

32-4159: Recombinant Human Melanoma Antigen Family A, 6

Alternative Name : Melanoma-associated antigen 6,Cancer/testis antigen 1.6,CT1.6,MAGE-6 antigen,MAGE3B antigen,MAGEA6,MAGE6,MAGE3B,MAGE-3b.

Description

Source : E.coli. MAGEA6 Human Recombinant produced in E.Coli is a single, non-glycosylated polypeptide chain containing 322 amino acids (1-314 a.a) and having a molecular mass of 35.9kDa.MAGEA6 is fused to an 8 amino acid His-tag at C-terminus & purified by proprietary chromatographic techniques. MAGEA6 belongs to the MAGEA family, which directs the expression of tumor antigens which are seen on a human melanoma by autologous cytolytic T lymphocytes (CTL). Members of the MAGEA family encode proteins with 50 to 80% sequence identity to each other. The MAGE genes, which are clustered at chromosomal location Xq28, were originally isolated from separate kinds of tumors, and based on their practically exclusive tumor-specific expression in adult tissues; they are objects for cancer immunotherapy. MAGEA genes' promoters and first exons exhibit substantial variability, implying that the existence of the MAGEA gene family enables the same function to be expressed under different transcriptional controls. MAGEA genes are implicated in several hereditary disorders, such as dyskeratosis congenita.

Product Info

Amount : 10 µg
Purification : Greater than 90% as determined by SDS-PAGE.
Content : MAGEA6 protein solution (1mg/ml) containing 20mM Tris-HCl buffer (pH 8.0), 0.1M NaCl, 10% glycerol and 1mM DTT.
Storage condition : Store at 4°C if entire vial will be used within 2-4 weeks. Store, frozen at -20°C for longer periods of time. For long term storage it is recommended to add a carrier protein (0.1% HSA or BSA).Avoid multiple freeze-thaw cycles.
Amino Acid : MPLEQRSQHC KPEEGLEARG EALGLVGAQA PATEEQEAAS SSSTLVEVTL GEVPAAESPD PPQSPQGASS LPTTMNYPLW SQSYEDSSNQ EEEGPSTFPD LESEFQAALS RKVAKLVHFL LLKYRAREPV TKAEMLGSSV GNWQYFFPVI FSKASDSLQL VFGIELMEVD PIGHVYIFAT CLGLSYDGLL GDNQIMPKTG FLIILAIIA KEGDCAPEEK IWEELSVLEV FEGREDSIFG DPKKLLTQYF VQENYLEYRQ VPGSDPACYE FLWGPRALIE TSYVKVLHMH VKISGGPRIS YPLLHEWALR EGEELEHHHH HH.