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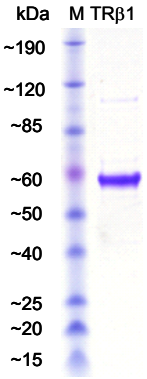
TRβ1 (Thyroid Hormone Receptor, β1 isoform)

Catalog Reference	Vial Size		Lot Number	Molecular Mass	Accession
P1023-01	10,000 units (ng)	☐	081204	53 kDa	NM_000461
P1023-02	25,000 units (ng)	☐			

Storage conditions:
Store at -80 °C

Description:
Nuclear receptors form the largest known family of transcription factors and have a crucial role in nearly all aspects of vertebrate development and adult physiology by transducing the effects of hormones into transcriptional responses (1). The family is defined by two domains: (a) the central, highly conserved, DNA-binding domain (DBD) of approximately 66 amino acids, and (b) the C-terminal, structurally conserved, ligand-binding domain (LBD) of approximately 250 amino acids (2, 3). The amino-terminal regions are least conserved among nuclear receptor sequences. This domain is highly divergent between TRα and TRβ isoforms, which suggests differential roles in transcriptional regulation. In addition, alternative splicing of the TRβ gene generates two isoforms, TRβ1 and TRβ2 with completely different amino-terminal domains (4). Unliganded TR inhibits the formation of a functional pre-initiation complex, through direct interaction with TBP and transcription factor IIB (5-7). In addition, in the absence of ligand TR has been shown to repress transcription through recruitment of a corepressor complex, which also includes Sin3A and histone deacetylase (8, 9). Ligand binding releases the corepressor complex and recruits a coactivator complex that includes multiple histone acetyltransferases, including a steroid receptor family coactivator, p300/CREB-binding protein–associated factor (PCAF), and CREB binding protein (CBP) (10-13).



Source:
Recombinant His tagged TR is isolated from an E. coli strain that carries the coding sequence of the human TRβ1 isoform under the control of a T7 promoter.

Applications:
TR has been applied in reconstituted in vitro transcription assays, protein-protein interactions assays and chromatin remodeling assays. **For Research Use Only**.

Quality Control:
Protein is greater than 95% homogeneous based on SDS-PAGE analysis.

Unit Definition:
1 unit is equal to 1 nanogram of purified protein. 20 units are sufficient for reconstituted transcription assay and 100 units are sufficient for a protein-protein interaction assay.

Concentration:
0.5 mg/ml (in 1x dilution buffer A)

Reagents Supplied:
1x dilution buffer A: 20 mM Tris-Cl (pH 8.0), 20% Glycerol, 100 mM KCl, 1 mM DTT and 0.2 mM EDTA

References:
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