

Product datasheet for **SC118289**

RPA70 (RPA1) (NM_002945) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	RPA70 (RPA1) (NM_002945) Human Untagged Clone
Tag:	Tag Free
Symbol:	RPA70
Synonyms:	HSSB; MST075; REPA1; RF-A; RP-A; RPA70
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL5</u>
E. coli Selection:	Ampicillin (100 ug/mL)



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Fully Sequenced ORF: >OriGene ORF within SC118289 sequence for NM_002945 edited (data generated by NextGen Sequencing)

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ATGGTCGGCCAGCTGAGCGAGGGGGCCATTGCGGCCATCATGCAGAAGGGGGATACAAAC
ATAAAGCCCATCTCCAAGTCATCAACATCCGTCCTTACTACGGGGAATAGTCCGCCG
CGTTATCGACTGCTCATGAGTGATGGATTGAACACTCTATCCTCTTTCATGTTGGCGACA
CAGTTGAACCCCTCTCGTGGAGGAAGAACAATTGCCAGCAACTGTGTATGCCAGATTCAC
AGATTTATTGTGAACACTCTGAAAGACGGAAGGAGAGTAGTTATCTTGTGGAATTAGAA
GTTTTGAAGTCAGCTGAAGCAGTTGGAGTGAAGATTGGCAATCCAGTGCCCTATAATGAA
GGACTCGGGCAGCCGCAAGTAGCTCCTCCAGCGCCAGCAGCCAGCCAGCAGCAAGCAGC
AGGCCCCAGCCGAGAATGGAAGCTCGGAATGGGTTCTACTGTTTCTAAGGCTTATGGT
GCTTCAAAGACATTTGAAAAGCTGCAGGTCCCAGCCTGTACACACTTCTGGGGGAACA
CAGTCCAAAGTGGTGCCATTGCCAGCCTCACTCCTTACCAGTCCAAGTGGACCATTTGT
GCTCGTGTACCAACAAAAGTCAGATCCGTACCTGGAGCAACTCCCAGGGGAAGGGAAG
CTTTTCTCCCTAGAACTGGTTGACGAAAGTGGTGAATCCGAGCTACAGCTTTCATGAG
CAAGTGGACAAGTCTTTCTCTTATTGAAGTGAACAAGGTGTATTATTTCTCGAAAGGC
ACCTGAAGATTGCTAACAAGCAGTTCACAGCTGTAAAAATGACTACGAGATGACCTTC
AATAACGAGACTTCCGTCATGCCCTGTGAGGACGACCATCATTTACCTACGGTTCAGTTT
GATTTACGGGGATTGATGACCTCGAGAACAAGTCGAAAGACTCACTTGTAGACATCATC
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TGGGGGAAGATGCTGATAAATTTGATGGTCTAGACAGCCCGTGTGGCTATCAAAGGA
GCCCCGAGTCTCTGATTTCCGTGGACGGAGCCTCTCCGTGCTGTCTCAAGCACTATCATT
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GCCTTAGATGGTGTTCATCTCTGATCTAAAGAGCGGCGGAGTCGGAGGGAGTAACACC
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TACTTTAGTTCTGTGGCCACAGTGGTGTATCTTCGCAAAGAGAACTGCATGTACCAAGCC
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GAGAAGTGCACACCGAATTTCCCAATTTCAAGTACCGCATGATCCTGTGAGTAAATATT
GCAGATTTTCAAGAGAATCAGTGGGTGACTTGTTCAGGAGTCTGCTGAAGCTATCCTT
GGACAAAATGCTGCTTATCTTGGGAATTAAGAGACAAGAATGAACAGGCATTTGAAGAA
GTTTTCCAGAATGCCAATTTCCGATCTTTCATATTCAGAGTCAGGGTCAAAGTGGAGACC
TACAACGACGAGTCTCGAATTAAGGCCACTGTGATGGACGTGAAGCCCGTGGACTACAGA
GAGTATGGCCGAAGGCTGGTCATGAGCATCAGGAGAAGTGCATTGATGTGA
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Clone variation with respect to NM_002945.3

12 a=>g

5' Read Nucleotide Sequence:	<p>>OriGene 5' read for NM_002945 unedited</p> <p>TATACGACTCACTATAGGCGGCCGCAAATTCGCACGAGGGGACCCGGTGGGAAGCTG GAGCTGTTGCGGGTCCGCGGGGAAGTCTTGGCGGTGGAGCCATGGTCGGCCAGCTGAGC GAGGGGGCCATTGCGGCCATCATGCAGAAGGGGATACAAACATAAAGCCCATCTCCAA GTCATCAACATCCGTCCTTACTACGGGAATAGTCCGCCGCTTATCGACTGCTCATG AGTGATGGATTGAACACTCTATCCTCTTTCATGTTGGCGACACAGTTGAACCTCTCGTG GAGGAAGAACAATTGTCCAGCACTGTGTATGCCAGATTACAGATTTATTGTGAACACT CTGAAAGACGGAAGGAGAGTAGTTATCTTGATGGATTTAGAAGTNTGAAGTCAGCTGAA GCAAGTTGGAGTGNAAGATTGGCAATCCAGTGCCCTATAATGAAGGACTCGGGCAGCCGA AGTAGCTCCTCCAGCGCCAGCAGCCAGCCAGCAAGCAGCAGGCCCCAGCCGAGAA TGGAAAGCTGGNAATGGGTTCTACTGTTTCTAGGGCTTATGGTGCTCAAAGACATTTG GAAAGGCTGCAGGTCCAGCCTGTACACACTTCTGGNGAACACAGTCNAAAGTGGTGC CCATTGCCAGCCTCACTCCTTACCAGTCAAAGTGACCCATTTGTGGCTCGTGTACCAA CANAAGTCAAAATCCGTACCTGGAGCACTNCCGAAGGGGAAAAGGAAAAGCTTTTCTCCC TAGAACCTGNTGACAAAAAGTGGTGGAAATCCGAGCTACAGCTTTTCAATGAGCAGTGGG ACCAAGTCTTTTTCTTTTTTGGAGTGAACCAGGGGTGATTATTTTTTCGAAAGGCACC CTTGAGAATGCAAAACAAGCGTTCACCAGCTGTTAAAATGACTACCAAATGACCTCATACG AACTTCGTCTGCCTTGGAAAGACACATATTACTCCGCGTTAATTGATCTCCGGGGGAAA GA</p>
3' Read Nucleotide Sequence:	<p>>OriGene 3' read for NM_002945 unedited</p> <p>GGACGCGCCGCAATCTAGAGTCGAGTTTTTTTTTTTTTTTTTTTAAACAACAAAGATATA CTGTTTATTAACAAAGCAAGGAAAACAAAAGGCTTCAAATCCTTTCCATGTAAACAT AGCTTTAGTCAAAAAAACAATAACATGAATGCAGGAATGTGTACAGGTAAAAAAGTA CGCACTACCAAGCGAAGCGCAGCATTAAATTGAAGTAAAAGTAAAGAAACGCTTTGTAG CCGCTCGGATTTCTTAGGGGACAGCAAGTCAATGCTTATCAGCGGTCTCAAAGAGAC AATTTTGATTAATATCAGACCACTCTGACTCAGTCTATTAACCCCTGAAGGAAGGATACT CTTCAGATATAGAAGATATGCCTTTGATTAATCATTCTACCCTATTGCCATTCGAAGCAT TACCAACTATGTAGCACCTCTAGAAAGAGAGAGCCTTGAATTCAGGAAGACACACTTA CTAAAATCCCCAGGTGCTCATGACCGCTTCTCAGCTCGCCCGCTGAGAAGAACCCTAAGT TGTGAGCGGGATGGNNGGGGGTGTGNACACCACTGGAGAAGCAAAAACCTAGTTACAT AATTTACTTCATGGTCTGCAGTTAGGGTCAAGTACTTACGACATAATTCTGCTTGATGA TAATGAAATTGACAGAAGNCCTGAGGCAGAGGGAGTACTGGTCTTGGCGTAGCCACTGG CTGACTCCGTAGGCCTGACACAGTCTACACCACAACACCTGAGCGTATTTTCTTTGCTA CCGATGGGGTCTGANAGCGCACGAGGGNAGGAATTGCTTANTCCACATCAAGAGCCTCT GCACTGGTACTACATGGGATCGTACACGGAGGGGGAAGAAAATGATTCCTTCTGGCTA TTGCAAAATTCGCCCGATTGGCCGTGGTCTTACATAAAGCAATTTTA</p>
Restriction Sites:	NotI-NotI
ACCN:	NM_002945
Insert Size:	3000 bp
OTI Disclaimer:	Our molecular clone sequence data has been matched to the reference identifier above as a point of reference. Note that the complete sequence of our molecular clones may differ from the sequence published for this corresponding reference, e.g., by representing an alternative RNA splicing form or single nucleotide polymorphism (SNP).
Components:	The ORF clone is ion-exchange column purified and shipped in a 2D barcoded Matrix tube containing 10ug of transfection-ready, dried plasmid DNA (reconstitute with 100 ul of water).

Reconstitution Method:	<ol style="list-style-type: none">1. Centrifuge at 5,000xg for 5min.2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.3. Close the tube and incubate for 10 minutes at room temperature.4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.5. Store the suspended plasmid at -20°C. The DNA is stable for at least one year from date of shipping when stored at -20°C.
RefSeq:	NM_002945.2 , NP_002936.1
RefSeq Size:	2824 bp
RefSeq ORF:	1851 bp
Locus ID:	6117
UniProt ID:	P27694
Cytogenetics:	17p13.3
Domains:	tRNA_anti, Rep-A_N
Protein Families:	Druggable Genome, Stem cell - Pluripotency
Protein Pathways:	DNA replication, Homologous recombination, Mismatch repair, Nucleotide excision repair
Gene Summary:	<p>This gene encodes the largest subunit of the heterotrimeric Replication Protein A (RPA) complex, which binds to single-stranded DNA (ssDNA), forming a nucleoprotein complex that plays an important role in DNA metabolism, being involved in DNA replication, repair, recombination, telomere maintenance, and co-ordinating the cellular response to DNA damage through activation of the ataxia telangiectasia and Rad3-related protein (ATR) kinase. The nucleoprotein complex protects the single-stranded DNA from nucleases, prevents formation of secondary structures that would interfere with repair, and co-ordinates the recruitment and departure of different genome maintenance factors. This subunit contains four oligonucleotide/oligosaccharide-binding (OB) domains, though the majority of ssDNA binding occurs in two of these domains. The heterotrimeric complex has two different modes of ssDNA binding, a low-affinity and high-affinity mode, determined by which ssDNA binding domains are utilized. The different binding modes differ in the length of DNA bound and in the proteins with which it interacts, thereby playing a role in regulating different genomic maintenance pathways. [provided by RefSeq, Sep 2017]</p>