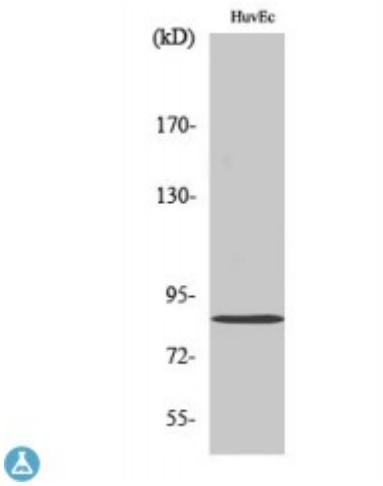
Anti-Mfn2 antibody



Description	Mfn2 is a protein encoded by the MFN2 gene which is approximately 86,4 kDa. Mfn2 is localised to the mitochondrion outer membrane. It is involved in pink/parkin mediated mitophagy, toll-like receptor signalling pathways and glucose / energy metabolism. It is a mitochondrial membrane protein that participates in mitochondrial fusion and contributes to the maintenance and operation of the mitochondrial network. Mfn2 is ubiquitously expressed at low levels. Mutations in the MFN2 gene may result in Charcot-Marie-Tooth disease. STJ94105 was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen. This polyclonal antibody detects endogenous levels of Mfn2 protein.

Model	STJ94105
Host	Rabbit
Reactivity	Human, Mouse, Rat
Applications	ELISA, IHC, WB
Immunogen	Synthesized peptide derived from human Mfn2.
Immunogen Region	Internal
Gene ID	9927
Gene Symbol	MFN2
Dilution range	WB 1:500-1:2000IHC 1:100-1:300ELISA 1:40000
Specificity	Mfn2 Polyclonal Antibody detects endogenous levels of Mfn2 protein.
Tissue Specificity	Ubiquitous; expressed at low level. Highly expressed in heart and kidney.

Purification	The antibody was affinity-purified from rabbit antiserum by affinity-chromatography using epitope-specific immunogen.
Note	For Research Use Only (RUO).
Protein Name	Mitofusin-2 Transmembrane GTPase MFN2
Molecular Weight	86 kDa
Clonality	Polyclonal
Conjugation	Unconjugated
Isotype	IgG
Formulation	Liquid in PBS containing 50% glycerol, 0.5% BSA and 0.02% sodium azide.
Concentration	1 mg/ml
Storage Instruction	Store at -20°C, and avoid repeat freeze-thaw cycles.
Database Links	HGNC:16877OMIM:601152
Alternative Names	Mitofusin-2 Transmembrane GTPase MFN2
Function	Mitochondrial outer membrane GTPase that mediates mitochondrial clustering and fusion . Mitochondria are highly dynamic organelles, and their morphology is determined by the equilibrium between mitochondrial fusion and fission events . Overexpression induces the formation of mitochondrial networks . Membrane clustering requires GTPase activity and may involve a major rearrangement of the coiled coil domains (Probable). Plays a central role in mitochondrial metabolism and may be associated with obesity and/or apoptosis processes . Plays an important role in the regulation of vascular smooth muscle cell proliferation . Involved in the clearance of damaged mitochondria via selective autophagy (mitophagy) . Is required for PRKN recruitment to dysfunctional mitochondria . Involved in the control of unfolded protein response (UPR) upon ER stress including activation of apoptosis and autophagy during ER stress . Acts as an upstream regulator of EIF2AK3 and suppresses EIF2AK3 activation under basal conditions .
Sequence and Domain Family	A helix bundle is formed by helices from the N-terminal and the C-terminal part of the protein. The GTPase domain cannot be expressed by itself, without the helix bundle. Rearrangement of the helix bundle and/or of the coiled coil domains may bring membranes from adjacent mitochondria into close contact, and thereby play a role in mitochondrial fusion.
Cellular Localization	Mitochondrion outer membrane. Colocalizes with BAX during apoptosis.
Post-translational Modifications	Phosphorylated by PINK1. Ubiquitinated by non-degradative ubiquitin by PRKN, promoting mitochondrial fusion; deubiquitination by USP30 inhibits mitochondrial fusion.