

## Gene Section

### Mini Review

# ARNT (aryl hydrocarbon receptor nuclear translocator)

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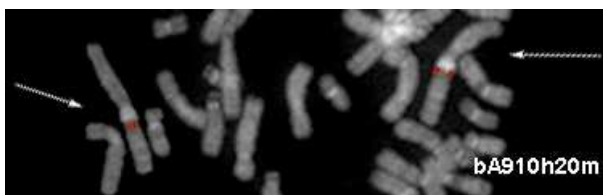
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## Identity

**Other names:** HIF-1b

**HGNC (Hugo):** ARNT

**Location:** 1q21



Probe(s) - Courtesy Mariano Rocchi, Resources for Molecular Cytogenetics.

## DNA/RNA

### Note

The gene is about 65 kb in size and has 22 exons.

### Transcription

Five alternative transcriptional start sites have been identified, located from 27 to 147 nucleotides 5' to the ATG translational initiation codon. There are two alternative polyadenylation sites, giving rise to transcripts of about 2600 and 4200 nucleotides. The 45 nucleotide exon 5 is an alternative exon and is spliced out in approximately half of the transcripts. This proportion does not seem to vary much between different tissues. No observable effects on the resulting protein due to omission of exon 5 have been noted. A transcript of about 1300 nucleotides is observed in some breast cancers and may be due to an alternative splicing event leading to elimination of the 3' end of the transcript.

### Pseudogene

No pseudogenes for ARNT are known.

## Protein

### Description

The 87 kDa protein is comprised of 789 amino acids (if exon 5 is included) or 774 amino acids (if exon 5 is excluded).

### Expression

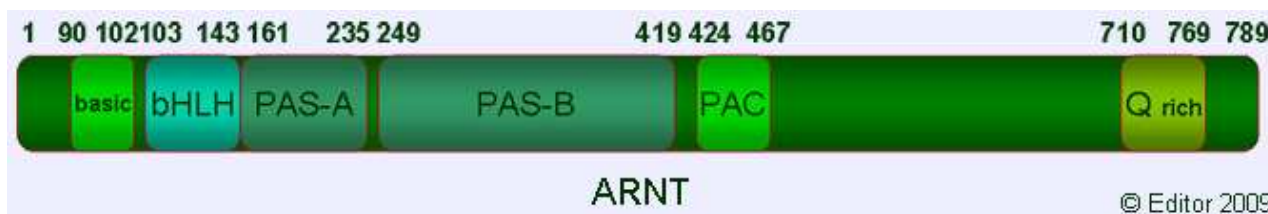
ARNT is expressed ubiquitously.

### Localisation

ARNT is a nuclear protein in most cell types, although it may also be located in the cytosol, particularly during embryogenesis.

### Function

ARNT serves as the dimerization partner for a number of other bHLH-PAS proteins, whose activity is modulated either by exogenous chemicals (the aryl hydrocarbon receptor (AHR)), or by hypoxia (hypoxia inducible factors 1, 2 and 3 alpha [HIF-1a, HIF-2a and HIF-3a]), or which show restricted expression (e.g. SIM-1). The AHR/ARNT dimer activates transcription of several genes involved in metabolism of foreign chemicals, including CYP1A1, CYP1B1, and NADP(H): oxidoreductase (NQO1). Transcriptional activation of these genes depends upon prior binding of AHR to xenobiotic ligands, including 2,3,7,8-tetrachlorodibenzo-p-dioxin (dioxin) and benzo(a)pyrene. The AHR/ARNT dimer and ARNT itself can also impact signaling by the estrogen receptor. The HIF-1a (and 2a and 3a) proteins are stabilized and activated by hypoxia (and hypoglycemia) and activate transcription of several genes involved in adapting to these adverse conditions,



bHLH, basic helix-loop-helix domain; PAS, Per/ARNT/Sim homology domain; A and B, the two approximately 50 amino-acid degenerative direct repeats within the PAS domain; Q-rich, glutamine-rich transactivation domain.

including the genes for erythropoietin (EPO), vascular endothelial growth factor (VEGF), and a number of enzymes of glycolysis. Unlike the AHR/ARNT and HIF/ARNT dimers, the SIM-1/ARNT dimer is probably not conditionally regulated. The above dimers bind specific DNA sequences in the regulatory regions of the responsive genes. The half-site for ARNT is on the 3' side of the recognition sequence and is 5'-GTG-3'. The sequence of the other half of the binding site depends upon the identity of the dimerization partner. DNA binding of ARNT is mediated by its basic region. There is evidence that the PAS region may also be involved. Dimerization between ARNT and other bHLH-PAS proteins is mediated by their HLH and PAS regions. The transcriptional activation domain of ARNT is located towards its carboxy terminus. ARNT appears capable of binding the E-box sequence 5'-CACGTG-3', although the affinity of ARNT for itself appears relatively low and no genes responsive to the homodimer have been identified.

### Homology

Two ARNT-related genes, ARNT-2 and ARNT-3 (also called BMAL-1 or MOP3) have been identified. ARNT-2 is more restricted in expression than ARNT, but appears to dimerize with the same partner proteins as ARNT. ARNT-3 has a somewhat different dimerization potential than ARNT.

## Mutations

### Germinal

Several polymorphisms have been identified. None has shown an association with any disease.

## Implicated in

### Note

Involved in a t(1;12)(q21;p13) translocation with EVT6 fusion in acute myeloblastic leukemia.

### Disease

Leukemia, Myelocytic, Acute AML-M2.

### Prognosis

Unknown.

### Hybrid/Mutated gene

Amino-terminal half of TEL fused to the complete coding sequence of ARNT except for its 8 amino-terminal amino acids. The reciprocal translocation

probably contributes little if at all to the cancer phenotype.

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*This article should be referenced as such:*

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