FKBP7 Protein, Human (199a.a, HEK293, His)

Cat. No.:	HY-P70949
Synonyms:	Peptidyl-Prolyl Cis-Trans Isomerase FKBP7; PPIase FKBP7; 23 kDa FK506-Binding Protein; 23 kDa FKBP; FKBP-23; FK506-Binding Protein 7; FKBP-7; Rotamase; FKBP7; FKBP23
Species:	Human
Source:	HEK293
Accession:	Q9Y680 (Q24-L222)
Gene ID:	51661
Molecular Weight:	25-32 kDa

PROPERTIES

AA Sequence	Q R Q K K E E S T E E V K I E V L H R P E N C S K T S K K G D L L N A H Y D G Y L A K D G S K F Y C S R T Q N E G H P K W F V L G V G Q V I K G L D I A M T D M C P G E K R K V V I P P S F A Y G K E G Y A E G K I P P D A T L I F E I E L Y A V T K G P R S I E T F K Q I D M D N D R Q L S K A E I N L Y L Q R E F E K D E K P R D K S Y Q D A V L E D I F K K N D H D G D G F I S P K E Y N V Y Q H D E L
Biological Activity	The enzyme activity of this recombinant protein is testing in progress, we cannot offer a guarantee yet.
Appearance	Solution.
Formulation	Supplied as a 0.2 μm filtered solution of 20 mM Tris-HCl, 150 mM NaCl, 1 mM $CaCl_2$, 10% Glycerol, pH 7.5.
Endotoxin Level	<1 EU/μg, determined by LAL method.
Reconsititution	N/A
Storage & Stability	Stored at -80°C for 1 year. It is stable at -20°C for 3 months after opening. It is recommended to freeze aliquots at -80°C for extended storage. Avoid repeated freeze-thaw cycles.
Shipping	Shipping with dry ice.

DESCRIPTION

Background	FKBP7 Protein stands out as a peptidyl-prolyl cis-trans isomerase (PPIase) that plays a pivotal role in expediting the folding of proteins, particularly during the intricate process of protein synthesis. Harnessing its enzymatic activity, FKBP7 contributes to the dynamic and timely conformational changes essential for the correct folding and maturation of proteins. As a member of the PPIase family, FKBP7 is adept at catalyzing the cis-trans isomerization of proline imidic peptide bonds, influencing the structural dynamics of nascent or misfolded polypeptides. This functional attribute underscores the protein's significance in maintaining cellular protein homeostasis and underscores its potential impact on cellular

physiology. Further investigations are warranted to unravel the specific molecular mechanisms through which FKBP7 actively participates in the intricate choreography of protein folding during synthesis.

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