

## Product datasheet for SC210783

### DNA Polymerase theta (POLQ) (NM\_199420) Human 3' UTR Clone

#### Product data:

Product Type:	3' UTR Clones
Product Name:	DNA Polymerase theta (POLQ) (NM_199420) Human 3' UTR Clone
Symbol:	DNA Polymerase theta
Synonyms:	PRO0327
Mammalian Cell Selection:	Neomycin
Vector:	pMirTarget (PS100062)
ACCN:	NM_199420
Insert Size:	903 bp
Insert Sequence:	<p>&gt;SC210783 3'UTR clone of NM_199420</p> <p>The sequence shown below is from the reference sequence of NM_199420. The complete sequence of this clone may contain minor differences, such as SNPs.</p> <p>Blue=Stop Codon Red=Cloning site</p>

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GGCAAGTTGGACGCCGCAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGAAAGATCGCCGTG
TAACAATTGGCAGAGCTCAGAATTCAAACGATCGCC
TGGGGAGAGCTAAAGGACTTTGATGTGTAACTGTGCTGTTGATGAAGTCCTCCAGGGAAGCCTGTGCA
GATGCAGTCACCTGGAAAGAACAGAGATTACCCTTTACCTACCTCAGCAAAACAACTTTCAAGTCTT
GATAGACTTAGCCTAGTAATTTTATAGTGAGAGTTTCAAATATATATCAGTGTCTATAGCATCAAAAA
CTTCTGGGGCGTGGGGGAAGTAGAATACCAAGTATAATAGTTACATTCACCTTTCAAAGAGCATCTATG
AATTTGCCTTTTGTAACTTACTGTGGCTTTAAACATATTGAGAACAGATGCTTGAAATATGCACTTAGC
ACTTTGGTTCCACATCTGTCTGGGTAAACCATGAAGAAATGAAGCTGCTGCCTCAATCGACCCAGACA
GCAGCCATAGGCAGATAAAGATTTGGTTTACCCTGGTGGTAGGCATCGTGTGTGACTTTTTTTCC
TCTAATATCAATTTTACAGTACGAAATAGTATTTTAAATAGTATTGGCTAATAAATTATGAATTCTA
TAAAGTAGTAAGACTTGGTATGGTTGGAGTGTAGGAATGAATATTCATGAATGTTTCTTATTGCTTTT
CCTTCCCTAATTCATACAATGAATGTATTTGGAATACTTACATATTATAAAATAAACTATACCTCTTCA
AGAGGTATCCTGTTCTGTAAGATCAGATGTTTTATTGCAGGTCAATATAATACTGCCAGAGACAGAAA
ATACCCCTTATCAGTCCCTTAGTGCCTCTTTCTGTTTGTGGCATGGTGAGAAAACCCATGCTGAAAAG
ATTGTACTTTGTATCCCAATCAGAGGGATGGAGCTAATCTTTTGTCTGTTGAAATAAAATGAATTTAT
GAGAAA
ACGCGTAAGCGGCCGCGGCATCTAGATTGGAAGAAATGACCGACCAAGCGACGCCAACCTGCCATCA
CGAGATTTGATTCCACCGCCGCTTCTATGAAAGG
  
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Restriction Sites: SgfI-MluI


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<b>OTI Disclaimer:</b>	Our molecular clone sequence data has been matched to the sequence identifier above as a point of reference. Note that the complete sequence of this clone is largely the same as the reference sequence but may contain minor differences , e.g., single nucleotide polymorphisms (SNPs).
<b>Components:</b>	The cDNA clone is shipped in a 2-D bar-coded Matrix tube as 10 ug dried plasmid DNA. The package also includes 100 pmols of both the corresponding 5' and 3' vector primers in separate vials.
<b>RefSeq:</b>	<a href="#">NM_199420.4</a>
<b>Summary:</b>	DNA polymerase that promotes microhomology-mediated end-joining (MMEJ), an alternative non-homologous end-joining (NHEJ) machinery triggered in response to double-strand breaks in DNA (PubMed:25642963, PubMed:25643323). MMEJ is an error-prone repair pathway that produces deletions of sequences from the strand being repaired and promotes genomic rearrangements, such as telomere fusions, some of them leading to cellular transformation (PubMed:25642963, PubMed:25643323). POLQ acts as an inhibitor of homology-recombination repair (HR) pathway by limiting RAD51 accumulation at resected ends (PubMed:25642963). POLQ-mediated MMEJ may be required to promote the survival of cells with a compromised HR repair pathway, thereby preventing genomic havoc by resolving unrepaired lesions (By similarity). The polymerase acts by binding directly the 2 ends of resected double-strand breaks, allowing microhomologous sequences in the overhangs to form base pairs. It then extends each strand from the base-paired region using the opposing overhang as a template. Requires partially resected DNA containing 2 to 6 base pairs of microhomology to perform MMEJ (PubMed:25643323). The polymerase activity is highly promiscuous: unlike most polymerases, promotes extension of ssDNA and partial ssDNA (pssDNA) substrates (PubMed:18503084, PubMed:21050863, PubMed:22135286). Also exhibits low-fidelity DNA synthesis, translesion synthesis and lyase activity, and it is implicated in interstrand-cross-link repair, base excision repair and DNA end-joining (PubMed:14576298, PubMed:18503084, PubMed:19188258, PubMed:24648516). Involved in somatic hypermutation of immunoglobulin genes, a process that requires the activity of DNA polymerases to ultimately introduce mutations at both A/T and C/G base pairs (By similarity). [UniProtKB/Swiss-Prot Function]
<b>Locus ID:</b>	10721
<b>MW:</b>	34.9