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# CtIP Rabbit pAb

Catalog # AP100241

## Product Information

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|---|---|
| **Application** | WB, IHC-P, IHC-F, IF, E |
| **Primary Accession** | Q99708 |
| **Other Accession** | Q99708 |
| **Predicted** | Rat, Pig, Human, Mouse, Chicken |
| **Host** | Rabbit |
| **Clonality** | Polyclonal |
| **Calculated MW** | 101942 |
| **Physical State** | Liquid |
| **Immunogen** | KLH conjugated synthetic peptide derived from human CtIP/RBBP8 |
| **Epitope Specificity** | 621-720/897 |
| **Isotype** | IgG |
| **Purity** | affinity purified by Protein A |
| **Buffer** | 0.01M TBS (pH7.4) with 1% BSA, 0.02% Proclin300 and 50% Glycerol. |
| **SIMILARITY** | Belongs to the COM1/SAE2/CtIP family. |
| **SUBUNIT** | Homodimer; dimerizes via the coiled coil domain. Interacts (via the PXDLS motif) with CTBP1; the interaction is disrupted via binding of the adenovirus E1A to CTBP1. Component of the BRCA1-RBBBP8 complex. Interacts (the Ser-327 phosphorylated form) with BRCA1 (via the C-terminal BRCA1 domains): the interaction occurs in the G2 phase, ubiquitinates RBBP8 and involves RBBP8 in BRCA1-dependent G2/M checkpoint control on DNA damage. Interacts with RB1. Interacts with the MRN complex. Interacts directly with MRE11A; the interaction is required for efficient homologous recombination (HR) and regulation of the MRN complex. Interacts directly with RAD50. Interacts directly with NBN. Interacts with SIRT6; the interaction deacetylates RBBP8 upon DNA damage. Interacts with LM04 (via the LIM zinc-binding 1 domain). |
| **Post-translational modifications** | Acetylated. Deacetylation by SIRT6 upon DNA damage promotes DNA end resection. Phosphorylated upon DNA damage, probably by ATM or ATR. Hyperphosphorylation upon ionizing radiation results in dissociation from BRCA1. Phosphorylation at Thr-847 by CDK1 is essential for the recruitment to DNA and the DNA repair function. Phosphorylated on Ser-327 as cells enter G2 phase. This phosphorylation is required for binding BRCA1 and for the G2/M DNA damage transition checkpoint control. Ubiquitinated. Ubiquitination at multiple sites by BRCA1 (via its N-terminal RING domain) does not lead to its proteosomal degradation but instead the ubiquitinated RBBP8 binds to chromatin following DNA damage and may play a role in G2/M checkpoint control. |
| **DISEASE** | Defects in RBBP8 are a cause of Seckel syndrome type 2 (SCKL2) [MIM:606744]. SCKL2 is a rare autosomal recessive disorder characterized by proportionate dwarfism of prenatal onset associated with low birth weight, growth retardation, severe microcephaly with a bird-headed like appearance, and mental retardation. Defects in RBBP8 are a cause of Jawad disease (JWDS) [MIM:251255]. JWDS is a syndrome characterized by congenital microcephaly, moderately severe mental retardation, and symmetrical digital anomalies. Digital malformations of variable degree inclued hallux valgus, syndactyly of |

toes 4 and 5, short fifth fingers, single flexion crease of fifth fingers, polydactyly and synpolydactyly. Note=Genetic variability in RBBP8 is noted as a factor in BRCA1-associated breast cancer risk. Exhibits sensitivity to tamoxifen in certain breast cancer cell lines.

**Important Note** This product as supplied is intended for research use only, not for use in human, therapeutic or diagnostic applications.

**Background Descriptions** The protein encoded by this gene is a ubiquitously expressed nuclear protein. It is found among several proteins that bind directly to retinoblastoma protein, which regulates cell proliferation. This protein complexes with transcriptional co-repressor CTBP. It is also associated with BRCA1 and is thought to modulate the functions of BRCA1 in transcriptional regulation, DNA repair, and/or cell cycle checkpoint control. It is suggested that this gene may itself be a tumor suppressor acting in the same pathway as BRCA1. Three transcript variants encoding two different isoforms have been found for this gene. More transcript variants exist, but their full-length natures have not been determined.

## Additional Information

**Gene ID** 5932

**Other Names** COM1; CTIP; JAWAD; JWDS; RIM; SAE2; SCKL2; 9930104E21Rik; RBBP-8; RGD1308872; CTIP_HUMAN; RBBP8; CtBP-interacting protein (CtIP); Retinoblastoma-binding protein 8 (RBBP-8); Retinoblastoma-interacting protein and myosin-like (RIM); Sporulation in the absence of SPO11 protein 2 homolog (SAE2); 3.1.-.-; CTIP_MOUSE; CTIP_RAT; RB binding protein 8, endonuclease; retinoblastoma-binding protein 8; Seckel syndrome 2; retinoblastoma binding protein 8; CTBP-interacting protein

**Dilution** WB=1:500-2000,IHC-P=1:100-500,IHC-F=1:100-500,IF=1:100-500,ELISA=1:5000-10000

**Storage** Store at -20 °C for one year. Avoid repeated freeze/thaw cycles. When reconstituted in sterile pH 7.4 0.01M PBS or diluent of antibody the antibody is stable for at least two weeks at 2-4 °C.

## Protein Information

**Name** RBBP8 ( HGNC:9891)

**Function** Endonuclease that cooperates with the MRE11-RAD50-NBN (MRN) complex in DNA-end resection, the first step of double-strand break (DSB) repair through the homologous recombination (HR) pathway (PubMed:17965729, PubMed:19202191, PubMed:19759395, PubMed:20064462, PubMed:23273981, PubMed:26721387, PubMed:27814491, PubMed:27889449, PubMed:30787182, PubMed:31802118). HR is restricted to S and G2 phases of the cell cycle and preferentially repairs DSBs resulting from replication fork collapse (PubMed:17965729, PubMed:19202191, PubMed:23273981, PubMed:27814491, PubMed:27889449, PubMed:30787182). Key determinant of DSB repair pathway choice, as it commits cells to HR by preventing classical non-homologous end-joining (NHEJ) (PubMed:19202191). Specifically promotes the endonuclease activity of the MRN complex to clear DNA ends containing protein adducts: recruited to DSBs by NBN following phosphorylation by CDK1, and promotes the endonuclease activity of MRE11 to clear protein-DNA adducts and generate clean double-strand break ends (PubMed:27814491, PubMed:27889449,

PubMed:30787182, PubMed:33836577). Functions downstream of the MRN complex and ATM, promotes ATR activation and its recruitment to DSBs in the S/G2 phase facilitating the generation of ssDNA (PubMed:16581787, PubMed:17965729, PubMed:19759395, PubMed:20064462). Component of the BRCA1-RBBP8 complex that regulates CHEK1 activation and controls cell cycle G2/M checkpoints on DNA damage (PubMed:15485915, PubMed:16818604). During immunoglobulin heavy chain class-switch recombination, promotes microhomology-mediated alternative end joining (A-NHEJ) and plays an essential role in chromosomal translocations (By similarity). Binds preferentially to DNA Y-junctions and to DNA substrates with blocked ends and promotes intermolecular DNA bridging (PubMed:30601117).

**Cellular Location**

Nucleus. Chromosome Note=Associates with sites of DNA damage in S/G2 phase (PubMed:10764811, PubMed:25349192). Recruited to DSBs by the MRE11- RAD50-NBN (MRN) complex following phosphorylation by CDK1, which promotes interaction with NBN (PubMed:27814491, PubMed:27889449, PubMed:33836577). Ubiquitinated RBBP8 binds to chromatin following DNA damage (PubMed:16818604).

**Tissue Location**

Expressed in ER-positive breast cancer lines, but tends to be down-regulated ER-negative cells (at protein level)

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