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Cleaved-Caspase-8 (Asp384) Rabbit Polyclonal Antibody

Catalog #: EAB10082

Host/Isotype	Clonality	Applications	MW (kDa)	Reactivity
Rabbit IgG	Polyclonal	WB, IHC-P, IF/ICC, ELISA	55	Human, Mouse, Rat

Applications Dilutions

The application notes include recommended starting dilutions; optimal dilutions/concentrations should be determined by the end user.

WB(Western Blotting)	1:500-2000
IHC-P(Immunohistochemistry-Paraffin)	1:50-300
IF/ICC(Immunofluorescence/Immunocytochemistry)	1:50-300
ELISA(Enzyme-linked Immunosorbent Assay)	1:5000-20000

Product Information

Conjugate	Unconjugate
Specificity	Cleaved-Caspase-8 (Asp384) Rabbit Polyclonal Antibody detects endogenous levels of Caspase-8 protein resulting from cleavage adjacent to Asp384.
Purification	Affinity purification
Concentration	1mg/ml
Format	Liquid
Formulation	In PBS, pH 7.4, Containing 0.02% sodium azide, 0.5% BSA and 50% Glycerol
Shipping	Gel Pack
Storage	Store at -20°C least 1 year from the date of shipment. Avoid repeated freeze/thaw cycles. Aliquots may be stored at +4°C for 1-2 weeks
UniProt ID	Q14790
Entrez-Gene Id	841

Product Descriotion

This gene encodes a member of the cysteine-aspartic acid protease (caspase) family. Sequential activation of caspases plays a central role in the execution-phase of cell apoptosis. Caspases exist as inactive proenzymes composed of a prodomain, a large protease subunit, and a small protease subunit. Activation of caspases requires proteolytic processing at conserved internal aspartic residues to generate a heterodimeric enzyme consisting of the large and small subunits. This protein is involved in the programmed cell death induced by Fas and various apoptotic stimuli. The N-terminal FADD-like death effector domain of this protein suggests that it may interact with Fas-interacting protein FADD. This protein was detected in the insoluble fraction of the affected brain region from Huntington disease patients but not in those from normal controls, which implicated the role in neurodegenerative diseases. Many alternatively spliced transcript variants encoding different isoforms have been described, although not all variants have had their full-length sequences determined.