ATXN7 Knockout cell line (U-2932)

Catalog Number: KOA44687

Product Information

Product Name	ATXN7 Knockout cell line (U-2932)
specification	1*10^6
Storage and transportation	Shipped on dry ice; Store in liquid nitrogen
Cell morphology	Human Lymphocyte-like, suspension
Passage ratio	1 : 2-1 : 4
species	Human
Gene	ATXN7
Gene ID	6314
Build method	Electroporation/Lentivirus
Mycoplasma testing	negative
Cultivation system	90%RPMI-1640+10%FBS
Price (USD)	Inquiry
Parental Cell Line	U-2932
Quality Control	Genotype: ATXN7 Knockout cell line (U-2932)>95% viability before freezing. All cells were tested and found to be free of bacterial, viruses,mycoplasma and other toxins.

Gene Information

Gene Official Full Name	ataxin 7provided by HGNC
Also known as	SCA7; OPCA3; SGF73; ADCAII
Gene Description	The autosomal dominant cerebellar ataxias (ADCA) are a heterogeneous group of neurodegenerative disorders characterized by progressive degeneration of the cerebellum, brain stem and spinal cord. Clinically, ADCA has been divided into three groups: ADCA types I-III. ADCAI is genetically heterogeneous, with five genetic loci, designated spinocerebellar ataxia (SCA) 1, 2, 3, 4 and 6, being assigned to five different chromosomes. ADCAII, which always presents with retinal degeneration (SCA7), and ADCAIII often referred to as the 'pure' cerebellar syndrome (SCA5), are most likely homogeneous disorders. Several SCA genes have been cloned and shown to contain CAG repeats in their coding regions. ADCA is caused by the expansion of the CAG repeats, producing an elongated polyglutamine tract in the corresponding protein. The expanded repeats are variable in size and unstable, usually increasing in size when transmitted to successive generations.

	This locus has been mapped to chromosome 3, and it has been determined that the diseased allele associated with spinocerebellar ataxia-7 contains 37-306 CAG repeats (near the N-terminus), compared to 4-35 in the normal allele. The encoded protein is a component of the SPT3/TAF9/GCN5 acetyltransferase (STAGA) and TBP-free TAF-containing (TFTC) chromatin remodeling complexes, and it thus plays a role in transcriptional regulation. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Jul 2016]
Expression	Ubiquitous expression in bone marrow (RPKM 8.0), testis (RPKM 6.7) and 25 other tissues See more