# Transmembrane Protein 231

**Alternative Names**
TMEM231

**Record Category**
Gene locus

**WHO-ICD**
N/A to gene loci

**Incidence per 100,000 Live Births**
N/A to gene loci

**OMIM Number**
614949

**Mode of Inheritance**
Autosomal recessive

**Gene Map Locus**
16q23.1

**Description**
The TMEM231 gene encodes a transmembrane ciliary protein that is a component of the tectonic-like complex, also known as the B9 or MKS complex. This complex localizes to the basal body, a ring like structure in the transition zone at the base of the primary cilia, and plays an important role in preventing the diffusion of transmembrane proteins between the cilia and plasma membranes. Knockdown of TMEM231 negatively affects ciliogenesis, probably because the diffusion barrier created by the B9 complex is essential for the formation and retention of ciliary components. The protein is also involved in the Sonic hedgehog signaling pathway. Based on studies of mouse orthologs, human TMEM231 protein is predicted to play a role in in-utero embryonic development, vasculature development, digit morphogenesis, eye development and neuroepithelial cell differentiation.

Mutations in the TMEM231 gene are associated with Meckel Syndrome, type 11 (MKS11) and Joubert Syndrome 20 (JBTS20). MKS11 is an often fatal ciliopathy defined by the presence of occipital encephalocele, polydactyly, and polycystic kidneys. JBTS20 is a phenotypically diverse disorder characterized by hypoplasia of the cerebellar vermis resulting in the neuroradiologic molar tooth sign, along with other neurological, ocular and renal manifestations.

**Molecular Genetics**
The gene is located on the long arm of chromosome 16. It spans a length of 19.5 kb and its coding sequence is spread across seven exons. The protein encoded by this gene has a molecular mass of 36 kDa and consists of 316 amino acids. Several additional isoforms of the TMEM231 protein exist due to alternative splicing. The gene is found to be overexpressed in the nasal epithelium. Mutations in TMEM231 associated with MKS11 and JBTS20 include homozygous and compound heterozygous missense mutations or frameshift and premature terminations.

**Epidemiology in the Arab World**

**Saudi Arabia**
Al-Hamed et al. (2016) determined the genetic mutations causing antenatal cystic kidney disease in a cohort of 44 Saudi families. In one family, the antenatal ultrasound found the fetus to have cystic kidneys, oligohydramnios/anhydramnios, encephalocele, corpus callosum agenesis, clubfoot and hepatic cysts. The case resulted in perinatal death. The patient, born to consanguineous parents, was found to be homozygous for the known TMEM231 mutation c.751G>A (p.V251I). The mutation appeared to be a missense change; however, it occurred at the last nucleotide of exon 4 and was hence predicted to cause a splicing defect. The proband had another affected sibling that also died in the perinatal period.

**References**
Al-Hamed MH, Kurdi W, Alsahan N, Alabdullah Z, Abudraz R, Tulbah M, Alnemer M, Khan R, Al-Jurayb H, Alahmed A, Tahir AI, Khalil D, Edwards N, Al Abdulaziz B, Binhumaid FS, Majid S, Faquih T, El-Kalioby M, Abouelhoda M, Altassan N, Monies D, Meyer B, Sayer JA, Albaqumi M. Genetic spectrum of Saudi Arabian patients with

antenatal cystic kidney disease and ciliopathy phenotypes using a targeted renal gene panel. J Med Genet. 2016; 53(5):338-47. PMID: 26862157.

## Related CTGA Records

Meckel Syndrome, type 11

## External Links

https://www.genecards.org/cgi-bin/carddisp.pl?gene=TMEM231

## Contributors

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