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Product datasheet for SC330728

ASH2L (NM_001261832) Human Untagged Clone

Product data:

Product Type: Expression Plasmids

Product Name: ASH2L (NM_001261832) Human Untagged Clone

Tag: Tag Free

Symbol: ASH2L

Synonyms: ASH2; ASH2L1; ASH2L2; Bre2

Vector: pCMV6-Entry (PS100001)

Fully Sequenced ORF:

>SC330728 representing NM_001261832.
Blue=Insert sequence Red=Cloning site Green=Tag(s)

ATGGATACTCAGGCGGGCTCCGTGGATGAAGAGAATGGCCGACAGTTGGGTGAGGTAGAGCTGCAATGT
GGGATTTGTACAAAATGGTTCACGGCTGACACATTTGGCATAGATACCTCATCCTGTCTACCTTTCATG
ACCAACTACAGTTTTCATTGCAACGTCTGCCATCACAGTGGGAATACCTATTTCCTCCGGAAGCAAGCA
AACTTGAAGGAAATGTGCCTTAGTGCTTTGGCCAACCTGACATGGCAGTCCCGAACACAGGATGAACAT
CCGAAGACAATGTTCTCCAAAGATAAGGATATTATACCATTTATTGATAAATACTGGGAGTGCATGACA
ACCAGACAGAGACCTGGGAAAATGACTTGGCCAAATAACATTGTTAAAACAATGAGTAAAGAAAGAGAT
GTATTCTTGGTAAAGGAACACCCAGATCCAGGCAGTAAAGATCCAGAAGAAGATTACCCCAAATTTGGA
CTTTTGGATCAGGACCTTAGTAACATTGGTCCTGCTTATGACAACCAAAAACAGAGCAGTGCTGTGTCT
ACTAGTGGGAATTTAAATGGGGGAATTGCAGCAGGAAGCAGCGGAAAAGGACGAGGAGCCAAGCGCAAA
CAGCAGGATGGAGGGACCACAGGGACCACCAAGAAGGCCCGGAGTGACCCTTTGTTTTCTGCTCAGCGC
CTTCCCCCTCATGGCTACCCATTGGAACACCCGTTTAACAAAGATGGCTATCGGTATATTCTAGCTGAG
CCTGATCCGCACGCCCCTGACCCCGAGAAGCTGGAACTTGACTGCTGGGCAGGAAAACCTATTCCTGGA
GACCTCTACAGAGCCTGCTTGTATGAACGGGTTTTGTTAGCCCTACATGATCGAGCTCCCCAGTTAAAG
ATCTCAGATGACCGGCTGACTGTGGTTGGAGAGAAGGGCTACTCTATGGTGAGGGCCTCTCATGGAGTA
CGGAAAGGTGCCTGGTATTTTGAAATCACTGTGGATGAGATGCCACCAGATACCGCTGCCAGACTGGGT
TGGTCCCAGCCCCTAGGAAACCTTCAAGCTCCTTTAGGTTATGATAAATTTAGCTATTCTTGGCGGAGC
AAAAAGGGAACCAAGTTCCACCAGTCCATTGGCAAACACTACTCTTCTGGCTATGGACAGGGAGACGTC
CTGGGATTTTATATTAATCTTCCTGAAGACACAGAGACAGCCAAGTCATTGCCAGACACATACAAAGAT
AAGGCTTTGATAAAATTCAAGAGTTATTTGTATTTTGAGGAAAAAGACTTTGTGGATAAAGCAGAGAAG
AGCCTGAAGCAGACTCCCCATAGTGAGGTTTCCATTAACTTTGGACCATGCTTCAAGTATCCTCCGAAG
GATCTCACTTACCGCCCTATGAGTGACATGGGCTGGGGCGCCGTGGTAGAGCACACCCTGGCTGACGTC
TTGTATCACGTGGAGACAGAAGTGGATGGGAGGCGCAGTCCCCCATGGGAACCCTGA

Restriction Sites: SgfI-MluI

ACCN: NM_001261832

Insert Size: 1506 bp

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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:	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_001261832.1
RefSeq Size:	2956 bp
RefSeq ORF:	1506 bp
Locus ID:	9070
UniProt ID:	Q9UBL3
Cytogenetics:	8p11.23
Protein Families:	Druggable Genome, Transcription Factors
MW:	56.5 kDa
Gene Summary:	Component of the Set1/Ash2 histone methyltransferase (HMT) complex, a complex that specifically methylates 'Lys-4' of histone H3, but not if the neighboring 'Lys-9' residue is already methylated. As part of the MLL1/MLL complex it is involved in methylation and dimethylation at 'Lys-4' of histone H3. May function as a transcriptional regulator. May play a role in hematopoiesis.[UniProtKB/Swiss-Prot Function] Transcript Variant: This variant (3) differs in the 5' UTR, initiates translation at a downstream, in-frame start codon and lacks an exon in the 3' coding region, but maintains the reading frame, compared to variant 1. The encoded isoform (c) is shorter than isoform a. 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.