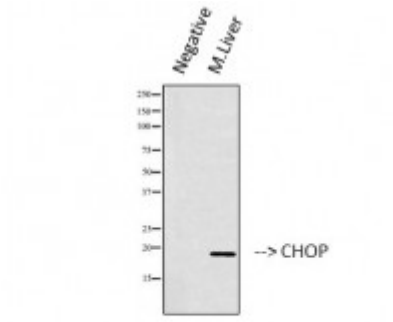
# Anti-CHOP antibody




Western Blot (WB) analysis of Mouse Liver cells using CHOP Mouse Monoclonal Antibody(2B1). (STJ97774)

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| **Description** | CHOP is a protein encoded by the DDIT3 gene which is approximately 19,1 kDa. CHOP is localised to the cytoplasm and nucleus. It is involved in the unfolded protein response, the MAPK signalling pathway and apoptosis modulation and signalling. This protein falls under the CCAAT/enhancer-binding protein family of transcription factors. It functions as a dominant-negative inhibitor by forming heterodimers with other C/EBP members, such as C/EBP and LAP and preventing their DNA binding activity. It is activated by endoplasmic reticulum stress and promotes apoptosis. CHOP is expressed in the muscle, nervous system, eye, liver and heart. Mutations in the DDIT3 gene may result in myxoid liposarcoma. STJ97774 was developed from clone 2B1 and was affinity-purified from mouse ascites by affinity-chromatography using specific immunogen. This primary antibody detects endogenous levels of DDIT3 |

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| **Model** | STJ97774 |
| **Host** | Mouse |
| **Reactivity** | Human, Mouse, Rat |
| **Applications** | IHC, WB |
| **Immunogen** | synthetic peptide derived from CHOP |
| **Immunogen Region** | 10-90 aa |
| **Gene ID** | 1649 |
| **Gene Symbol** | DDIT3 |
| **Dilution range** | WB 1:1000-2000IHC 1:100-200 |
| **Specificity** | CHOP Mouse Monoclonal Antibody (2B1) detects endogenous levels of |

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| | DDIT3 |
| **Purification** | The antibody was affinity-purified from mouse ascites by affinity-chromatography using specific immunogen. |
| **Clone ID** | 2B1 |
| **Note** | For Research Use Only (RUO). |
| **Protein Name** | DNA damage-inducible transcript 3 protein DDIT-3 C/EBP zeta C/EBP-homologous protein CHOP C/EBP-homologous protein 10 CHOP-10 CCAAT/enhancer-binding protein homologous protein Growth arrest and DNA damage-in |
| **Clonality** | Monoclonal |
| **Conjugation** | Unconjugated |
| **Isotype** | IgG1 |
| **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:2726OMIM:126337 |
| **Alternative Names** | DNA damage-inducible transcript 3 protein DDIT-3 C/EBP zeta C/EBP-homologous protein CHOP C/EBP-homologous protein 10 CHOP-10 CCAAT/enhancer-binding protein homologous protein Growth arrest and DNA damage-in |
| **Function** | Multifunctional transcription factor in ER stress response. Plays an essential role in the response to a wide variety of cell stresses and induces cell cycle arrest and apoptosis in response to ER stress. Plays a dual role both as an inhibitor of CCAAT/enhancer-binding protein (C/EBP) function and as an activator of other genes. Acts as a dominant-negative regulator of C/EBP-induced transcription: dimerizes with members of the C/EBP family, impairs their association with C/EBP binding sites in the promoter regions, and inhibits the expression of C/EBP regulated genes. Positively regulates the transcription of TRIB3, IL6, IL8, IL23, TNFRSF10B/DR5, PPP1R15A/GADD34, BBC3/PUMA, BCL2L11/BIM and ERO1L. Negatively regulates; expression of BCL2 and MYOD1, ATF4-dependent transcriptional activation of asparagine synthetase (ASNS), CEBPA-dependent transcriptional activation of hepcidin (HAMP) and CEBPB-mediated expression of peroxisome proliferator-activated receptor gamma (PPARG). Inhibits the canonical Wnt signaling pathway by binding to TCF7L2/TCF4, impairing its DNA-binding properties and repressing its transcriptional activity. Plays a regulatory role in the inflammatory response through the induction of caspase-11 (CASP4/CASP11) which induces the activation of caspase-1 (CASP1) and both these caspases increase the activation of pro-IL1B to mature IL1B which is involved in the inflammatory response. |
| **Sequence and Domain Family** | The N-terminal region is necessary for its proteasomal degradation, transcriptional activity and interaction with EP300/P300. |
| **Cellular Localization** | Cytoplasm. Nucleus. Present in the cytoplasm under non-stressed conditions and ER stress leads to its nuclear accumulation. |

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| **Post-translational Modifications** | Ubiquitinated, leading to its degradation by the proteasome. Phosphorylation at serine residues by MAPK14 enhances its transcriptional activation activity while phosphorylation at serine residues by CK2 inhibits its transcriptional activation activity. |