Recombinant Human URB

Catalog Number: 3410-UR

DESCRIPTION

Source	Mouse myeloma cell line, NS0-derived Met129-Tyr950 & Ser79-Tyr950, both with C-terminal 6-His tag Accession # Q76M96
N-terminal Sequence Analysis	Met129 & Ser79
Predicted Molecular Mass	100.1 kDa

SPECIFICATIONS

SDS-PAGE	125-150 kDa, reducing conditions
Activity	Measured by its ability to inhibit proliferation of HT-29 human colon adenocarcinoma cells. The ED_{50} for this effect is 1-4 µg/mL.
Endotoxin Level	<0.10 EU per 1 µg of the protein by the LAL method.
Purity	>95%, by SDS-PAGE under reducing conditions and visualized by silver stain.
Formulation	Lyophilized from a 0.2 µm filtered solution in PBS. See Certificate of Analysis for details.

PREPARATION AND STORAGE

Reconstitution	Reconstitute at 250 µg/mL in sterile PBS.
Shipping	The product is shipped at ambient temperature. Upon receipt, store it immediately at the temperature recommended below.
Stability & Storage	**Use a manual defrost freezer and avoid repeated freeze-thaw cycles.** ● 12 months from date of receipt, -20 to -70 °C as supplied. ● 1 month, 2 to 8 °C under sterile conditions after reconstitution. ● 3 months, -20 to -70 °C under sterile conditions after reconstitution.

BACKGROUND

URB (**up**regulated in **B**RS-3 deficient mice) is a 150 kDa, secreted glycoprotein that belongs to the sushi-repeat-containing protein superfamily (1, 2). Sushi repeats, otherwise known as short consensus repeats (SCRs), are 60 amino acid (aa) sequences usually involved in protein-protein interaction. They are characterized by the presence of four Cys, two Pro, one Gly and one Trp (3). Human URB is synthesized as a 950 aa precursor that contains a 21 aa signal sequence and a 929 aa mature region. The mature molecule contains three extended sushi/SCR domains of approximately 140 aa each. They bear resemblance to the fifth sushi-repeat in human SPRX (4). The three lie between aa 141 - 281, 615 - 760, and 771 - 913, respectively. Between the first and second SCR lie two amino acid-rich regions, a Thr-rich domain (aa 347 - 404), and a Lys-rich domain (aa 487 - 588). Three potential N-linked glycosylation sites exist in the last two SCR's, while six potential bipartite nuclear localization signals (NLS) occur between aa 420 - 780. There are two potential alternate splice forms for human URB. One is 594 aa in length, and shows a simple truncation at Ser594. This effectively removes the second and third SCRs and two bipartite NLS (5). The second is 553 aa in length and shows a simple truncation after Lys553. This eliminates four bipartite NLSs, the second and third SCRs, and part of the Lys-rich domain (6). Full-length human URB is 83%, 84% and 87% aa identical to rat, mouse and bovine URB, respectively. URB is found in chondrocytes and appears to be downregulated upon CFU-Fibroblast differentiation (1). Thus, it may play a role in skeletogenesis.

References:

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2. Aoki, K. *et al.* (2002) Biochem. Biophys. Res. Commun. **290**:1282.
3. Anatova, J. *et al.* (1989) Biochemistry **28**:4754.
4. Meindl, A. *et al.* (1995) Hum. Mol. Genet. **4**:2339.
5. Isogai, T. *et al.* (2002) GenBank Accession # BAC11475.
6. Strausberg, R.L. *et al.* (2002) GenBank Accession # AAH86876.

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