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32-6919: TDP1 Human, Sf9

Alternative Name : Tyrosyl-DNA phosphodiesterase 1, Tyr-DNA phosphodiesterase 1, TDP1, FLJ11090, MGC104252.

Description

Source: Sf9, Baculovirus cells.
Sterile Filtered clear solution.
TDP1 belongs to the phospholipase D family and contains two PLD phosphodiesterase domains. TDP1 is involved in repairing stalled topoisomerase I-DNA complexes by catalyzing the hydrolysis of the phosphodiester bond between the tyrosine residue of topoisomerase I and the 3-prime phosphate of DNA. TDP1 may also remove glycolate from single-stranded DNA containing 3-prime phosphoglycolate, suggesting a role in repair of free-radical mediated DNA double-strand breaks. Mutations in the TDP1 gene are linked to the disease spinocerebellar ataxia with axonal neuropathy (SCAN1).
TDP1 Human Recombinant produced in Sf9 Baculovirus cells is a single, glycosylated polypeptide chain containing 617 amino acids (1-608) and having a molecular mass of 69.5kDa. TDP1 is fused to 9 amino acid His-Tag at C-terminus and purified by proprietary chromatographic techniques.Â

Product Info

Amount :	1 µg / 5 µg
Purification :	Greater than 90.0% as determined by SDS-PAGE.
Content :	TDP1 protein solution (0.25mg/ml) containing Phosphate Buffered Saline (pH 7.4) and 10% glycerol.
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 :	ADPMSQEGDY GRWTISSSDE SEEEKPKPDK PSTSSLLCAR QGAANEPRYT CSEAQKAAHK RKISPVKFSN TDSVLPPKRQ KSGSQEDLGW CLSSSDDELQ PEMPQKQAEK VVIKKEKDIS APNDGTAQRT ENHGAPACHR LKEEEDEYET SGEGQDIWDM LDKGNPFQFY LTRVSGVKPK YNSGALHIKD ILSPLFGTLV SSAQFNYCFD VDWLVKQYPP EFRKKPILLV HGDKREAKAH LHAQAKPYEN ISLCQAKLDI AFGTHHTKMM LLLYEEGLRV VIHTSNLIHA DWHQKTQGIW LSPLYPRIAD GTHKSGESPT HFKADLISYL MAYNAPSLKE WIDVIHKHDL SETNVYLIGS TPGRFQGSQK DNWGHFRLKK LLKDHASSMP NAESWPVVGQ FSSVGSLGAD ESKWLCSEFK ESMLTLGKES KTPGKSSVPL YLIYPSVENV RTSLEGYPAG GSLPYSIQTA EKQNWLHSYF HKWSAETSGR SNAMPHIKTY MRPSPDFSKI AWFLVTSANL SKAAWGALEK NGTQLMIRSY ELGVLFLPSA FGLDSFKVKQ KFFAGSQEPM ATFPVPYDLP PELYGSKDRP WIWNIPYVKA PDTHGNMWVP SHHHHHH.