

# Transcriptional Regulation

## Topoisomerase I

### Technical tip

Human DNA Topoisomerase I (Topo I) is a monomeric protein of 765 amino acids encoded by a single-copy gene. Based on its function, DNA Topoisomerase I has been subdivided into four distinct domains. The N-terminal 214 amino acids of topo I comprise a highly charged N-terminal domain involved in protein-protein interactions with a number of cellular proteins. The highly conserved core domain expanded from amino acids 215 to 636 contains most catalytic residues and retains DNA binding activity. The active C-terminal domain (residues 713-765) is connected to the core domain by a poorly conserved linker domain (residues 636-712).

Human DNA Topoisomerase I is the best studied member of the DNA Topoisomerase family. It catalyzes the relaxation of both positive and negative supercoiled DNAs without the requirement of energy. In addition to DNA replication and transcriptional activation, DNA Topoisomerase I also plays a major role in pre-mRNA splicing, cell cycle, and other gene regulatory pathways during cell growth and development. Since Topo I can cause large amounts of single-strand DNA breaks and this kind of DNA damage closely relates to most cancer, it is therefore believed that DNA Topo I can be an important target for antitumor agents. The wild type DNA Topoisomerase I protein (765 amino acids) was expressed in baculovirus system and purified by using an affinity column and FPLC chromatography. Purified Topo I has been used for in vitro transcriptional activation, pre-mRNA splicing/phosphorylation, DNA binding, and DNA relaxation assays.

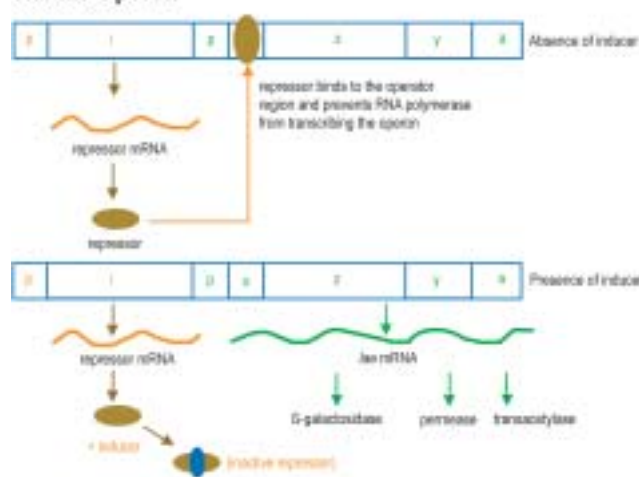
#### Related products :

Topoisomerase I Core	FQ4370	2 µg
Topoisomerase I NTD	FQ4390	2 µg
Topoisomerase I Y723F	FQ4360	2 µg
One Tube RT-PCR Kit	UPS53944	100 tests

The control of transcriptional initiation and rate is the major point of regulation of gene expression in prokaryotes. In eukaryotes, these processes are combined to many different pathways. The regulation apply to clustered genes (operons) to perform coordinated function (and protein expression).

In prokaryotes, the initiation is controlled by two DNA sequence elements that are approximately 35 bases and 10 bases, respectively, upstream of the site of transcriptional initiation, termed **promoter sequences**, because they promote recognition of transcriptional start sites by RNA polymerase. The consensus sequence for the 35-position is TTGACA, and for the 10-position, TATAAT. The 10-position is also known as the Pribnow-box. Several regulatory proteins can act both positively (**activators**) and negatively (**repressors**), interacting with sequences generally termed **operators**. A classic example of catabolite-regulated operons is the bacterail *lac* operon (with one regulatory gene (*i*) and three structural genes (*z*, *y*, and *a*)), and a classic example of an attenuated operon is the *trp* operon.

### The lac Operon



In eukaryotic cells, the transcription regulation of genes may be more complicated. Specific factors that exert initiation control include the **strength of promoter** elements within the DNA sequences of a given gene, the presence or absence of **enhancer sequences** (which enhance the activity of RNA polymerase at a given promoter by binding specific transcription factors), and the interaction between multiple **activator proteins and inhibitor proteins**. Eukaryotic transcribed mRNAs must be capped and

polyadenylated, and the introns must be accurately removed. Several **regulatory genes** have been identified that undergo tissue-specific patterns of alternative splicing, which generate biologically different proteins from the same gene.

Finally, the transcription also depends on Chromatin Structure (regulated by transcription factors, histones and CpG methylation), and biologically active proteins expression control depends on RNA Transport, Transcript Stability, Translational Initiation and modifications, Protein Transport, and Control of Protein Stability.

### Human, Recombinant, Sf9 insect cells

Our purified Topo I protein is greater than 95% homogeneous and contains no detectable protease, DNase, and RNase activity.

Description	Cat.#	Qty
Topoisomerase I	FQ4400	2 µg

### Topoisomerase I (C651-765)

Human DNA Topoisomerase I, C-terminal domain(CTD)

Human DNA Topoisomerase I catalyzes the relaxation of both positive and negative supercoils without the requirement of energy. In addition to DNA replication and transcriptional activation, DNA Topoisomerase I also plays a major role in pre-mRNA splicing, recombination, chromatin remodeling, and other DNA or RNA templating activities.

The 713-765 amino acids C-terminal domain of DNA Topoisomerase I is highly conserved and connected to the core domain by a poorly conserved linker domain (residues 636-713). An active site tyrosine has been characterized at position 723. Mutation from tyrosine to phenylalanine at position 723 preferentially binds the supercoiled DNA rather than relaxed DNA in the mixture of supercoiled and relaxed DNAs.

The C-terminal domain of DNA Topoisomerase I protein (residues 651-765) was expressed in baculovirus system and purified by using an affinity column and FPLC chromatography. Purified Topo I protein (CTD) is greater than 95% homogeneous and contains no detectable protease, DNase, and RNase activity.

Description	Cat.#	Qty
Topoisomerase I (C651-765)	FQ4380	2 µg