A, NM_000252.2:c.969dupA, NM_000252.2:c.969delA, NM_000252.2:c.1261-10A>G, NM_000252.2:c.1306_1310dupCCTAT, NM_000252.2:c.1357_1358delCC, NM_000252.2:c.1415_1416delGT	X-linked centronuclear myopathy follows an X-linked pattern of inheritance and is caused by pathogenic variants in the MTM1 gene located on chromosomal region Xq28. The age of onset is infantile, etc/. This disease is characterized by severe phenotype in males presenting at birth with marked weakness, hypotonia and respiratory failure. The incidence is 1/50,000 newborn man.	600

MTMR2	Charcot-Marie-Tooth disease, type 4B1	NM_016156.5	NM_016156.5:c.1276C>T, NM_016156.5:c.304C>T	Charcot-Marie-Tooth disease type 4B1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MTMR2 gene located on chromosomal region 11q21. The age of onset is early infantile. This disease is characterized by distal and proximal muscular weakness starting in the lower extremities, sensory loss and cranial nerve involvement, foot deformities and diaphragmatic and facial involvement.	600
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
MYO5A	Griscelli syndrome, type 1	NM_000259.3	NM_000259.3:c.2332C>T, NM_000259.3:c.1145delC	Griscelli disease type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the MYO5A gene located on chromosomal region 15q21.2. The age of onset is infantile. This disease is characterized by is characterised by silvery gray sheen of the hair and hypopigmentation of the skin which can be associated to neurological impairment. The prevalence is <1:1,000,000.	600
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
NAGS	N-acetylglutamate synthase deficiency	NM_153006.2	NM_153006.2:c.916-2A>T, NM_153006.2:c.971G>A, NM_153006.2:c.1025delG, NM_153006.2:c.1289T>C, NM_153006.2:c.1299G>C, NM_153006.2:c.1307dupT	N-acetylglutamate synthetase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NAGS gene located on chromosomal region 17q21.31. The age of onset is infantile, etc/. This disease is characterized by hyperammonemia, vomiting, hyperactivity or lethargy, diarrhoea, poor feeding, seizures, hypotonia, delayed psychomotor development and respiratory distress. The prevalence is <1:1,000,000.	600
NDRG1	Charcot-Marie-Tooth disease, type 4D	NM_001135242.1	NM_001135242.1:c.928C>T, NM_001135242.1:c.538-1G>A, NM_001135242.1:c.442C>T, NM_001135242.1:c.16C>T	Charcot-Marie-Tooth disease type 4D follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NDRG1 gene located on chromosomal region 8q24.22. The age of onset is infantile, etc/. This disease is characterized by demyelination and hearing loss.	600
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
NEFL	Charcot-Marie-Tooth disease, type 1F	NM_006158.4	NM_006158.4:c.628G>T, NM_006158.4:c.418G>T, NM_006158.4:c.361G>T	Charcot-Marie-Tooth disease type 1F follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NEFL gene located on chromosomal region 8p21.2. The age of onset is infantile. This disease is characterized by a progressive peripheral motor and sensory neuropathy with variable clinical, distal weakness and wasting of the muscles of the lower limbs. The prevalence is 15:100,000-20:100,000.	600
NEUROG3	Diarrhea type 4, malabsorptive, congenital	NM_020999.3	NM_020999.3:c.319C>A, NM_020999.3:c.278G>T	Congenital malabsorptive diarrhea type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NEUROG3 gene located on chromosomal region 10q22.1. The age of onset is early infantile. This disease is characterized by severe, life-threatening watery diarrhea associated with generalized malabsorption and a paucity of enteroendocrine cells. The prevalence is <1:1,000,000.	600

NHP2	Dyskeratosis congenita, autosomal recessive type 2	NM_017838.3	NM_017838.3:c.460T>A, NM_017838.3:c.415T>C, NM_017838.3:c.289_290delAT	Dyskeratosis congenita type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NHP2 gene located on chromosomal region 5q35.3. The age of onset is variable from infancy to adult. It is a multisystem disorder caused by defective telomere maintenance. Clinical manifestations include mucocutaneous abnormalities, bone marrow failure, and an increased predisposition to cancer, among other variable features.	600
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
NOP10	Dyskeratosis congenita, autosomal recessive type 1	NM_018648.3	NM_018648.3:c.100C>T	Dyskeratosis congenita autosomal recessive type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NOP10 gene located on chromosomal region 15q14. The age of onset is infantile. This disease is characterized by the mucocutaneous triad of abnormal skin pigmentation, nail dystrophy and mucosal leucoplakia. The prevalence is 1:1,000,000.	600
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
NPHP1	Joubert syndrome type 4	NM_000272.3	NM_000272.3:c.1884+1G>T, NM_000272.3:c.1184dupC, NM_000272.3:c.829C>T, NM_000272.3:c.555dupA, NM_000272.3:c.455C>G, NM_000272.3:c.80T>A, NM_000272.3:c.1delA	Joubert syndrome type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NPHP1 gene located on chromosomal region 2q13. This is a disorder presenting with cerebellar ataxia, oculomotor apraxia, hypotonia, neonatal breathing abnormalities and psychomotor delay. Additional variable features include retinal dystrophy and renal disease. Joubert syndrome type 4 is a phenotypically mild form.	600
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
NR0B1	Adrenal hypoplasia, congenital	NM_000475.4	NM_000475.4:c.1319A>T, NM_000475.4:c.1316T>G, NM_000475.4:c.1107G>A, NM_000475.4:c.890T>C, NM_000475.4:c.873G>C, NM_000475.4:c.847C>T, NM_000475.4:c.813C>G, NM_000475.4:c.800G>C, NM_000475.4:c.788T>A, NM_000475.4:c.704G>A, NM_000475.4:c.591C>A, NM_000475.4:c.513G>A, NM_000475.4:c.388_389delTA, NM_000475.4:c.273C>A	Congenital adrenal hypoplasia follows an X-linked pattern of inheritance and is caused by pathogenic variants in the NR0B1 gene located on chromosomal region Xp21.2. The age of onset is infantile. This disease is characterized by adrenal insufficiency with vomiting, feeding difficulty, dehydration, and shock caused by a salt-wasting episode and hypoglycemia.	600
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
NTRK1	Insensitivity to pain, congenital, with anhidrosis	NM_002529.3	NM_002529.3:c.1076A>G, NM_002529.3:c.1727delT, NM_002529.3:c.1729G>C, NM_002529.3:c.1759A>G, NM_002529.3:c.1926_1927insT, NM_002529.3:c.2084C>T, NM_002529.3:c.2339G>C	Insensitivity to pain, congenital, with anhidrosis follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NTRK1 gene located on chromosomal region 1q23.1. The age of onset is infantile. This disease is characterized by anhidrosis, insensitivity to pain, self-mutilating behavior and episodes of fever.	600
NUP62	Striatonigral degeneration, infantile	NM_001193357.1	NM_001193357.1:c.1172A>C	Infantile striatal degeneration follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the NUP62 gene located on chromosomal region 19q13.33. The age of onset is infantile. This disease is characterized by choreoathetosis, dystonia, rigidity, spasticity, dysphagia, optic atrophy, intellectual deficit, developmental regression of motor and verbal skills, failure to thrive, myoclonus, quadriparesis, cerebellar ataxia and nystagmus. The prevalence is <1:1,000,000.	600
NYX	Night blindness, congenital stationary (complete), type 1A, X-linked	NM_022567.2	NM_022567.2:c.1049G>A	Congenital stationary night blindness follows an X-linked pattern of inheritance and is caused by pathogenic variants in the NYX gene located on chromosomal region Xp11.4. The age of onset is infantile. This disease is characterized by hemeralopia with a moderate loss of visual acuity.	600
OAT	Gyrate atrophy of choroid and retina	NM_000274.3	NM_000274.3:c.1276C>T, NM_000274.3:c.1250C>T, NM_000274.3:c.1205T>C, NM_000274.3:c.994G>A, NM_000274.3:c.955C>T, NM_000274.3:c.952delG, NM_000274.3:c.952G>A, NM_000274.3:c.901-2A>G, NM_000274.3:c.824G>A, NM_000274.3:c.812G>A, NM_000274.3:c.677C>T, NM_000274.3:c.627T>A, NM_000274.3:c.596C>A, NM_000274.3:c.539G>C, NM_000274.3:c.533G>A, NM_000274.3:c.278G>T, NM_000274.3:c.268C>G, NM_000274.3:c.159delC	Gyrate atrophy of choroid and retina follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the OAT gene located on chromosomal region 10q26.13. The age of onset is infantile. This disease is characterized by gyrate atrophy of the choroid and retina that begins during childhood with myopia and night blindness, followed by concentric shrinking of the visual field (tunnel vision) and a peculiar aspect of retinopathy on the funduscopy. Patients can also present with ornithinemia.	600
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

OCRL	Lowe Syndrome; Dent disease type 2	NM_001318784.1	NM_001318784.1:c.912_913delAG, NM_001318784.1:c.1502G>A, NM_001318784.1:c.2302C>T, NM_001318784.1:c.2406dupA, NM_001318784.1:c.2533C>T, NM_001318784.1:c.2538delA	Dent disease type 2 and Lowe syndrome follow an X-linked pattern of inheritance and are caused by pathogenic variants in the OCRL gene located on chromosomal region Xq25-q26. Dent disease type 2 is a type of Dent disease in which patients have the manifestations of Dent disease type 1 associated with extra-renal features: hypercalciuria and low-molecular-weight (LMW) proteinuria. In addition, these patients may also have nephrocalcinosis, nephrolithiasis, hematuria, hypophosphatemia and/or renal insufficiency. The features of Lowe syndrome are hydrophthalmia, cataract, mental retardation, vitamin D-resistant rickets, amino aciduria, and reduced ammonia production by the kidney.	600
OFD1	Joubert syndrome type 10; Orofaciodigital syndrome type 1	NM_003611.2	NM_003611.2:c.43_44delAG, NM_003611.2:c.52G>T, NM_003611.2:c.65dupA, NM_003611.2:c.62_63insT, NM_003611.2:c.221C>T, NM_003611.2:c.224A>C, NM_003611.2:c.235G>A, NM_003611.2:c.241C>G, NM_003611.2:c.243C>G, NM_003611.2:c.247C>T, NM_003611.2:c.260A>G, NM_003611.2:c.275_276delCT, NM_003611.2:c.274T>C, NM_003611.2:c.277G>T, NM_003611.2:c.290A>G, NM_003611.2:c.312+1delG, NM_003611.2:c.312+2_312+7delTAAAGT, NM_003611.2:c.413-10T>G, NM_003611.2:c.454C>T, NM_003611.2:c.518-1G>A, NM_003611.2:c.541dupG, NM_003611.2:c.594_598delAAAGC, NM_003611.2:c.602delA, NM_003611.2:c.607_610delTATA, NM_003611.2:c.616_617delGA, NM_003611.2:c.614_617delGAGA, NM_003611.2:c.619_624delATAGAA, NM_003611.2:c.628C>T, NM_003611.2:c.653delA, NM_003611.2:c.654+2_654+3delTA, NM_003611.2:c.1268_1272delAAAAC, NM_003611.2:c.1303A>C, NM_003611.2:c.1318delC, NM_003611.2:c.1319delT, NM_003611.2:c.1322_1326delAAGAA, NM_003611.2:c.1323_1326delAGAA, NM_003611.2:c.1360_1363delCTTA, NM_003611.2:c.1358T>A, NM_003611.2:c.1365_1368delACAA, NM_003611.2:c.1612C>T, NM_003611.2:c.1757delG, NM_003611.2:c.1821delG, NM_003611.2:c.1840delG, NM_003611.2:c.1859_1860delCCinsG, NM_003611.2:c.2261-1G>T, NM_003611.2:c.2321_2322insT, NM_003611.2:c.2349delC, NM_003611.2:c.2387+1G>C, NM_003611.2:c.2582dupT	Joubert syndrome type 10 and Orofaciodigital syndrome type 1 follow an X-linked pattern of inheritance and are caused by pathogenic variants in the OFD1 gene located on chromosomal region Xp22.2. Joubert syndrome type 10 is a disorder presenting with cerebellar ataxia, oculomotor apraxia, hypotonia, neonatal breathing abnormalities and psychomotor delay. Neuroradiologically, it is characterized by cerebellar vermian hypoplasia/aplasia, thickened and reoriented superior cerebellar peduncles, and an abnormally large interpeduncular fossa, giving the appearance of a molar tooth on transaxial slices (molar tooth sign). Additional variable features include retinal dystrophy and renal disease. Orofaciodigital syndrome type 1 is characterized by malformations of the face, oral cavity, and digits and is transmitted as an X-linked dominant condition with lethality in males. The central nervous system may also be involved in as many as 40% of cases.	600
OPA3	3-methylglutaconic aciduria, type 3	NM_001017989.2	NM_001017989.2:c.221delG	3-methylglutaconic aciduria type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the OPA3 gene located on chromosomal region 19q13.32. The age of onset is infantile. This disease is characterized by the association of optic atrophy and choreoathetosis with 3-methylglutaconic aciduria. The prevalence is 1:10,000-5:10,000.	600
OSTM1	Osteopetrosis, autosomal recessive type 5	NM_014028.3	NM_014028.3:c.415_416delAG	Osteopetrosis, autosomal recessive type 5 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the OSTM1 gene located on chromosomal region 6p21. The age of onset is infantile. This disease is characterized by osteopetrosis, agenesis del cuerpo calloso, atrofia cerebral e hipocampo pequeï¿½o.	600
OTC	Ornithine transcarbamylase deficiency	NM_000531.5	NM_000531.5:c.77G>A, NM_000531.5:c.118C>T, NM_000531.5:c.119G>A, NM_000531.5:c.134T>C, NM_000531.5:c.148G>T, NM_000531.5:c.238A>G, NM_000531.5:c.245T>G, NM_000531.5:c.259G>A, NM_000531.5:c.275G>A, NM_000531.5:c.332T>C, NM_000531.5:c.421C>T, NM_000531.5:c.460G>T, NM_000531.5:c.563G>T, NM_000531.5:c.589G>T, NM_000531.5:c.617T>G, NM_000531.5:c.646C>G, NM_000531.5:c.674C>T, NM_000531.5:c.717+2T>C, NM_000531.5:c.829C>T	Ornithine transcarbamylase deficiency follows an X-linked pattern of inheritance and is caused by pathogenic variants in the OTC gene located on chromosomal region Xp11.4. The age of onset is infantile. This disease is characterized by severe neonatal hyperammonemic coma that generally proves to be fatal, in males. Females may be also affected by symptoms with various degrees of intensity, ranging from dislike for proteins to chronic vomiting, growth retardation, hypotonia, psychomotor retardation, hyperammonemic coma, or psychiatric disorders. The prevalence is 1:80,000.	600
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
P3H1	Osteogenesis imperfecta, type 8	NM_001243246.1	NM_001243246.1:c.1656C>A, NM_001243246.1:c.1473+1G>T, NM_001243246.1:c.1365_1366delAGinsC, NM_001243246.1:c.1102C>T, NM_001243246.1:c.747delC	Osteogenesis imperfecta type 8 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the P3H1 gene located on chromosomal region 1p34.2. The age of onset is infantile. This disease is characterized by bone fragility, low bone mass and susceptibility to bone fractures. The prevalence is 6:100,000-7:100,000.	600
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
PDE6C	Cone dystrophy type 4	NM_006204.3	NM_006204.3:c.85C>T, NM_006204.3:c.180_186delCCTGTGC, NM_006204.3:c.256_257insAG, NM_006204.3:c.481-12T>A, NM_006204.3:c.633G>C, NM_006204.3:c.826C>T, NM_006204.3:c.881G>A, NM_006204.3:c.1066G>T, NM_006204.3:c.1363A>G, NM_006204.3:c.1682dupA, NM_006204.3:c.1805A>T, NM_006204.3:c.2036+1G>T, NM_006204.3:c.2283+1G>C, NM_006204.3:c.2457T>A	Cone dystrophy type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PDE6C gene located on chromosomal region 10q23.33. The age of onset is infantile. This disease is characterized by reduced visual acuity, achromatopsia, pendular nystagmus, increased sensitivity to light (photophobia), a small central scotoma, eccentric fixation, and reduced or complete loss of color discrimination.	600
PDE6G	Retinitis pigmentosa type 57	NM_002602.3	NM_002602.3:c.187+1G>T	Retinitis pigmentosa type 57 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PDE6G gene located on chromosomal region 17q25.3. 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.	600
PDHA1	Pyruvate dehydrogenase E1-alpha deficiency	NM_001173454.1	NM_001173454.1:c.887A>C, NM_001173454.1:c.901C>G	Pyruvate dehydrogenase E1-alpha deficiency follows an X-linked pattern of inheritance and is caused by pathogenic variants in the PDHA1 gene located on chromosomal region Xp22.12. The age of onset is variable. This disease is characterized by primary lactic acidosis in children. It is associated with a broad clinical spectrum ranging from fatal lactic acidosis in the newborn to chronic neurologic dysfunction with structural abnormalities in the central nervous system without systemic acidosis.The prevalence is >1:40,000 newborn.	600

PDP1	Pyruvate dehydrogenase phosphatase deficiency	NM_001161779.1	NM_001161779.1:c.352G>T, NM_001161779.1:c.672_676delCTTTA, NM_001161779.1:c.878delC, NM_001161779.1:c.926_928delTTC, NM_001161779.1:c.1681C>T	Pyruvate dehydrogenase phosphatase deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PDP1 gene located on chromosomal region 8q22.1. The age of onset is neonatal. This disease is characterized by lactic acidosis and hypotonia.	600
PDSS1	Coenzyme Q10 deficiency, primary, type 2	NM_014317.4	NM_014317.4:c.319dupT, NM_014317.4:c.924T>G	Coenzyme Q10 deficiency, primary, type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PDSS1 gene located on chromosome 10p12.1. The age of onset is neonatal/infantile. This disease is characterized by multisystem disorder with early-onset deafness, optic atrophy, mild mental retardation, peripheral neuropathy, obesity and cardiac valvulopathy.	600
PDSS2	Coenzyme Q10 deficiency, primary, type 3	NM_020381.3	NM_020381.3:c.1145C>T, NM_020381.3:c.964C>T, NM_020381.3:c.129dupC	Coenzyme Q10 deficiency, primary, type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PDSS2 gene located on chromosomal region 6q21. The age of onset is infantile. This disease is characterized by onset of symptoms typically between age three and 12 months, often following a viral infection. Neurologic features include hypotonia, spasticity, movement disorders, cerebellar ataxia, and peripheral neuropathy.	600
PDX1	Pancreatic agenesis type 1	NM_000209.3	NM_000209.3:c.492G>T, NM_000209.3:c.532G>A, NM_000209.3:c.533A>G	Pancreatic agenesis type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PDX1 gene located on chromosomal region 13q12.1. The age of onset is infantile. This disease is characterized by isolated hypoplasia or agenesis of the pancreas, pancreatic beta-cell failure resulting in neonatal insulin-dependent diabetes mellitus, and exocrine pancreatic insufficiency.	600
PDZD7	Usher syndrome, type 2C, GPR98/PDZD7 digenic	NM_001195263.1	NM_001195263.1:c.2107delA, NM_001195263.1:c.1543C>T, NM_001195263.1:c.166dupC, NM_001195263.1:c.144dupA	Usher syndrome type 2C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the GPR98 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
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
PEX12	Peroxisome biogenesis disorder type 3A (Zellweger)	NM_000286.2	NM_000286.2:c.959C>T, NM_000286.2:c.894delC, NM_000286.2:c.888_889delCT, NM_000286.2:c.771delC, NM_000286.2:c.538C>T, NM_000286.2:c.455_459dupGGAAA	Peroxisome biogenesis disorder 3A (Zellweger) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PEX12 gene located on chromosomal region 17q12. The peroxisomal biogenesis disorder (PBD) Zellweger syndrome (ZS) is an autosomal recessive multiple congenital anomaly syndrome resulting from disordered peroxisome biogenesis. Affected children present in the newborn period with profound hypotonia, seizures, and inability to feed. Characteristic craniofacial anomalies, eye abnormalities, neuronal migration defects, hepatomegaly, and chondrodysplasia punctata are present. Children with this condition do not show any significant development and usually die in the first year of lifeï¾	600
PEX2	Peroxisome biogenesis disorder type 5A (Zellweger)	NM_000318.2	NM_000318.2:c.789_790delCT, NM_000318.2:c.163G>A	Peroxisome biogenesis disorder 5A (Zellweger) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PEX2 gene located on chromosomal region 8q21.13. The peroxisomal biogenesis disorder (PBD) Zellweger syndrome (ZS) is an autosomal recessive multiple congenital anomaly syndrome resulting from disordered peroxisome biogenesis. Affected children present in the newborn period with profound hypotonia, seizures, and inability to feed. Characteristic craniofacial anomalies, eye abnormalities, neuronal migration defects, hepatomegaly, and chondrodysplasia punctata are present. Children with this condition do not show any significant development and usually die in the first year of lifeï¾	600

PEX26	Peroxisome biogenesis disorder type 7A (Zellweger)	NM_001127649.2	NM_001127649.2:c.254dupT, NM_001127649.2:c.265G>A, NM_001127649.2:c.292C>T	Peroxisome biogenesis disorder 7A (Zellweger) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PEX26 gene located on chromosomal region 22q11.21. The peroxisomal biogenesis disorder (PBD) Zellweger syndrome (ZS) is an autosomal recessive multiple congenital anomaly syndrome resulting from disordered peroxisome biogenesis. Affected children present in the newborn period with profound hypotonia, seizures, and inability to feed. Characteristic craniofacial anomalies, eye abnormalities, neuronal migration defects, hepatomegaly, and chondrodysplasia punctata are present. Children with this condition do not show any significant development and usually die in the first year of lifeï¾	600
PEX5	Peroxisome biogenesis disorder type 2A (Zellweger)	NM_001300789.1	NM_001300789.1:c.1342C>T, NM_001300789.1:c.1641T>G	Peroxisome biogenesis disorder 2A (Zellweger) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PEX5 gene located on chromosomal region 12p13.31. The peroxisomal biogenesis disorder (PBD) Zellweger syndrome (ZS) is an autosomal recessive multiple congenital anomaly syndrome resulting from disordered peroxisome biogenesis. Affected children present in the newborn period with profound hypotonia, seizures, and inability to feed. Characteristic craniofacial anomalies, eye abnormalities, neuronal migration defects, hepatomegaly, and chondrodysplasia punctata are present. Children with this condition do not show any significant development and usually die in the first year of lifeï¾	600
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
PGM1	Congenital disorder of glycosylation, type 1t	NM_001172818.1	NM_001172818.1:c.397A>G, NM_001172818.1:c.415G>C, NM_001172818.1:c.841G>T, NM_001172818.1:c.1561C>T	Congenital disorder of glycosylation, type 1T follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PGM1 gene located on chromosomal region 1p31.3. The age of onset is infantile. It is a multisystem disorder caused by a defect in glycoprotein biosynthesis and characterized by under-glycosylated serum glycoproteins. Congenital disorders of glycosylation result in a wide variety of clinical features, such as defects in the nervous system development, psychomotor retardation, dysmorphic features, hypotonia, coagulation disorders, and immunodeficiency. The broad spectrum of features reflects the critical role of N-glycoproteins during embryonic development, differentiation, and maintenance of cell functions. The prevalence is <1:1,000,000.	600
PHKG2	Glycogen storage disease type 9c	NM_000294.2	NM_000294.2:c.130C>T, NM_000294.2:c.393-2A>G, NM_000294.2:c.553C>T, NM_000294.2:c.958C>T	Glycogen storage disease type 9C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PHKG2 gene located on chromosomal region 16p12.1-p11.2. The age of onset is infantile. This disease is characterized by hepatomegaly, growth retardation, and mild delay in motor development during childhood. The incidence is <1:100.000 births.	600
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

PJVK	Deafness, autosomal recessive type 59	NM_001042702.3	NM_001042702.3:c.113dupT, NM_001042702.3:c.122delA, NM_001042702.3:c.161C>T, NM_001042702.3:c.420delT, NM_001042702.3:c.726delT, NM_001042702.3:c.823dupT, NM_001042702.3:c.988delG	Autosomal recessive nonsyndromic sensorineural deafness type 59 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PJVK gene located on chromosomal region 2q31.2. The age of onset is neonatal/infantile. This disease is characterized by congenital, non-progressive, mild-to-profound sensorineural hearing impairment.	600
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
PLA2G6	Infantile neuroaxonal dystrophy type 1	NM_003560.2	NM_003560.2:c.2370T>G, NM_003560.2:c.2239C>T, NM_003560.2:c.1903C>T, NM_003560.2:c.1894C>T, NM_003560.2:c.1634A>C, NM_003560.2:c.1612C>T, NM_003560.2:c.929T>A, NM_003560.2:c.109C>T	Infantile neuroaxonal dystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PLA2G6 gene located on chromosomal region 22q13.1. The age of onset is infantile. This disease is a type of neurodegeneration with brain iron accumulation characterized by psychomotor delay and regression, increasing neurological involvement with symmetrical pyramidal tract signs and spastic tetraplegia. INAD may be classic or atypical and patients present with symptoms anywhere along a continuum between the two.	600
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
PLEC	Epidermolysis bullosa simplex with muscular dystrophy	NM_201380.3	NM_201380.3:c.12373dupG, NM_201380.3:c.11776G>T, NM_201380.3:c.11301_11302delGA, NM_201380.3:c.9580_9581delCT, NM_201380.3:c.9415C>T, NM_201380.3:c.7285C>T, NM_201380.3:c.1243C>T, NM_201380.3:c.1236+1G>A	Epidermolysis bullosa simplex with muscular dystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PLEC gene located on chromosomal region 8q24. The age of onset is early. This disease is characterized by generalized blistering associated with muscular dystrophy, dystrophic nails, and focal keratoderma of the palms and soles. The prevalence is 1:30,000-1:50,000.	600

PLEKHG5	Charcot-Marie-Tooth disease, recessive intermediate C	NM_001265592.1	NM_001265592.1:c.3172C>T, NM_001265592.1:c.2177T>C	Charcot-Marie-Tooth disease, intermediate type C follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PLEKHG5 gene located on chromosomal region 1p36.31. The age of onset is infantile. This disease is a disorder of the peripheral nervous system, characterized by progressive weakness and atrophy, initially of the peroneal muscles and later of the distal muscles of the arms. Recessive intermediate forms of Charcot-Marie-Tooth disease are characterized by clinical and pathologic features intermediate between demyelinating and axonal peripheral neuropathies, and motor median nerve conduction velocities ranging from 25 to 45 m/sec.	600
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
PLOD1	Ehlers-Danlos syndrome, kyphoscoliotic type, 1	NM_001316320.1	NM_001316320.1:c.607+1G>A, NM_001316320.1:c.1096C>T, NM_001316320.1:c.1674C>G, NM_001316320.1:c.1977G>C, NM_001316320.1:c.2149C>T, NM_001316320.1:c.2173G>A	Ehlers-Danlos syndrome kyphoscoliotic type, 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PLOD1 gene located on chromosomal region 1p36. The age of onset is early. This disease is characterized by progressive scoliosis from birth, severe muscle hypotonia, hyperextensible joints and fragile eyeballs. The weakness can lead to ocular retinal hemorrhage, glaucoma, coloring of the sclera or even to rupture of the globe. The prevalence is <1:5,000.	600
PLP1	Pelizaeus-Merzbacher disease	NM_000533.4	NM_000533.4:c.3G>A, NM_000533.4:c.128C>T, NM_000533.4:c.231_232insC, NM_000533.4:c.487T>C, NM_000533.4:c.593delG, NM_000533.4:c.725C>T, NM_000533.4:c.737G>C	Pelizaeus-Merzbacher disease follows an X-linked pattern of inheritance and is caused by pathogenic variants in the PLP1 gene located on chromosomal region Xq22.2. The age of onset is infantile. It is a hypomyelinative leukodystrophy in which myelin is not formed properly in the central nervous system. It is characterized clinically by nystagmus, spastic quadriplegia, ataxia, and developmental delay.	600
PLP1	Pelizaeus-Merzbacher disease	NM_001305004.1	NM_001305004.1:c.5-1G>T	Pelizaeus-Merzbacher disease follows an X-linked pattern of inheritance and is caused by pathogenic variants in the PLP1 gene located on chromosomal region Xq22.2. The age of onset is infantile. It is a hypomyelinative leukodystrophy in which myelin is not formed properly in the central nervous system. It is characterized clinically by nystagmus, spastic quadriplegia, ataxia, and developmental delay.	600
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
PNPO	Pyridoxamine 5'-phosphate oxidase deficiency	NM_018129.3	NM_018129.3:c.674G>A, NM_018129.3:c.685C>T	Pyridoxamine 5'-phosphate oxidase (PNPO) deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PNPO gene located on chromosomal region 17q21.32. The age of onset is early. This disease is characterized by onset of severe seizures within hours of birth that are not responsive to anticonvulsants.	600

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
POU1F1	Pituitary hormone deficiency, combined, type 1	NM_001122757.2	NM_001122757.2:c.826G>T, NM_001122757.2:c.793C>T, NM_001122757.2:c.766G>A, NM_001122757.2:c.655T>C, NM_001122757.2:c.593G>A, NM_001122757.2:c.592C>T, NM_001122757.2:c.550G>C, NM_001122757.2:c.511A>T, NM_001122757.2:c.506G>A, NM_001122757.2:c.482T>G, NM_001122757.2:c.469G>T, NM_001122757.2:c.71C>T	Pituitary hormone deficiency, combined, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the POU1F1 gene located on chromosomal region 3p11.2. The age of onset is early. This disease is characterized by short stature, cognitive alterations or delayed puberty. The prevalence is 1:8,000.	600
POU3F4	Deafness, X-linked type 2 (DFNX2)	NM_000307.4	NM_000307.4:c.499C>T, NM_000307.4:c.604A>T	X-linked deafness type 2 (DFNX2, also known as DFN3) follows an X-linked pattern of inheritance and is caused by pathogenic variants in the POU3F4 gene located on chromosomal region Xq21.1. The age of onset is infantile. This disease is characterized by progressive conductive and sensorineural hearing loss and a pathognomonic temporal bone deformity that includes dilatation of the inner auditory canal and a fistulous connection between the internal auditory canal and the cochlear basal turn, resulting in a perilymphatic fluid 'gusher' during stapes surgery (summary by de Kok et al., 1995 and Song et al., 2010). Note: Choroideremia, deafness, and mental retardation (OMIM 303110), is caused by a contiguous gene deletion syndrome involving the POU3F4 and CHM genes on Xq21. This deletion is not detected by this CGT test.	600

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
PRCD	Retinitis pigmentosa, type 36	NM_001077620.2	NM_001077620.2:c.52C>T, NM_001077620.2:c.64C>T	Retinitis pigmentosa, type 36 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PRCD gene located on chromosomal region 17q25.1. 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.	600
PRKRA	Dystonia, type 16	NM_003690.4	NM_003690.4:c.665C>T	Dystonia, type 16 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PRKRA gene located on chromosomal region 2q31.2. The age of onset is early. This disease is characterized by progressive limb dystonia, laryngeal and oromandibular dystonia and parkinsonism.	600
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
PROP1	Pituitary hormone deficiency, combined, type 2	NM_006261.4	NM_006261.4:c.469dupT, NM_006261.4:c.358C>T, NM_006261.4:c.349T>A, NM_006261.4:c.310delC, NM_006261.4:c.301_302delAG, NM_006261.4:c.295C>T, NM_006261.4:c.263T>C, NM_006261.4:c.247C>T, NM_006261.4:c.218G>A, NM_006261.4:c.217C>T, NM_006261.4:c.157delA, NM_006261.4:c.150delA, NM_006261.4:c.112_124delTCGAGTGCTCCAC, NM_006261.4:c.4delG, NM_006261.4:c.2T>C	Pituitary hormone deficiency, combined, type 2, genetic forms follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PROP1 gene located on chromosomal region 5q35.3. The age of onset is early. This disease is characterized by short stature, cognitive alterations or delayed puberty.	600
PRPS1	Deafness, X-linked 1 (DFNX1); Arts syndrome; PRPS1-related disorders	NM_002764.3	NM_002764.3:c.193G>A, NM_002764.3:c.344T>C, NM_002764.3:c.398A>C, NM_002764.3:c.869T>C, NM_002764.3:c.916G>A	The DFNX1 locus (PRPS1 gene) is associated with phenotypically heterogeneous non-syndromic hearing loss. In general, hearing impairment in male patients with PRPS1 mutations is bilateral, moderate to profound, and can be pre- or post-lingual, progressive or non-progressive. Female carriers may also be affected by unilateral or bilateral hearing impairment. Mutations in PRPS1 might also result in a spectrum of syndromic conditions, including PRS-I superactivity (OMIM #300661), Charcot-Marie Tooth neuropathy type X-5 (CMTX5 or Rosenberg-Chutorian syndrome, OMIM #311070) and Arts syndrome. Arts syndrome is an X-linked disorder characterized by mental retardation, early-onset hypotonia, ataxia, delayed motor development, hearing impairment, and optic atrophy (de Brouwer et al., 2007). In the Arts syndrome, susceptibility to infections, especially of the upper respiratory tract, can result in early death.	600
PRX	Charcot-Marie-Tooth disease, type 4F	NM_181882.2	NM_181882.2:c.3208C>T, NM_181882.2:c.2857C>T, NM_181882.2:c.2553_2556delTCTC, NM_181882.2:c.2145T>A, NM_181882.2:c.2098delG, NM_181882.2:c.1362delA, NM_181882.2:c.1102C>T, NM_181882.2:c.247delC	Charcot-Marie-Tooth disease, type 4F follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PRX gene located on chromosomal region 19q13.2. The age of onset is infantile. This disease is characterized by delayed motor milestones, and proximal and distal muscle weakness. The prevalence is <1:1,000,000.	600

PSAP	Combined SAP deficiency	NM_001042465.2	NM_001042465.2:c.1297C>T, NM_001042465.2:c.1055T>C, NM_001042465.2:c.643A>C, NM_001042465.2:c.607C>T	Combined saposin (SAP) deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PSAP gene located on chromosomal region 10q22.1. The age of onset is neonatal/infancy. This disease is characterized by hypotonia, massive myoclonic bursts, abnormal ocular movements and dystonia. Grand mal seizures and seizures triggered by tactile stimuli have been described. Patients also develop hepatosplenomegaly. Death between 1 and 4 months usually occurs from respiratory failure following repeated pulmonary infections. The prevalence is below 1/1,000,000.	600
PSAP	Combined SAP deficiency	NM_002778.3	NM_002778.3:c.1A>T	Combined saposin (SAP) deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PSAP gene located on chromosomal region 10q22.1. The age of onset is neonatal/infancy. This disease is characterized by hypotonia, massive myoclonic bursts, abnormal ocular movements and dystonia. Grand mal seizures and seizures triggered by tactile stimuli have been described. Patients also develop hepatosplenomegaly. Death between 1 and 4 months usually occurs from respiratory failure following repeated pulmonary infections. The prevalence is below 1/1,000,000.	600
PSAT1	Neu-Laxova syndrome, type 2	NM_058179.3	NM_058179.3:c.299A>C, NM_058179.3:c.1033_1034delCT	Neu-Laxova syndrome, type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the PSAT1 gene located on chromosomal region 9q21.2. The age of onset is prenatal. This disease is characterized by severe congenital malformations leading to prenatal or early postnatal lethality. Affected patients have abnormal craniofacial features, microcephaly, intrauterine growth retardation, ichthyosis, flexion deformities, limb malformations, and edema of the hands and feet. Some patients have malformations of the central nervous system. The prevalence is below 1/1,000,000.	600
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
RAB23	Carpenter syndrome	NM_001278666.1	NM_001278666.1:c.434T>A, NM_001278666.1:c.407dupC	Carpenter syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RAB23 gene located on chromosomal region 6p11.2. The age of onset is early. This disease is characterized by acrocephaly, peculiar facies, brachydactyly and syndactyly in the hands, and preaxial polydactyly and syndactyly of the toes. The prevalence is <1:1,000,000.	600
RAB27A	Griscelli syndrome, type 2	NM_004580.4	NM_004580.4:c.454G>C, NM_004580.4:c.389T>C, NM_004580.4:c.382dupA, NM_004580.4:c.352C>T, NM_004580.4:c.259G>C, NM_004580.4:c.217T>G	Griscelli disease type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RAB27A gene located on chromosome 15q15-q21.1. The age of onset is infantile. This disease is characterized by immune system abnormalities in addition to having hypopigmented skin and hair. Affected individuals are prone to recurrent infections. They also develop an immune condition called hemophagocytic lymphohistiocytosis, in which the immune system produces too many activated immune cells called T-lymphocytes and macrophages (histiocytes).	600
RAB3GAP1	Warburg micro syndrome, type 1	NM_001172435.1	NM_001172435.1:c.497_498delTT, NM_001172435.1:c.748+1G>A, NM_001172435.1:c.899+1G>A, NM_001172435.1:c.937dupA, NM_001172435.1:c.1395_1398delTATG, NM_001172435.1:c.1410C>A, NM_001172435.1:c.1734G>A, NM_001172435.1:c.2011C>T	Warburg micro syndrome type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RAB3GAP1 gene located on chromosomal region 2q21.3. The age of onset is infantile. This disease is characterized by microcephaly, microphthalmia, microcornia, congenital cataracts, optic atrophy, cortical dysplasia, in particular corpus callosum hypoplasia, severe mental retardation, spastic diplegia, and hypogonadism. The prevalence is <1:1,000,000.	600

RAB3GAP2	Martsolf syndrome	NM_012414.3	NM_012414.3:c.1648C>T, NM_012414.3:c.1485C>A, NM_012414.3:c.1276C>T, NM_012414.3:c.325_328delAAAG	Warburg micro syndrome type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RAB3GAP2 gene located on chromosomal region 1q41. The age of onset is early. This disease is characterized by microcephaly, microphthalmia, microcornia, congenital cataracts, optic atrophy, cortical dysplasia, in particular corpus callosum hypoplasia, severe mental retardation, spastic diplegia, and hypogonadism. The prevalence is <1:1,000,000.	600
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
RAG2	Omenn syndrome; Severe combined immunodeficiency, B cell-negative	NM_000536.3	NM_000536.3:c.1352G>C, NM_000536.3:c.601C>T, NM_000536.3:c.283G>A, NM_000536.3:c.230C>A, NM_000536.3:c.115A>G	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
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

RDX	Deafness, autosomal recessive, type 24	NM_001260492.1	NM_001260492.1:c.1405dupG, NM_001260492.1:c.342_346delGATAT	Autosomal recessive nonsyndromic sensorineural deafness type DFNB24 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RDX gene located on chromosomal region 11q22.3. 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
RELN	Lissencephaly 2 (Norman-Roberts type)	NM_005045.3	NM_005045.3:c.6646C>T, NM_005045.3:c.5615-1G>A	Lissencephaly syndrome 2, Norman-Roberts type follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the RELN gene located on chromosomal region 7q22. The age of onset is early. This disease is characterized by craniofacial anomalies (severe microcephaly, a low sloping forehead, a broad and prominent nasal bridge and widely set eyes) and postnatal growth retardation, severe intellectual deficit, spasticity and epilepsy. The prevalence is 1:1,000,000-9:1,000,000.	600
REN	Renal tubular dysgenesis	NM_000537.3	NM_000537.3:c.404C>A, NM_000537.3:c.145C>T, NM_000537.3:c.127C>T	Renal tubular dysgenesis deficiency follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in REN gene located on chromosomal region 1q32.1. 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
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
RP2	Retinitis pigmentosa, type 2, X-linked	NM_006915.2	NM_006915.2:c.235delG, NM_006915.2:c.305dupT, NM_006915.2:c.352delC, NM_006915.2:c.353G>A, NM_006915.2:c.353G>T, NM_006915.2:c.358C>T, NM_006915.2:c.453delC, NM_006915.2:c.453C>G, NM_006915.2:c.631delC	Retinitis pigmentosa type 2 (RP2) follows an X-linked (XLRP) pattern of inheritance and is caused by pathogenic variants in the RP2 gene located on chromosomal region Xp11.23. The age of onset is variable. This condition primarily affects males, causing night blindness in early childhood followed by progressive daytime vision loss. RP2 gene mutations account for 10 to 15 percent of all cases of X-linked retinitis pigmentosa. A gradual loss of photoreceptors underlies the progressive vision loss characteristic of retinitis pigmentosa (RP). The prevalence of RP2 is 1:3,500.	600
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

RPGR	Retinitis pigmentosa, type 3, X-linked	NM_001034853.1	NM_001034853.1:c.846_847delAA, NM_001034853.1:c.823G>A, NM_001034853.1:c.806G>A, NM_001034853.1:c.703C>T, NM_001034853.1:c.674_675delCC, NM_001034853.1:c.654_655delGA, NM_001034853.1:c.642_656delTGGAGAACCTGAGAAinsC, NM_001034853.1:c.517G>C, NM_001034853.1:c.505G>T, NM_001034853.1:c.389T>G, NM_001034853.1:c.296C>A, NM_001034853.1:c.179G>T, NM_001034853.1:c.173_174insA, NM_001034853.1:c.155-2A>G	Retinitis pigmentosa type 3 (RP3) follows an X-linked (XLRP) pattern of inheritance and is caused by pathogenic variants in the RPGR gene located on chromosomal region Xp11.4. XLRP are severe forms of inherited retinal degeneration that primarily affects the rod photoreceptors (Demirci et al., 2002). It typically causes an early-onset night blindness and loss of peripheral vision, often causing patients to become legally blind by the age of 30 to 40 years. Mutation in the RPGR gene is believed to account for approximately 70% of XLRP (RP3)(Vervoort et al., 2000). In RP3, affected males have a severe phenotype, and carrier females show a wide spectrum of clinical features ranging from completely asymptomatic to severe RP (Jin et al., 2007). Mutations in the RPGR gene can also cause X-linked cone-rod dystrophy (CORDX1; 304020) and a syndromic form of retinitis pigmentosa (RP) with deafness and sinorespiratory infections (300455). Cone-rod dystrophy is a group of related [to RP] eye disorders that causes vision loss, which becomes more severe over time. These disorders affect the retina, which is the layer of light-sensitive tissue at the back of the eye. In people with cone-rod dystrophy, vision loss occurs as the light-sensing cells of the retina gradually deteriorate. X-linked cone-rod dystrophy is a rare, progressive visual disorder primarily affecting cone photoreceptors (Demirci et al., 2002). Affected individuals, essentially all of whom are males, present with decreased visual acuity, myopia, photophobia, abnormal color vision, full peripheral visual fields, decreased photopic electroretinographic responses, and granularity of the macular retinal pigment epithelium. The degree of rod photoreceptor involvement is variable, with increasing degeneration. Although penetrance appears to be nearly 100%, there is variable expressivity with respect to age at onset, severity of symptoms, and findings (Hong et al., 1994).	600
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
SBF2	Charcot-Marie-Tooth disease, type 4B2	NM_030962.3	NM_030962.3:c.5536_5539dupATCT, NM_030962.3:c.3586C>T, NM_030962.3:c.3154A>T, NM_030962.3:c.2875C>T, NM_030962.3:c.1459C>T	Charcot-Marie-Tooth disease, type 4B2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SBF2 gene located on chromosomal region 11p15.4. The age of onset is infantile. This disease is characterized by muscle weakness, sensory loss, reduced nerve conduction velocities, characteristic myelin outfoldings and a severe disease course.	600
SC5D	Lathosterolosis	NM_001024956.2	NM_001024956.2:c.86G>A	Lathosterolosis follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SC5D gene located on chromosomal region 11q23.3. The age of onset is early. This disease is characterized by malformations, intellectual deficit and liver disease. The prevalence is <1:1,000,000.	600

SCNN1A	Pseudohypoaldosteronism, type 1	NM_001159576.1	NM_001159576.1:c.1942C>T, NM_001159576.1:c.1699C>T, NM_001159576.1:c.1659delC, NM_001159576.1:c.1482delC, NM_001159576.1:c.517G>A, NM_001159576.1:c.380_381delTC	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
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
SELENON	Muscular dystrophy, rigid spine, type 1	NM_020451.2	NM_020451.2:c.713dupA, NM_020451.2:c.818G>A, NM_020451.2:c.943G>A, NM_020451.2:c.1315C>T, NM_020451.2:c.1384T>G	Rigid spine syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SELENON gene located on chromosomal region 1p36.11. The age of onset is infantile. This disease is characterized by contractures of the spinal extensor muscles associated with abnormal posture (limitation of neck and trunk flexure), progressive scoliosis of the spine, early marked cervico-axial muscle weakness with relatively preserved strength and function of the extremities and progressive respiratory insufficiency. The prevalence is 3.5:100,000ï¾–5:100,000.	600
SEMA4A	Cone-rod dystrophy, type 10; Retinitis pigmentosa, type 35	NM_001193300.1	NM_001193300.1:c.1033G>C, NM_001193300.1:c.1049T>G	Cone-rod dystrophy, type 10 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SEMA4A gene located on chromosomal region 1q22. The age of onset is childhood/adolescent. This disease is characterized by retinal pigment deposits visible on fundus examination, predominantly in the macular region, and initial loss of cone photoreceptors followed by rod degeneration. This leads to decreased visual acuity and sensitivity in the central visual field, followed by loss of peripheral vision. Severe loss of vision occurs earlier than in retinitis pigmentosa, due to cone photoreceptors degenerating at a higher rate than rod photoreceptors. The prevalence is 1-9/100,000. Retinitis pigmentosa-35 (RP35) can be caused by compound heterozygous mutation in the SEMA4A gene. RP35 is characterized by retinal pigment deposits and primary loss of rod photoreceptor cells followed by secondary loss of cone photoreceptors. Patients typically have night vision blindness and loss of midperipheral visual field. As their condition progresses, they lose their far peripheral visual field and eventually central vision as well.	600
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
SGCB	Muscular dystrophy, limb-girdle, type 2E	NM_000232.4	NM_000232.4:c.552T>G, NM_000232.4:c.452C>G, NM_000232.4:c.341C>T, NM_000232.4:c.323T>G, NM_000232.4:c.299T>A, NM_000232.4:c.272G>T, NM_000232.4:c.272G>C	Autosomal recessive limb-girdle muscular dystrophy type 2E follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SGCB gene located on chromosomal region 4q12. The age of onset is variable. This disease is characterized by limb-girdle weakness, particularly of the pelvic girdle muscles.	600
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
SH2D1A	Lymphoproliferative syndrome, X-linked, type 1	NM_002351.4	NM_002351.4:c.3G>T, NM_002351.4:c.95G>C, NM_002351.4:c.163C>T, NM_002351.4:c.164G>T, NM_002351.4:c.172C>T, NM_002351.4:c.203C>T, NM_002351.4:c.302C>T	X-linked lymphoproliferative disease type 1 follows an X-linked pattern of inheritance and is caused by pathogenic variants in the SH2D1A gene located on chromosomal region Xq25. The age of onset is infantile. This disease is characterized by an inadequate immune response to infection with the Epstein-Barr virus: fulminant infectious mononucleosis, macrophage-activation syndrome or hemophagocytic lymphohistiocytosis (HLH) (see these terms), and/or progressive hypogammaglobulinemia and/or lymphomas. The prevalence is 1:1, 000,000 men.	600
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
SIL1	Marinesco-Sjogren syndrome	NM_001037633.1	NM_001037633.1:c.1312C>T, NM_001037633.1:c.331C>T	Marinesco-Sjï¿½gren syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SIL1 gene located on chromosomal region 5q31.2. The age of onset is infantile. This disease is characterized by dysarthria, nystagmus, muscle weakness and hypotonia. The prevalence is <1:1,000,000.	600
SIX6	Optic disc anomalies with retinal and/or macular dystrophy	NM_007374.2	NM_007374.2:c.532_536delAACCG	Optic disc anomalies with retinal and/or macular dystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SIX6 gene located on chromosomal region 14q23.1. The age of onset is neonatal. This disease is characterized by optic nerve dysplasia, optic disk anomalies, chorioretinal dystrophy and macular atrophy. Some patients have microphthalmia. The prevalence is <1/1,000,000.	600
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

SLC12A6	Agenesis of the corpus callosum with peripheral neuropathy	NM_133647.1	NM_133647.1:c.3031C>T, NM_133647.1:c.2023C>T, NM_133647.1:c.1584_1585delCTinsG, NM_133647.1:c.619C>T, NM_133647.1:c.366T>G, NM_133647.1:c.316+1G>A	Corpus callosum agenesis with neuronopathy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC12A6 gene located on chromosomal region 15q13-q14. The age of onset is early. This disease is characterized by a delay in developmental milestones, a severe sensory-motor polyneuropathy with areflexia, a variable degree of agenesis of the corpus callosum, amyotrophy, hypotonia, and cognitive impairment. The prevalence is 1:2,117.	600
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
SLC25A13	Citrullinemia, adult-onset, type 2	NM_001160210.1	NM_001160210.1:c.1816C>T, NM_001160210.1:c.1804G>T, NM_001160210.1:c.1804G>A, NM_001160210.1:c.1802dupA, NM_001160210.1:c.1595G>A, NM_001160210.1:c.1414_1415delCT, NM_001160210.1:c.1314+1G>A, NM_001160210.1:c.1234-1G>A, NM_001160210.1:c.1180+1G>A, NM_001160210.1:c.1081C>T, NM_001160210.1:c.852_855delTATG, NM_001160210.1:c.674C>A, NM_001160210.1:c.615+5G>A, NM_001160210.1:c.615+1G>C	Citrullinemia, adult-onset, type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC25A13 gene located on chromosomal region 7q21.3. This disease is characterized by hyperammonemia and associated neuropsychiatric symptoms such as nocturnal delirium, confusion, restlessness, disorientation, drowsiness, memory loss, abnormal behavior (aggression, irritability, and hyperactivity), seizures, and coma. The prevalence is 1:17,000-1:230,000.	600
SLC25A15	Hyperornithinemia-hyperammonemia-homocitrullinemia syndrome	NM_014252.3	NM_014252.3:c.110T>G, NM_014252.3:c.212T>A, NM_014252.3:c.535C>T, NM_014252.3:c.538G>A, NM_014252.3:c.562_564delTTC, NM_014252.3:c.569G>A, NM_014252.3:c.658G>A, NM_014252.3:c.815C>T, NM_014252.3:c.824G>A	Hyperornithinemia-hyperammonemia-homocitrullinuria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC25A15 gene located on chromosomal region 13q14.11. The age of onset is early. This disease is characterized by coma due to hyperammonemia, convulsions, and hypotonia. The prevalence is 1:5,500.	600
SLC25A22	Epileptic encephalopathy, early infantile, type 3	NM_001191060.1	NM_001191060.1:c.706G>T, NM_001191060.1:c.617C>T	Early infantile epileptic encephalopathy, type 3 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC25A22 gene located on chromosomal region 11p15.5. The age of onset is early. This disease is characterized by the onset of tonic spasms within the first 3 months of life leading to psychomotor impairment and death. The prevalence is <1:1,000,000.	600
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
SLC35A1	Congenital disorder of glycosylation, type 2f	NM_006416.4	NM_006416.4:c.277_280delGTGCinsTG	Congenital disorder of glycosylation type 2F follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC35A1 gene located on chromosomal region 6q15. The age of onset is early. This disease is characterized by repeated hemorrhagic incidents, including severe pulmonary hemorrhage.	600

SLC35C1	Congenital disorder of glycosylation, type 2c	NM_018389.4	NM_018389.4:c.91G>T, NM_018389.4:c.290dupG, NM_018389.4:c.439C>T, NM_018389.4:c.503_505delTCT, NM_018389.4:c.923C>G	Congenital disorder of glycosylation type 2c follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC35C1 gene located on chromosomal region 11p11.2. The age of onset is infantile. This disease is characterized by recurrent bacterial infections, severe growth delay and severe intellectual deficit.	600
SLC35D1	Schneckenbecken dysplasia	NM_015139.2	NM_015139.2:c.932G>A, NM_015139.2:c.319C>T	Schneckenbecken dysplasia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC35D1 gene located on chromosomal region 1p31.3. The age of onset is fetal. This disease is characterized by nail-like configuration of the hypoplastic iliac bone, flattened hypoplastic vertebral bodies, short ribs, short and wide fibulae, short and broad long bones with a dumbbell-like appearance, and precocious ossification of the tarsus.	600
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
SLC45A2	Albinism, oculocutaneous, type 4	NM_016180.4	NM_016180.4:c.1121delT, NM_016180.4:c.986delC, NM_016180.4:c.469G>A	Oculocutaneous albinism type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SLC45A2 gene located on chromosomal region 5p13.2. The age of onset is early. This disease is characterized by skin and hair hypopigmentation, numerous ocular changes and misrouting of the optic nerves at the chiasm. The prevalence is 1:100.000.	600
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
SLC6A8	Cerebral creatine deficiency syndrome, type 1	NM_005629.3	NM_005629.3:c.321_323delCTT, NM_005629.3:c.395G>T, NM_005629.3:c.1011C>G, NM_005629.3:c.1141G>C, NM_005629.3:c.1222_1224delTTC, NM_005629.3:c.1540C>T	Cerebral creatine deficiency syndrome type 1 follows an X-linked pattern of inheritance and is caused by pathogenic variants in the SLC6A8 gene located on chromosomal region Xq28. The age of onset is infantile. People with this disorder have intellectual disability, which can range from mild to severe, and delayed speech development. Some affected individuals develop behavioral disorders such as attention deficit hyperactivity disorder or autistic behaviors that affect communication and social interaction. They may also experience seizures. The disorder has been estimated to account for between 1 and 2 percent of males with intellectual disability. Carrier females may show mild neuropsychologic impairment (summary by van de Kamp et al., 2011). The prevalence is 11:1,000.	600

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
SNAP29	Cerebral dysgenesis, neuropathy, ichthyosis, and palmoplantar keratoderma syndrome	NM_004782.3	NM_004782.3:c.487dupA	Cerebral dysgenesis, neuropathy, ichthyosis, and palmoplantar keratoderma syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SNAP29 gene located on chromosomal region 22q11.2. The age of onset is early. This disease is characterized by severe developmental abnormalities of the nervous system and aberrant differentiation of the epidermis. The prevalence is <1:1,000,000.	600
SPART	Spactic paraplegia, type 20, autosomal recessive	NM_001142294.1	NM_001142294.1:c.1110delA, NM_001142294.1:c.364_365delAT	Spactic paraplegia, type 20 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SPART gene located on chromosomal region 13q13.3. The age of onset is infancy. 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. SPG20 is characterized by dysarthria, distal amyotrophy, mild developmental delay and short stature. The prevalence is <1/1,000,000.	600
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
STAR	Lipoid adrenal hyperplasia	NM_000349.2	NM_000349.2:c.772C>T, NM_000349.2:c.749G>A, NM_000349.2:c.577C>T, NM_000349.2:c.562C>T, NM_000349.2:c.559G>A, NM_000349.2:c.545G>T, NM_000349.2:c.545G>A	Lipoid adrenal hyperplasia follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the STAR gene located on chromosomal region 8p11.23. The age of onset is neonatal/infancy. This disease is characterized by a defect in the conversion of cholesterol to pregnenolone, the first step in adrenal and gonadal steroidogenesis. All affected individuals are phenotypic females with a severe salt-losing syndrome that is fatal if not treated in early infancy. The prevalence is unknown.	600
STIL	Microcephaly, type 7, primary, autosomal recessive	NM_001048166.1	NM_001048166.1:c.3846_3849delACAG, NM_001048166.1:c.3718C>T, NM_001048166.1:c.3658delG, NM_001048166.1:c.2829+1G>A	Microcephaly, type 7, primary, autosomal recessive follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the STIL gene located on chromosomal region 1p33. The age of onset is prenatal/neonatal. This disease is characterized by a head circumference more than 3 standard deviations below the age-related mean. Brain weight is markedly reduced and the cerebral cortex is disproportionately small. Despite this marked reduction in size, the gyral pattern is relatively well preserved, with no major abnormality in cortical architecture. Affected individuals are mentally retarded. Primary microcephaly is further defined by the absence of other syndromic features or significant neurological deficits due to degenerative brain disorder. The prevalence is unknown.	600
STRA6	Microphthalmia, isolated, with coloboma, type 8	NM_001199042.1	NM_001199042.1:c.2081G>A, NM_001199042.1:c.2080C>T, NM_001199042.1:c.2048C>T, NM_001199042.1:c.1816C>T, NM_001199042.1:c.1795G>C, NM_001199042.1:c.1638-1G>A, NM_001199042.1:c.1027_1028delGGinsAA, NM_001199042.1:c.995C>T, NM_001199042.1:c.644dupG, NM_001199042.1:c.394_395insCC, NM_001199042.1:c.264delC, NM_001199042.1:c.186G>A, NM_001199042.1:c.169_170delTAinsC	Microphthalmia, isolated, with coloboma, type 8 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the STRA6 gene located on chromosomal region 15q24.1. This disease is characterized by bilateral clinical anophthalmia, pulmonary hypoplasia/aplasia, cardiac malformations, and diaphragmatic defects. The phenotype is variable, ranging from isolated clinical anophthalmia or microphthalmia to complex presentations involving the cardiac, pulmonary, diaphragmatic, and renal systems. At its most severe, infants are born without pulmonary structures and die soon after birth.	600
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
SUCLG1	Mitochondrial DNA depletion syndrome, type 9 (encephalomyopathic, type with methylmalonic aciduria)	NM_003849.3	NM_003849.3:c.152_153delAT	Mitochondrial DNA depletion syndrome, type 9 (encephalomyopathic, type with methylmalonic aciduria) follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SUCLG1 gene located on chromosomal region 2p11.2. The age of onset is early. This disease is characterized by polypnea, severe hypotonia, lethargy, and vomiting, after a silent period during which the children were considered as normal. Facial dysmorphism and cerebral malformations may be noted, as well as diverse organ involvement such as hypertrophic myocardiopathy, tubulopathy, or liver insufficiency.	600
SUOX	Sulfite oxidase deficiency	NM_000456.2	NM_000456.2:c.37C>T, NM_000456.2:c.650G>A, NM_000456.2:c.794C>A, NM_000456.2:c.894_895delCT	Sulfocysteinuria follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the SUOX gene located on chromosome 12q13.13. The age of onset is early. This disease is characterized by seizures, reduced muscle tone, psychomotor retardation, lens dislocation.	600

TAT	Tyrosinemia, type 2	NM_000353.2	NM_000353.2:c.1297C>T, NM_000353.2:c.1249C>T, NM_000353.2:c.668C>G, NM_000353.2:c.236-5A>G, NM_000353.2:c.169C>T	Tyrosinemia type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TAT gene located on chromosomal region 16q22.1. The age of onset is early. This disease is characterized by hypertyrosinemia with oculocutaneous manifestations and, in some cases, intellectual deficit. The prevalence is 1:100,000-1:120,000 newborn.	600
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
TECTA	Deafness, autosomal recessive, type 21	NM_005422.2	NM_005422.2:c.651dupC, NM_005422.2:c.2428C>T, NM_005422.2:c.2941+1G>A, NM_005422.2:c.4371_4384dupTCAGTGCGACCCGC, NM_005422.2:c.4601G>A	Autosomal recessive nonsyndromic sensorineural deafness type DFNB21 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TECTA gene located on chromosomal region 11q23.3. 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
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

TH	Segawa syndrome, recessive	NM_199292.2	NM_199292.2:c.1481C>T, NM_199292.2:c.1234C>A, NM_199292.2:c.826A>C, NM_199292.2:c.707T>C, NM_199292.2:c.698G>A	Segawa syndrome, autosomal recessive follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TH gene located on chromosomal region 11p15.5. This disease is characterized by dystonia presenting in infancy or early childhood. Dystonia is defined by the presence of sustained involuntary muscle contractions, often leading to abnormal postures. Some cases present with parkinsonian symptoms in infancy. Unlike all other forms of dystonia, it is an eminently treatable condition, due to a favorable response to L-DOPA. The prevalence is 1:1,000,000-9:1,000,000.	600
TIMM8A	Mohr-Tranebjaerg syndrome	NM_004085.3	NM_004085.3:c.238C>T, NM_004085.3:c.198C>G, NM_004085.3:c.112C>T	Mohr-Tranebjaerg syndrome follows an X-linked pattern of inheritance and is caused by pathogenic variants in the TIMM8A gene located on chromosomal region Xq22. The age of onset is infantile. This disease is characterized by hearing loss, followed by adolescent onset progressive dystonia or ataxia, visual impairment from early adulthood onwards and dementia from the 4th decade onwards. The prevalence is <1:1,000,000.	600
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
TMC1	Deafness, autosomal recessive, type 7	NM_138691.2	NM_138691.2:c.100C>T, NM_138691.2:c.425G>A, NM_138691.2:c.454-1G>C, NM_138691.2:c.1165C>T, NM_138691.2:c.1763+3A>G, NM_138691.2:c.1842G>A, NM_138691.2:c.1960A>G	Autosomal recessive nonsyndromic sensorineural deafness type DFNB7 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TMC1 gene located on chromosomal region 9q21.13. 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
TMEM216	Joubert syndrome, type 2; Meckel syndrome, type 2	NM_001173991.2	NM_001173991.2:c.79_82delAACG, NM_001173991.2:c.218G>A, NM_001173991.2:c.218G>T, NM_001173991.2:c.230G>C, NM_001173991.2:c.253C>T, NM_001173991.2:c.341T>G	Joubert syndrome (JBTS) type 2 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TMEM216 gene located on chromosomal region 11q12.2. 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 (manifesting with either Leber congenital amaurosis or progressive retinal dystrophy) and nephronophthisis (usually juvenile). The prevalence is 1:100,000. The TMEM216 gene is also associated with other ciliopathies, as Meckel syndrome type 2, 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.	600

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
TMIE	Deafness, autosomal recessive, type 6	NM_147196.2	NM_147196.2:c.170G>A, NM_147196.2:c.241C>T, NM_147196.2:c.250C>T	Autosomal recessive nonsyndromic sensorineural deafness type DFNB6 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TMIE gene located on chromosomal region 21q22.3. The age of onset is early. This disease is characterized by hearing loss and deafness.	600
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
TNNT1	Nemaline myopathy , type 5, Amish type	NM_003283.5	NM_003283.5:c.538G>T	Nemaline myopathy 5, Amish type follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TNNT1 gene located on chromosomal region 19q13.4. The age of onset is from birth to adulthood. 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 1:50,000 newborn.	600
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
TPRN	Deafness, autosomal recessive, type 79	NM_001128228.2	NM_001128228.2:c.1427delC, NM_001128228.2:c.1239G>A	Autosomal recessive nonsyndromic sensorineural deafness type DFNB79 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TPRN gene located on chromosomal region 9q34.3. The age of onset is early. This disease is characterized by hearing loss and deafness.	600
TREX1	Aicardi-Goutieres syndrome, type 1	NM_016381.5	NM_016381.5:c.309dupC, NM_016381.5:c.506G>A, NM_016381.5:c.655C>T	Aicardi-Goutiï¿½res syndrome 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TREX1 gene located on chromosomal region 3p21.31. The age of onset is early. This disease is characterized by subacute encephalopathy (feeding problems, irritability and psychomotor regression or delay) associated with epilepsy (53% of cases), chilblain skin lesions on the extremities (43% of cases) and episodes of aseptic febrile illness (40% of cases). The prevalence is <1:1,000,000.	600

TRIM32	Muscular dystrophy, limb-girdle, type 2H	NM_001099679.1	NM_001099679.1:c.1459G>A, NM_001099679.1:c.1560delC	Autosomal recessive limb-girdle muscular dystrophy type 2H follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TRIM32 gene located on chromosomal region 9q31-q33. The age of onset is variable. This disease is characterized by proximal muscle weakness and facial muscle wasting.	600
TRIM37	Mulibrey nanism	NM_001005207.3	NM_001005207.3:c.2212delG, NM_001005207.3:c.2056C>T, NM_001005207.3:c.1668-1G>C, NM_001005207.3:c.1478_1479delAG, NM_001005207.3:c.1411C>T, NM_001005207.3:c.1346dupA, NM_001005207.3:c.1037_1040dupAGAT, NM_001005207.3:c.965G>T, NM_001005207.3:c.745C>T, NM_001005207.3:c.496_500delAGGAA, NM_001005207.3:c.326G>C, NM_001005207.3:c.227T>C	Mulibrey nanism follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TRIM37 gene located on chromosomal region 17q22. The age of onset is prenatal. This disease is characterized by pre- and postnatal growth restriction, characteristic craniofacial features with scaphocephaly, triangular face, high and broad forehead, low nasal bridge and yellowish dots in retinal mid peripheral region. The prevalence is <1:1,000,000.	600
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
TSHB	Hypothyroidism, congenital, nongoitrous, type 4	NM_000549.4	NM_000549.4:c.94G>T, NM_000549.4:c.145G>A, NM_000549.4:c.205C>T	Hypothyroidism, congenital, nongoitrous 4, also known as isolated thyroid-stimulating hormone (TSH) deficiency is a type of central congenital hypothyroidism, a permanent thyroid deficiency that is present from birth, characterized by low levels of thyroid hormones due to a deficiency in TSH synthesis.	600
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
TULP1	Leber congenital amaurosis, type 15	NM_003322.4	NM_003322.4:c.1511_1521delTGCAGTTCGGC, NM_003322.4:c.1471T>C, NM_003322.4:c.1444C>T, NM_003322.4:c.1376T>A, NM_003322.4:c.1318C>T, NM_003322.4:c.1259G>C, NM_003322.4:c.1204G>T, NM_003322.4:c.1198C>T	Leber congenital amaurosis 15 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TULP1 gene located on chromosomal region 6p21.31. 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
TWNK	Mitochondrial DNA depletion syndrome, type 7 (hepatocerebral type); Perrault syndrome type 5	NM_021830.4	NM_021830.4:c.526dupG, NM_021830.4:c.952G>A, NM_021830.4:c.955A>G, NM_021830.4:c.1287C>T, NM_021830.4:c.1370C>T, NM_021830.4:c.1523A>G	Mitochondrial DNA depletion syndrome, hepatocerebrorenal form follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the TWNK gene located on chromosomal region 10q24. The age of onset is neonatal/infantile. It is a severe disease associated with mitochondrial dysfunction. Some patients are affected by progressive atrophy of the cerebellum, brain stem, the spinal cord, and sensory axonal neuropathy. Clinical features include hypotonia, athetosis, ataxia, ophthalmoplegia, sensorineural hearing deficit, sensory axonal neuropathy, epileptic encephalopathy and female hypogonadism. In some individuals liver dysfunction and multi-organ failure is present. On the other hand, Perrault syndrome is a rare condition that causes different patterns of signs and symptoms in affected males and females. A key feature of this condition is hearing loss, which occurs in both males and females. Affected females also have abnormalities of the ovaries. Neurological problems occur in some affected males and females.	600
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
UBR1	Johanson-Blizzard syndrome	NM_174916.2	NM_174916.2:c.4254G>A, NM_174916.2:c.1537C>T, NM_174916.2:c.1281+1G>T, NM_174916.2:c.869C>G	Johanson-Blizzard syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the UBR1 gene located on chromosomal region 15q15.2. The age of onset is early. This disease is characterized by congenital exocrine pancreatic insufficiency and aplasia/hypoplasia of alae nasi, together with a variety of other abnormalities including aplasia cutis, anorectal anomalies and failure to thrive. The prevalence is <1:1,000,000.	600

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
UQCRQ	Mitochondrial complex III deficiency, nuclear, type 4	NM_014402.4	NM_014402.4:c.134C>T	Mitochondrial complex III deficiency, nuclear type 4 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the UQCRQ gene located on chromosomal region 5q31.1. The age of onset is infantile. This disease is characterized by severe psychomotor retardation and extrapyramidal signs. Neurologic features included dystonia, athetoid movements, ataxia, mild axial hypotonia, increased tone, hyperreflexia, and inability to walk unsupported.	600
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
USH1G	Usher syndrome, type 1G	NM_173477.4	NM_173477.4:c.805C>T, NM_173477.4:c.649C>T, NM_173477.4:c.394dupG, NM_173477.4:c.186_187delCA	Usher syndrome type 1G follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the USH1G gene located on chromosomal region 17q25.1. 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.	600
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
VDR	Rickets, vitamin D-resistant, type 2A	NM_001017536.1	NM_001017536.1:c.1135G>A, NM_001017536.1:c.1065C>G, NM_001017536.1:c.1035C>A, NM_001017536.1:c.971G>T, NM_001017536.1:c.389G>A, NM_001017536.1:c.299G>A, NM_001017536.1:c.287G>A, NM_001017536.1:c.238C>T	Vitamin D-dependent rickets type 2A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the VDR gene located on chromosomal region 12q13.11. The age of onset is early. This disease is characterized by hypocalcemia, severe rickets and in many cases alopecia. The prevalence is 1:10,000-5:10,000.	600
VLDLR	Cerebellar hypoplasia and mental retardation with or without quadrupedal locomotion, type 1	NM_003383.4	NM_003383.4:c.769C>T, NM_003383.4:c.844C>T, NM_003383.4:c.2302_2303delGA, NM_003383.4:c.2339delT	Cerebellar hypoplasia and mental retardation with or without quadrupedal locomotion, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the VLDLR gene located on chromosomal region 9p24.2. The age of onset is early. This disease is characterized by non-progressive congenital ataxia that is predominantly truncal and results in delayed ambulation, moderate-to-profound intellectual disability, dysarthria, strabismus, and seizures. The prevalence is 1:100,000-9:100,000.	600

VPS13A	Choreoacanthocytosis	NM_033305.2	NM_033305.2:c.622C>T, NM_033305.2:c.2898T>G, NM_033305.2:c.3091delG, NM_033305.2:c.9109C>T, NM_033305.2:c.9275+1G>T	Chorea-acanthocytosis follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the VPS13A gene located on chromosomal region 9q21. The age of onset is adult. This disease is characterized by progressive neurological symptoms including movement disorders, psychiatric manifestations and cognitive disturbances.	600
VPS33B	Arthrogryposis, renal dysfunction and cholestasis, type 1	NM_018668.4	NM_018668.4:c.1594C>T, NM_018668.4:c.1480-1G>T, NM_018668.4:c.1312C>T, NM_018668.4:c.1246C>T, NM_018668.4:c.603+2T>A, NM_018668.4:c.440_449delCTCTTGATGT	Arthrogryposis, renal dysfunction and cholestasis type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the VPS33B gene located on chromosomal region 15q26.1. The age of onset is early. This disease is characterized by neurogenic arthrogryposis multiplex congenita, renal tubular dysfunction and neonatal cholestasis. The prevalence is <1:1,000,000.	600
WAS	Wiskott-Aldrich syndrome; Thrombocytopenia, X-linked	NM_000377.2	NM_000377.2:c.134C>T, NM_000377.2:c.167C>T, NM_000377.2:c.173C>G, NM_000377.2:c.809T>C, NM_000377.2:c.814T>C, NM_000377.2:c.881T>C, NM_000377.2:c.1442T>A	Wiskott-Aldrich syndrome (WAS) is an X-linked recessive primary immunodeficiency disease characterized by microthrombocytopenia, eczema, recurrent infections and an increased risk for autoinmmune manifestations and malignancies. WAS usually manifests in infancy but onset may also occur during the neonatal period. The incidence of WAS has been estimated at less than 1 in 100,000 live births. Thrombocytopaenia is defined by a decrease in the number of platelets in circulating blood, resulting in the potential for increased bleeding and decreased ability for clotting. Both conditions follow an X-linked pattern of inheritance and are caused by pathogenic variants in the WAS gene located on chromosomal region Xp11.23.	600
WDR62	Microcephaly, type 2, primary, autosomal recessive, with or without cortical malformations	NM_001083961.1	NM_001083961.1:c.193G>A, NM_001083961.1:c.557G>A, NM_001083961.1:c.671G>C, NM_001083961.1:c.702dupG, NM_001083961.1:c.1313G>A, NM_001083961.1:c.1408C>T, NM_001083961.1:c.3514+1delG, NM_001083961.1:c.3574delA	Autosomal recessive primary microcephalyc type 2 with or without cortical malformations follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the WDR62 gene located on chromosomal region 19q13.12. The age of onset is early. This disease is characterized by reduced head circumference at birth without gross anomalies of brain architecture and variable degrees of intellectual impairment. The incidence is 1:1,000,000.	600
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

WNT7A	Fuhrmann syndrome	NM_004625.3	NM_004625.3:c.874C>T, NM_004625.3:c.325G>A	Fuhrmann syndrome follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the WNT7A gene located on chromosomal region 3p25.1. The age of onset is neonatal/infancy. This disease is characterized by bowing of the femora, aplasia or hypoplasia of the fibulae and poly-, oligo-, and syndactyly. Most of the patients also have a hypoplastic pelvis and hypoplasia of the fingers and fingernails. Some had congenital dislocation of the hip, absence or fusion of tarsal bones, absence of various metatarsals, and hypoplasia and aplasia of the toes. The prevalence is <1:1,000,000.	600
XPA	Xeroderma pigmentosum, group A	NM_000380.3	NM_000380.3:c.727C>T, NM_000380.3:c.619C>T, NM_000380.3:c.501delG, NM_000380.3:c.348T>A	Xeroderma pigmentosum complementation group A follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the gene XPA located on chromosomal region 9q22.33. The age of onset is variable. This disease is characterized by photosensitivity of skin with burning, freckling, and skin cancers. It is associated with a spectrum of mild to severe neurological anomalies (e.g. cognitive deterioration, dysarthria, balance disturbance, areflexia) and sometimes delay of growth and sexual development. The prevalence is 1:1,000,000.	600
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
ZMPSTE24	Mandibuloacral dysplasia with, type B lipodystrophy	NM_005857.4	NM_005857.4:c.54dupT, NM_005857.4:c.121C>T, NM_005857.4:c.955-1G>A, NM_005857.4:c.1018T>C, NM_005857.4:c.1085dupT, NM_005857.4:c.1263dupT, NM_005857.4:c.1349G>A	Mandibuloacral dysplasia with type B lipodystrophy follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ZMPSTE24 gene located on chromosomal region 1p34.2. The age of onset is early. This disease is characterized by postnatal growth retardation, craniofacial anomalies and skeletal malformations, such as mandibular and clavicular hypoplasia; mottled cutaneous pigmentation and generalized lipoatrophy.	600
ZNF469	Brittle cornea syndrome, type 1	NM_001127464.2	NM_001127464.2:c.4174G>T	Brittle cornea syndrome, type 1 follows an autosomal recessive pattern of inheritance and is caused by pathogenic variants in the ZNF469 gene located on chromosomal region 16q24.2. The age of onset is infantile. This disease is characterized by severe ocular manifestations due to extreme corneal thinning and fragility with rupture in the absence of significant trauma. BCS generally progresses to blindness. The prevalence is <1:1,000,000.	600