## 32-6943: UGT1A1 Human

UDP Glucuronosyltransferase 1 Family, Polypeptide A1, UGT1, GNT1, UDP Glycosyltransferase 1 Family, Polypeptide A1, Bilirubin-Specific UDPGT Isozyme 1, UDP-Glucuronosyltransferase 1-A, UDP-

## Alternative

Name : Glucuronosyltransferase 1A1, EC 2.4.1.17, UDPGT 1-1, BILIQTL1, HUG-BR1, UGT1-01, UGT-1A, UGT1*1, UGT1.1, UGT1A, Bilirubin UDP-Glucuronosyltransferase Isozyme 1, Bilirubin UDP-Glucuronosyltransferase 1-1, UDP-Glucuronosyltransferase 1-1, UDPGT, UDP-glucuronosyltransferase 1-1.

## Description

Source: Escherichia Coli.
Sterile Filtered clear solution.
UDP Glucuronosyltransferase 1 Family Polypeptide A1, also known as UGT1A1 has a main importance in the conjugation as well as subsequent elimination of potentially toxic xenobiotics and endogenous compounds. UGT1A1 is also capable of catalyzing glucuronidation of 17beta, 17alpha, 1-hydroxypyrene, 4-methylumbelliferone, 1-naphthol, paranitrophenol, scopoletin, and umbelliferone.
UGT1A1 Human Recombinant produced in E.Coli is a single, non-glycosylated polypeptide chain containing 488 amino acids (26-490 a.a) and having a molecular mass of 54.7 kDa . UGT1A1 is fused to a 23 amino acid His-tag at N -terminus \& purified by proprietary chromatographic techniques.

## Product Info

## Amount :

## Purification :

 Content :
## Storage condition :

Amino Acid :

## $5 \mu \mathrm{~g} / 20 \mu \mathrm{~g}$

Greater than $90.0 \%$ as determined by SDS-PAGE.
UGT1A1 protein solution ( $1 \mathrm{mg} / \mathrm{ml}$ ) containing 20 mM Tris- $\mathrm{HCl}(\mathrm{pH} 8.0)$ and $10 \%$ glycerol.
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.
MGSSHHHHHH SSGLVPRGSH MGSHAGKILL IPVDGSHWLS MLGAIQQLQQ RGHEIVVLAP DASLYIRDGA FYTLKTYPVP FQREDVKESF VSLGHNVFEN DSFLQRVIKT YKKIKKDSAM LLSGCSHLLH NKELMASLAE SSFDVMLTDP FLPCSPIVAQ YLSLPTVFFL HALPCSLEFE ATQCPNPFSY VPRPLSSHSD HMTFLQRVKN MLIAFSQNFL CDVVYSPYAT LASEFLQREV TVQDLLSSAS VWLFRSDFVK DYPRPIMPNM VFVGGINCLH QNPLSQEFEA YINASGEHGI VVFSLGSMVS EIPEKKAMAI ADALGKIPQT VLWRYTGTRP SNLANNTILV KWLPQNDLLG HPMTRAFITH AGSHGVYESI CNGVPMVMMP LFGDQMDNAK RMETKGAGVT LNVLEMTSED LENALKAVIN DKSYKENIMR LSSLHKDRPV EPLDLAVFWV EFVMRHKGAP HLRPAAHDLT WYQYHSLD.

