

Product datasheet for **SC328923**

UBAP1 (NM_001171201) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	UBAP1 (NM_001171201) Human Untagged Clone
Tag:	Tag Free
Symbol:	UBAP1
Synonyms:	NAG20; SPG80; UAP; UBAP; UBAP-1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)

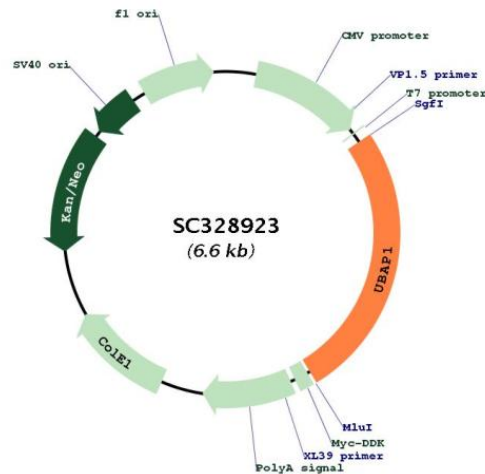


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Fully Sequenced ORF: >SC328923 representing NM_001171201.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGGCCGGGAATTCGTGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGAGTGGGGCGGTGAGGGGAAGGAGGAGGAAGTAGGACTTCAACATGGCGGCTGCGGCACTGGCGGT
GGCTACGGTGACGGCCTGGCCCGGAGCGGGCAGAGTTGGAGGTGGTGGCGTTTCGCTCTCCCTAGGGGCT
GTCGGGAGCTCAGCGGGGACCGAGCCTGGGAGGCCGGCCGGTCCAGCACCTTTCGGCTTCTGAGACGG
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GCCGAGCGGGAAGCAGAGTGCAAAATTCGCGAAGCAGAAGCTAAAGTGAATTCAGAGTGGCCAGAG
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CTGCCAGCTTGAGCACAACAGCATCCTCACACCAACTCGGGTCAGCAGTAGTCCACGAAACAGAAA
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GATAATCTGGAGTTAAAAACTATTGATGAGAAGGAAGAGCTGAGAAATATTCTGGTAGGAACCACTGGA
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GAGGTCCTGGCATCCTTGGAACGGGCAACCCTAGATTTCAAGCCTCTTCAAAAGTGTCCCTCCCCCTATACCT
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AGTGGCACAGAGATGCCAGCCCTGACATCCTCCAGATGCCTCCCTCTCTGTTTTGTCTGTGTGCACA
GAGGAATCATCACCTCCAATACTGGTCCACGGTCACCCCTCCTAATTTCTCAGTGTACAAGTGCCC
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GAGACGGTGGTCAACATGGGCTACTCGTACGAGTGTGTCCTCAGAGCCATGAAGAAGAAAGGAGAGAAT
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AAATTTAAGGAGATGGGCTTTGAGCTGAAAGACATTAAGGAAGTTTGTATTACACAACAATGACCAG
GACAATGCTTTGGAAGACCTCATGGCTCGGGCAGGAGCCAGCTGA
ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
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Restriction Sites: Sgfl-Mlul

Plasmid Map:


ACCN: NM_001171201

Insert Size: 1701 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).

OTI Annotation: This TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.

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:

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_001171201.1](#)

RefSeq Size: 2702 bp

RefSeq ORF: 1701 bp

Locus ID: 51271

UniProt ID: [Q9NZ09](#)

Cytogenetics: 9p13.3

MW: 61.8 kDa

Gene Summary: This gene is a member of the UBA domain family, whose members include proteins having connections to ubiquitin and the ubiquitination pathway. The ubiquitin associated domain is thought to be a non-covalent ubiquitin binding domain consisting of a compact three helix bundle. This particular protein originates from a gene locus in a refined region on chromosome 9 undergoing loss of heterozygosity in nasopharyngeal carcinoma (NPC). Taking into account its cytogenetic location, this UBA domain family member is being studied as a putative target for mutation in nasopharyngeal carcinomas. Multiple alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Jan 2010]

Transcript Variant: This variant (4) lacks an internal coding exon, which results in an in-frame upstream AUG start codon, as compared to variant 1. The resulting isoform (2) is longest and has a different N-terminus, as compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on transcript alignments.