

SMARCA4 gene

SWI/SNF related BAF chromatin remodeling complex subunit ATPase 4

Normal Function

The *SMARCA4* gene provides instructions for making a protein called BRG1, which forms one piece (subunit) of several different protein groupings called SWI/SNF protein complexes. SWI/SNF complexes regulate gene activity (expression) by a process known as chromatin remodeling. Chromatin is the network of DNA and protein that packages DNA into chromosomes. The structure of chromatin can be changed (remodeled) to alter how tightly DNA is packaged. Chromatin remodeling is one way gene expression is regulated during development; when DNA is tightly packed, gene expression is lower than when DNA is loosely packed. The BRG1 protein uses a molecule called ATP to provide energy for chromatin remodeling, although the protein's specific role in remodeling is unclear.

Through their ability to regulate gene activity, SWI/SNF complexes are involved in many processes, including repairing damaged DNA; copying (replicating) DNA; and controlling the growth, division, and maturation (differentiation) of cells. Through these processes, the BRG1 protein and other SWI/SNF subunits are thought to act as tumor suppressors, which keep cells from growing and dividing too rapidly or in an uncontrolled way.

Health Conditions Related to Genetic Changes

Coffin-Siris syndrome

Approximately 40 variants (also known as mutations) in the *SMARCA4* gene have been found to cause Coffin-Siris syndrome. This condition is characterized by delayed development, abnormalities of the fifth (pinkie) fingers or toes, and characteristic facial features that are described as coarse. The *SMARCA4* gene variants involved in Coffin-Siris syndrome are germline variants, which means that they are present in cells throughout the body. The variants change single protein building blocks (amino acids) in or remove an amino acid from the BRG1 protein. Although it is unclear how these changes affect SWI/SNF complexes, researchers suggest that *SMARCA4* gene variants result in abnormal chromatin remodeling. Disturbance of this process alters the activity of many genes and disrupts several cellular processes, which could explain the diverse signs and symptoms of Coffin-Siris syndrome. People with Coffin-Siris syndrome do not appear to have an increased risk of cancer (see below).

Rhabdoid tumor predisposition syndrome

At least six germline variants in the *SMARCA4* gene have been identified in people with rhabdoid tumor predisposition syndrome (RTPS). RTPS is characterized by a high risk of developing cancerous (malignant) growths called rhabdoid tumors. These tumors most often occur in the brain and spinal cord (central nervous system) or in the kidney, but they can occur in other organs and tissues of the body. Some affected children also develop noncancerous (benign) tumors called schwannomas, which grow on nerves. Women with RTPS are at increased risk of developing a rare type of ovarian cancer called small cell cancer of the ovary, hypercalcemic type (SCCOHT).

In addition to the germline variant affecting one copy of the *SMARCA4* gene in each cell, an additional genetic change that deletes the normal copy of the gene is needed for a tumor to develop. This additional change is present only in the cancerous cells. Such changes are known as somatic variants. In combination, the germline and somatic variants lead to the absence of BRG1 protein. This absence likely impairs the tumor suppressor functions of the protein, but the specific mechanism that leads to rhabdoid tumors is unknown.

Lung cancer

MedlinePlus Genetics provides information about Lung cancer

Other cancers

Somatic variants in both copies of the *SMARCA4* gene, which result in the absence of SMARCA4 protein, cause noninherited (sporadic) rhabdoid tumors in children. Somatic variants in the *SMARCA4* gene have also been found in certain other types of cancer, particularly lung cancer and other cancers in the chest called *SMARCA4*-deficiency thoracic sarcomas. The mechanism by which variants in the *SMARCA4* gene contribute to these tumors is unknown, although it is thought that changes in SWI/SNF complexes are involved. These changes may impair normal cell differentiation, which leads to the overgrowth of certain cell types, causing cancer. Alternatively, abnormal SWI/SNF complexes may disrupt the regulation of genes that help control the growth and division of cells, which leads to cancer. It is likely that other genetic changes in addition to *SMARCA4* gene variants are necessary for cancer development.

Other Names for This Gene

- ATP-dependent helicase SMARCA4
- BAF190
- brahma protein-like 1
- BRG1
- BRG1-associated factor 190A
- BRM/SWI2-related gene 1
- protein BRG-1

- RTPS2
- SMCA4_HUMAN
- SNF2
- SWI2
- transcription activator BRG1

Additional Information & Resources

Tests Listed in the Genetic Testing Registry

- Tests of SMARCA4 ([https://www.ncbi.nlm.nih.gov/gtr/all/tests/?term=6597\[geneid\]](https://www.ncbi.nlm.nih.gov/gtr/all/tests/?term=6597[geneid]))

Scientific Articles on PubMed

- PubMed (<https://pubmed.ncbi.nlm.nih.gov/?term=%28SMARCA4%5BTIAB%5D%29+AND+%28%28Genes%5BMH%5D%29+OR+%28Genetic+Phenomena%5BMH%5D%29%29+AND+english%5Bla%5D+AND+human%5Bmh%5D+AND+%22last+1800+days%22%5Bdp%5D>)

Catalog of Genes and Diseases from OMIM

- SWI/SNF-RELATED, MATRIX-ASSOCIATED, ACTIN-DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY A, MEMBER 4; SMARCA4 (<https://omim.org/entry/603254>)

Gene and Variant Databases

- NCBI Gene (<https://www.ncbi.nlm.nih.gov/gene/6597>)
- ClinVar ([https://www.ncbi.nlm.nih.gov/clinvar?term=SMARCA4\[gene\]](https://www.ncbi.nlm.nih.gov/clinvar?term=SMARCA4[gene]))

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Genomic Location

The *SMARCA4* gene is found on chromosome 19 (<https://medlineplus.gov/genetics/chromosome/19/>).

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