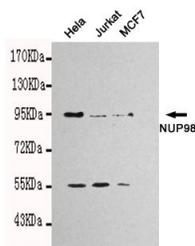




NUP98

Mouse monoclonal Antibody

#53131

Catalog Number: 53131**Amount:** 100µg/100µl**Swiss-Prot No. :** P52948**Gene name:** nup98**Gene id:** 4928**Clone Number:** 3B8-D7-H10**Form of Antibody:** Purified mouse monoclonal in buffer containing 0.1M Tris-Glycine (pH 7.4, 150 mM NaCl) with 0.2% sodium azide, 50% glycerol**Storage/Stability:** Store at -20°C/1 year**Immunogen:** Purified recombinant human NUP98 protein fragments expressed in E.coli**Purification:** affinity-chromatography**Specificity/Sensitivity:** This antibody detects endogenous levels of NUP98 and does not cross-react with related proteins**Reactivity:** Human**Applications:** Predicted MW: 98kd WB: 1:1000

Western blot detection of NUP98 in HeLa, Jurkat and MCF7 cell lysates using NUP98 mouse mAb (1:1000 diluted). Predicted band size: 98kDa. Observed band size: 98kDa.

Background:

Signal-mediated nuclear import and export proceed through the nuclear pore complex (NPC), which is comprised of approximately 50 unique proteins collectively known as nucleoporins. The 98 kDa nucleoporin is generated through a biogenesis pathway that involves synthesis and proteolytic cleavage of a 186 kDa precursor protein. This cleavage results in the 98 kDa nucleoporin as well as a 96 kDa nucleoporin, both of which are localized to the nucleoplasmic side of the NPC. Rat studies show that the 98 kDa nucleoporin functions as one of several docking site nucleoporins of transport substrates. The human gene has been shown to fuse to several genes following chromosome translocations in acute myelogenous leukemia (AML) and T-cell acute lymphocytic leukemia (T-ALL). This gene is one of several genes located in the imprinted gene domain of 11p15.5, an important tumor-suppressor gene region. Alterations in this region have been associated with the Beckwith-Wiedemann syndrome, Wilms tumor, rhabdomyosarcoma, adrenocortical carcinoma, and lung, ovarian, and breast cancer. Alternative splicing of this gene results in several transcript variants; however, not all variants have been fully described.