

Product datasheet for **SC119100**

HIF1 beta (ARNT) (NM_001668) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	HIF1 beta (ARNT) (NM_001668) Human Untagged Clone
Tag:	Tag Free
Symbol:	HIF1 beta
Synonyms:	bHLHe2; HIF-1-beta; HIF-1beta; HIF1-beta; HIF1B; HIF1BETA; TANGO
Mammalian Cell Selection:	None
Vector:	<u>pCMV6-XL4</u>
E. coli Selection:	Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene sequence for NM_001668 edited
GGCGGTGACAGCGCCGCTTCTGGGGAGTGGCCTTTCTTTTCCCCTCCCTCCCGGTTCCGGTGG
GCGCGGCTCCTCCCACTGGGGGGGGTGGCGCGCGCGGCGGTCATCTGCGGCCATGGC
GGCGACTACTGCCAACCCGAAAATGACATCAGATGTACCATCACTGGGTCCAGCCATTGC
CTCTGAAAACCTGGACCTGGAATTCAAGGTGGAGGAGCCATTGTCCAGAGGGCTATTA
GCGGCGACAGGGCTGGATTTTGTATGATGATGGAGAAGGGAACAGTAAATTTTGTAGGTG
TGATGATGATCAGATGTCTAACGATAAGGAGCGGTTTGGCAGGTCGGATGATGAGCAGAG
CTCTGCGGATAAAGAGAGACTTGGCAGGAAAATCACAGTAAATTTGAACGGCGGCGACG
GAACAAGATGACAGCCTACATCACAGAAGTGTGATATGGTACCCACCTGTAGTGCCCT
GGCTCGAAAACCCAGACAAGCTAACCATCTTACGCATGGCAGTTTCTCACATGAAGTCCTT
GCGGGAACTGGCAACACATCCACTGATGGCTCCTATAAGCCGCTTTTCCCTCACTGATCA
GGAAGTAAACATTTGATCTTGGAGGCAGCAGATGGCTTTCTGTTTATTGTCTCATGTGA
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ATTGCAGGTAAGTCTCCCAACTGTACAGACATGAGTAATGTTTGTCAACCAACAGA
GTTTCATCTCCCGACACAATTGAGGGTATCTTCACTTTTGTGGATCACCCTGTGTGGC
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TGAAGACCAGCAGCTTCTAAGAGACAGCTTCCAACAGGTAGTGAATTTAAAGGCCAAGT
GCTGTCTGTATGTTCCGGTCCGGTCTAAGAACCAAGAATGGCTCTGGATGAGAACCAG
CTCCTTTACTTTCCAGAACCCTTACTCAGATGAAATTGAGTACATCATCTGTACCAACAC
CAATGTGAAGAACTCTAGCCAAGAACCAGGCCTACACTCTCCAACAATCCAGAGGCC



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ACAACTAGGTCCACAGCTAATTTACCCCTGGAGATGGGCTCAGGACAGCTGGCACCCAG
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GAGTAAGTGAGAGAGAGTGTGTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGCGCACAC
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TTACCTTTGTCTTTCTGTGTACTTTTCAAAGAGTCCTAAGGAGTTAAATCTTCCAGGTAT
TTTCCACTAGTATTGCAGCCAAAGAATATTTAAATAAACGTCTTTGCTGCGCTTGCAAA
AAAAAAAAAAAAA
    
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- Restriction Sites:** NotI-NotI
- ACCN:** NM_001668
- Insert Size:** 3200 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:** The ORF of this clone has been fully sequenced and found to be a perfect match to NM_001668.2.
- 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_001668.2](#), [NP_001659.1](#)

RefSeq Size: 4846 bp

RefSeq ORF: 2370 bp

Locus ID: 405

UniProt ID: [P27540](#)

Cytogenetics: 1q21.3

Domains: PAS, HLH, PAC

Protein Families: Druggable Genome, Transcription Factors

Protein Pathways: Pathways in cancer, Renal cell carcinoma

Gene Summary: This gene encodes a protein containing a basic helix-loop-helix domain and two characteristic PAS domains along with a PAC domain. The encoded protein binds to ligand-bound aryl hydrocarbon receptor and aids in the movement of this complex to the nucleus, where it promotes the expression of genes involved in xenobiotic metabolism. This protein is also a co-factor for transcriptional regulation by hypoxia-inducible factor 1. Chromosomal translocation of this locus with the ETV6 (ets variant 6) gene on chromosome 12 have been described in leukemias. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Oct 2013]

Transcript Variant: This variant (1) encodes the longest 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.