

Product datasheet for **SC324457**

NAT13 (NAA50) (NM_025146) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	NAT13 (NAA50) (NM_025146) Human Untagged Clone
Tag:	Tag Free
Symbol:	NAT13
Synonyms:	hNaa50p; MAK3; NAT5; NAT5P; NAT13; NAT13P; SAN
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-AC (PS100020)
E. coli Selection:	Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene sequence for NM_025146.1
GCGCGGCAGCGGTCTGGCTGGCGGCAGCGGGAGGGAGCCGAGAGACCCGAGTGCAC
GTGTGGAGAAGCGCGGCACAAGCGCGGGCGGGAGACTCCCGCCCCACCAGACTC
AAGCCCTCACTCGACTCTCGCGGCTTCGTTGCTCGCACAGCTCCCTGCCAGGCTAGGA
GGCCGGCTTTCGGGGTTGAGTGGCCGAGCTAAGGGTGCAGGAGACCAAGGGCGGCGACT
ACGACGGCGTTGATATCGGTGGTAACGACGGCCTCAGCAGGCGGGGAAGATGAAAGGTAG
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GCTAGCAAACTTGCCATTTCAATGATATTGCTGTAGGTGCAGTATGCTGTAGGGTGG
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GATTGTTACTAGTGGCATTAACTTTTGAATTTGGGCTGGTGGATTAATTTTTTTAAT



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ATCCCAGCTAGAGATATGGCCTTTAACTGACCTAAAGAGGTGTGTGTGATTTAATTTTT
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AAGTTTACTTGGTGCAGTTAAGAATTA AACTTGTCAATTTAACATTGCTGTTACATCTG
AAATAA ACTTATGTGATGTTCTGGTAAAAAAAAAAAAAAAAAAAAA

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- Restriction Sites:** Please inquire
- ACCN:** NM_025146
- 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_025146.1](#), [NP_079422.1](#)

RefSeq Size: 3576 bp

RefSeq ORF: 510 bp

Locus ID: 80218

UniProt ID: [Q9GZZ1](#)

Cytogenetics: 3q13.31

Domains: Acetyltransf

Gene Summary: N-alpha-acetyltransferase that acetylates the N-terminus of proteins that retain their initiating methionine (PubMed:19744929, PubMed:22311970, PubMed:21900231, PubMed:27484799). Has a broad substrate specificity: able to acetylate the initiator methionine of most peptides, except for those with a proline in second position (PubMed:27484799). Also displays N-epsilon-acetyltransferase activity by mediating acetylation of the side chain of specific lysines on proteins (PubMed:19744929). Autoacetylates in vivo (PubMed:19744929). The relevance of N-epsilon-acetyltransferase activity is however unclear: able to acetylate H4 in vitro, but this result has not been confirmed in vivo (PubMed:19744929). Component of a N-alpha-acetyltransferase complex containing NAA10 and NAA15, but NAA50 does not influence the acetyltransferase activity of NAA10: this multiprotein complex probably constitutes the major contributor for N-terminal acetylation at the ribosome exit tunnel, with NAA10 acetylating all amino termini that are devoid of methionine and NAA50 acetylating other peptides (PubMed:16507339, PubMed:27484799). Required for sister chromatid cohesion during mitosis by promoting binding of CDCA5/sororin to cohesin: may act by counteracting the function of NAA10 (PubMed:17502424, PubMed:27422821).[UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (1) represents the longer transcript and encodes the longer 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.