## 32-4191: Recombinant Human Mediator Complex Subunit 20


#### Abstract

Alternative $\quad$ Mediator complex subunit 7, cofactor required for Sp1 transcriptional activation subunit 9 Name: 33 kDa, Activator-recruited cofactor 34 kDa component, Transcriptional coactivator CRSP33,RNA polymerase transcriptional regulation mediator subunit 7 homolog,


## Description

Source : E.coli. MED7 Human Recombinant produced in E. coli is a single polypeptide chain containing 256 amino acids (1-233) and having a molecular mass of 29.7 kDa.MED7 is fused to a 23 amino acid His-tag at N-terminus \& purified by proprietary chromatographic techniques. MED7 is a member of the Mediator complex subunit 7 family. The activation of gene transcription is a multistep course which is initiated by factors which identify transcriptional enhancer sites in DNA and collaborate with co-activators to direct transcriptional initiation by the RNA polymerase II apparatus. The gene encode a subunit of the CRSP (cofactor required for SP1 activation) complex, that, together with TFIID, is needed for effective activation by SP1. Additionally, MED7 is also an element of other multisubunit complexes e.g. thyroid hormone receptor-(TR) associated proteins that cooperate with TR and enables TR function on DNA templates in conjunction with initiation factors and cofactors.

## Product Info

| Amount : | $20 \mu \mathrm{~g}$ |
| :---: | :---: |
| Purification : | Greater than $85 \%$ as determined by SDS-PAGE. |
| Content : | The MED7 solution ( $0.5 \mathrm{mg} / 1 \mathrm{ml}$ ) contains 20 mM Tris- HCl buffer ( pH 8.0 ), 0.1 M NaCl , and $10 \%$ glycerol. |
| Storage condition : | Store at $4^{\circ} \mathrm{C}$ if entire vial will be used within $2-4$ weeks. Store, frozen at $-20^{\circ} \mathrm{C}$ 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 : | MGSSHHHHHH SSGLVPRGSH MGSMGEPQQV SALPPPPMQY IKEYTDENIQ EGLAPKPPPP IKDSYMMFGN QFQCDDLIIR PLESQGIERL HPMQFDHKKE LRKLNMSILI NFLDLLDILI RSPGSIKREE KLEDLKLLFV HVHHLINEYR PHQARETLRV MMEVQKRQRL ETAERFQKHL ERVIEMIQNC LASLPDDLPH SEAGMRVKTE PMDADDSNNC TGQNEHOREN SGHRRDOIIE KDAALCVLID EMNERP |



