

## Product datasheet for **SC334728**

### CEBP Alpha (CEBPA) (NM\_001285829) Human Untagged Clone

#### Product data:

Product Type:	Expression Plasmids
Product Name:	CEBP Alpha (CEBPA) (NM_001285829) Human Untagged Clone
Tag:	Tag Free
Symbol:	CEBP Alpha
Synonyms:	C/EBP-alpha; CEBP
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>NCBI ORF sequence for NM_001285829, the custom clone sequence may differ by one or more nucleotides

```

ATGCCCGGGGAGCGCACGGGCCCGCCGGCTACGGCTGCGCGGCCGCGGCTACCTGGACGGCAGGC
TGGAGCCCTGTACGAGCGCGTGGGGCGCCGGCGCTGCGGCCGCTGGTGATCAAGCAGGAGCCCCGCGA
GGAGGATGAAGCCAAGCAGCTGGCGCTGGCCGGCCTCTCCCTTACCAGCCGCCGCCGCCGCCGCCGCC
TCGCACCCGCACCCGCACCCGCCCGCCGCGCACCTGGCCGCCCGCCACCTGCAGTTCCAGATCGCGCACT
GCGGCCAGACCACCATGCACCTGCAGCCCGGTACCCACGCCGCCGCCGCCGCCCGTGCCAGCCCGCA
CCCCGCGCCCGCGCTCGGTGCCCGCGCCTGCCGGCCCTGGCAGCGCGCTCAAGGGGCTGGCGCCGCG
CACCCGACCTCCGCGCGAGTGGCGGCAGCGGCGCGGCAAGGCCAAGAAGTCGGTGGACAAGAACAGCA
ACGAGTACCGGTGCGGCGGAGCGCAACAACATCGCGGTGCGCAAGAGCCGCGACAAGGCCAAGCAGCG
CAACGTGGAGACGCAGCAGAAGGTGCTGGAGCTGACCAAGTGAATGACCGCCTGCGCAAGCGGGTGGAA
CAGCTGAGCCGCGAACTGGACACGCTGCGGGGCATCTCCGCCAGCTGCCAGAGAGCTCCTTGGTCAAGG
CCATGGGCAACTGCGCGTGA
  
```

Restriction Sites:	Sgfl-MluI
ACCN:	NM_001285829
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).


[View online »](#)

<b>Components:</b>	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).
<b>Reconstitution Method:</b>	<ol style="list-style-type: none"> <li>1. Centrifuge at 5,000xg for 5min.</li> <li>2. Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>3. Close the tube and incubate for 10 minutes at room temperature.</li> <li>4. Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
<b>Note:</b>	Plasmids are not sterile. For experiments where strict sterility is required, filtration with 0.22um filter is required.
<b>RefSeq:</b>	<u>NM_001285829.1, NP_001272758.1</u>
<b>RefSeq Size:</b>	2631 bp
<b>RefSeq ORF:</b>	720 bp
<b>Locus ID:</b>	1050
<b>UniProt ID:</b>	<u>P49715</u>
<b>Cytogenetics:</b>	19q13.11
<b>Protein Families:</b>	Druggable Genome, ES Cell Differentiation/IPS
<b>Protein Pathways:</b>	Acute myeloid leukemia, Pathways in cancer
<b>Gene Summary:</b>	<p>This intronless gene encodes a transcription factor that contains a basic leucine zipper (bZIP) domain and recognizes the CCAAT motif in the promoters of target genes. The encoded protein functions in homodimers and also heterodimers with CCAAT/enhancer-binding proteins beta and gamma. Activity of this protein can modulate the expression of genes involved in cell cycle regulation as well as in body weight homeostasis. Mutation of this gene is associated with acute myeloid leukemia. The use of alternative in-frame non-AUG (GUG) and AUG start codons results in protein isoforms with different lengths. Differential translation initiation is mediated by an out-of-frame, upstream open reading frame which is located between the GUG and the first AUG start codons. [provided by RefSeq, Dec 2013]</p> <p>Transcript Variant: This variant (1) can initiate translation from an upstream non-AUG (GUG) site, and also from three downstream, in-frame AUG sites. The isoform (b, also known as C/EBP-30) represented in this RefSeq results from translation initiation at the third AUG start codon. Isoform b has a shorter N-terminus, compared to isoform c. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>