OriGene Technologies, Inc.
9620 Medical Center Drive, Ste 200
Rockville, MD 20850, US
Phone: +1-888-267-4436
https://www.origene.com
techsupport@origene.com
EU: info-de@origene.com
CN: techsupport@origene.cn

Product datasheet for SC328488

BHMT2 (NM_001178005) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	BHMT2 (NM_001178005) Human Untagged Clone
Tag:	Tag Free
Symbol:	BHMT2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC328488 representing NM_001178005. Blue=Insert sequence Red=Cloning site Green=Tag(s) GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTG GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC ATGGCACCTGCTGGACGCCCGGGGGCCAAGAAGGGGATTTTGGAGCGCCTGGAGAGTGGGGAGGTTGTG ATTGGAGATGGCAGCTTTCTCATTACTCTGGAGAAGAGAGGCTATGTGAAGGCTGGGCTCTGGACTCCA GAGGCAGTGATAGAACACCCAGACGCAGTTCGTCAACTTCACATGGAATTCTTGAGAGCAGGATCAAAT GTCATGCAGACTTTTACCTTTTCTGCCAGTGAGGACAATATGGAAAGCAAGTATTTTGAGCACGTTGAA GAAGCTGTGTGGGCTGTGGAAGTCTTAAAAGAATCAGATAGACCCGTGGCAGTTACCATGTGCATAGGC CCAGAGGGAGACATGCATGATATAACCCCCGGAGAATGTGCTGTGAGGCTGGTGAAGGCAGGGGCTTCC ATCGTTGGCGTGAACTGCCGCTTTGGGCCCGACACCAGCTTGAAGACGATGGAGCTCATGAAGGAGGGT CTTGAGTGGGCAGGGCTGAAAGCGCACCTCATGGTGCAGCCTCTGGGGTTCCACGCGCCTGACTGTGGC AAAGAGGGGTTTGTGGATCTCCCAGAATATCCCTTTGGACTGGAGTCCAGAGTTGCCACCAGATGGGAT ATTCAAAAATACGCCAGAGAGGCCTACAACCTGGGGGTCAGGTACATTGGCGGGTGCTGTGGATTTGAG CCCTACCACATCAGGGCAATTGCAGAGGAGCTGGCCCCAGAAAGGGGCTTTTTGCCACCAGCTTCAGAA AAACACGGCAGCTGGGGAAGTGGTTTGGACATGCACACCAAACCCTGGATTAGAGCAAGGGCTCGAAGG GAGTATTGGGAGAATCTGCTGCCAGCTTCAGGCAGACCTTTCTGTCCTTCGCTGTCAAAGCCAGACTTC TAA ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
Restriction Sites:	SgfI-MluI

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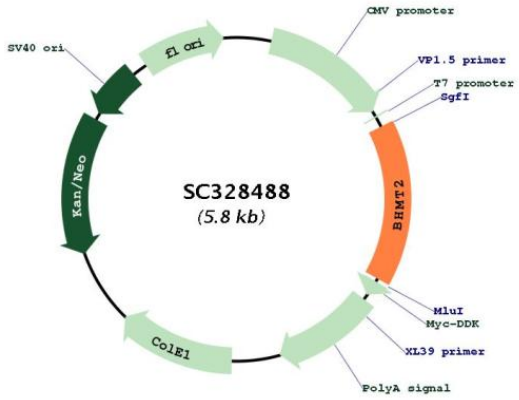
Plasmid Map:



ACCN:	NM_001178005
Insert Size:	900 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_001178005.1
RefSeq Size:	2459 bp

RefSeq ORF:	900 bp
Locus ID:	23743
UniProt ID:	Q9H2M3
Cytogenetics:	5q14.1
MW:	33.2 kDa
Gene Summary:	Homocysteine is a sulfur-containing amino acid that plays a crucial role in methylation reactions. Transfer of the methyl group from betaine to homocysteine creates methionine, which donates the methyl group to methylate DNA, proteins, lipids, and other intracellular metabolites. The protein encoded by this gene is one of two methyl transferases that can catalyze the transfer of the methyl group from betaine to homocysteine. Anomalies in homocysteine metabolism have been implicated in disorders ranging from vascular disease to neural tube birth defects such as spina bifida. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, May 2010] Transcript Variant: This variant (2) lacks an in-frame exon in the CDS, as compared to variant 1. The resulting isoform (2) lacks an internal segment, 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.