10320 Camino Santa Fe, Suite G
San Diego, CA 92121
Tel: 858.875.1900 Fax: 858.875.1999

KD-Validated Anti-DNA Polymerase gamma Rabbit Monoclonal Antibody

Rabbit monoclonal antibody
Catalog # AGI1650

Product Information

Application	WB, FC, ICC
Primary Accession	P54098
Reactivity	Rat, Human, Mouse
Clonality	Monoclonal
Isotype	Rabbit IgG
Clone Names	24GB1085
Calculated MW	139562
Gene Name	POLG
Aliases	DNA Polymerase Gamma, Catalytic Subunit; POLG1; POLGA; Mitochondrial DNA Polymerase Catalytic Subunit; Polymerase (DNA) Gamma, Catalytic Subunit; Polymerase (DNA Directed), Gamma; DNA Polymerase Subunit Gamma-1; PolG-Alpha; EC 2.7.7.7; MDP1; Mitochondrial Polymerase Gamma Catalytic Subunit; MTDPS4A; MTDPS4B; MIRAS; SANDO; SCAE; PEO
Immunogen	A synthesized peptide derived from human DNA Polymerase gamma

Additional Information

Gene ID	5428
Other Names	DNA polymerase subunit gamma-1, 2.7.7.7, 3'-5' exodeoxyribonuclease, 3.1.11.-, 5'-deoxyribose-phosphate lyase, 4.2.99.-, Mitochondrial DNA polymerase catalytic subunit, PolG-alpha, POLG {ECO:0000303|PubMed:10827171, ECO:0000312|HGNC:HGNC:9179}

Protein Information

Name	POLG {ECO:0000303|PubMed:10827171, ECO:0000312|HGNC:HGNC:9179}
Function	Catalytic subunit of DNA polymerase gamma solely responsible for replication of mitochondrial DNA (mtDNA). Replicates both heavy and light strands of the circular mtDNA genome using a single-stranded DNA template, RNA primers and the four deoxyribonucleoside triphosphates as substrates (PubMed:11477093, PubMed:11897778, PubMed:15917273, PubMed:19837034, PubMed:9558343). Has 5' -> 3' polymerase activity. Functionally interacts with TWNK and SSBP1 at the replication fork to form a highly processive replisome, where TWNK unwinds the double- stranded DNA template prior to replication and SSBP1 covers the parental heavy strand to enable continuous replication of the entire mitochondrial genome. A single nucleotide incorporation cycle includes binding of the incoming nucleotide at the insertion site, a phosphodiester bond formation reaction that extends the

3'-end of the primer DNA, and translocation of the primer terminus to the post- insertion site. After completing replication of a mtDNA strand, mediates 3' -> 5' exonucleolytic degradation at the nick to enable proper ligation (PubMed:11477093, PubMed:11897778, PubMed:15167897, PubMed:15917273, PubMed:19837034, PubMed:26095671, PubMed:9558343). Highly accurate due to high nucleotide selectivity and 3' -> 5' exonucleolytic proofreading. Proficiently corrects base substitutions, single-base additions and deletions in non-repetitive sequences and short repeats, but displays lower proofreading activity when replicating longer homopolymeric stretches. Exerts exonuclease activity toward single-stranded DNA and double-stranded DNA containing 3'- terminal mispairs. When a misincorporation occurs, transitions from replication to a pro-nucleolytic editing mode and removes the missincorporated nucleoside in the exonuclease active site. Proceeds via an SN2 nucleolytic mechanism in which Asp-198 catalyzes phosphodiester bond hydrolysis and Glu-200 stabilizes the leaving group. As a result the primer strand becomes one nucleotide shorter and is positioned in the post-insertion site, ready to resume DNA synthesis (PubMed:10827171, PubMed:11477094, PubMed:11504725, PubMed:37202477). Exerts 5'-deoxyribose phosphate (dRP) lyase activity and mediates repair-associated mtDNA synthesis (gap filling) in base-excision repair pathway. Catalyzes the release of the 5'-terminal 2-deoxyribose-5-phosphate sugar moiety from incised apurinic/apyrimidinic (AP) sites to produce a substrate for DNA ligase. The dRP lyase reaction does not require divalent metal ions and likely proceeds via a Schiff base intermediate in a beta-elimination reaction mechanism (PubMed:9770471).

Cellular Location Mitochondrion. Mitochondrion matrix, mitochondrion nucleoid

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