

## Product datasheet for **SC334566**

### **PAX5 (NM\_001280551) Human Untagged Clone**

#### **Product data:**

<b>Product Type:</b>	Expression Plasmids
<b>Product Name:</b>	PAX5 (NM_001280551) Human Untagged Clone
<b>Tag:</b>	Tag Free
<b>Symbol:</b>	PAX5
<b>Synonyms:</b>	ALL3; BSAP
<b>Mammalian Cell Selection:</b>	Neomycin
<b>Vector:</b>	pCMV6-Entry (PS100001)
<b>E. coli Selection:</b>	Kanamycin (25 ug/mL)
<b>Fully Sequenced ORF:</b>	>NCBI ORF sequence for NM_001280551, the custom clone sequence may differ by one or more nucleotides

```
ATGTTTGCTGGGAGATCAGGGACCGGCTGCTGGCAGAGCGGGTGTGTGACAATGACACCGTGCCTAGCG
TCAGTTCCATCAACAGGATCATCCGGACAAAAGTACAGCAGCCACCCAACCAACCAGTCCCAGTCCAG
TCACAGCATAGTGTCCACTGGCTCCGTGACGCAGGTGTCTCGGTGAGCAGGATTCGGCCGGCTCGTGC
TACTCCATCAGCGGCATCCTGGGCATCAGTCCCCAGCGCCGACACCAACAAGCGCAAGAGAGACGAAG
GTATTCAGGAGTCTCCGGTGCCGAACGGCCACTCGCTCCGGGCAGAGACTTCTCCGGAAGCAGATGCG
GGGAGACTTGTTACACAGCAGCAGCTGGAGGTGCTGGACCGGTGTTTGGAGGGCAGCACTACTCAGAC
ATCTTCACCACCACAGAGCCCATCAAGCCCGAGCAGACCACAGATATTCAGCCATGGCCTCGCTGGCTG
GTGGGCTGGACGACATGAAGGCCAATCTGGCCAGCCCCACCCCTGCTGACATCGGGAGCAGTGTGCCAGG
CCCGCAGTCTACCCATTGTGACAGGCTCCCCCTACTATTATAGCGCTGCCGCCGAGGAGCCGCCCA
CCTGCAGCCGCCACTGCCTATGACCGTCACTGA
```

<b>Restriction Sites:</b>	Sgfl-MluI
<b>ACCN:</b>	NM_001280551
<b>OTI Disclaimer:</b>	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).
<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).



**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\\_001280551.1](#), [NP\\_001267480.1](#)

**RefSeq Size:** 8554 bp

**RefSeq ORF:** 663 bp

**Locus ID:** 5079

**Cytogenetics:** 9p13.2

**Protein Families:** Transcription Factors

**Gene Summary:** This gene encodes a member of the paired box (PAX) family of transcription factors. The central feature of this gene family is a novel, highly conserved DNA-binding motif, known as the paired box. Paired box transcription factors are important regulators in early development, and alterations in the expression of their genes are thought to contribute to neoplastic transformation. This gene encodes the B-cell lineage specific activator protein that is expressed at early, but not late stages of B-cell differentiation. Its expression has also been detected in developing CNS and testis and so the encoded protein may also play a role in neural development and spermatogenesis. This gene is located at 9p13, which is involved in t(9;14)(p13;q32) translocations recurring in small lymphocytic lymphomas of the plasmacytoid subtype, and in derived large-cell lymphomas. This translocation brings the potent E-mu enhancer of the IgH gene into close proximity of the PAX5 promoter, suggesting that the deregulation of transcription of this gene contributes to the pathogenesis of these lymphomas. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Jul 2013]

**Transcript Variant:** This variant (6) lacks several exons and initiates translation at a downstream start codon, compared to variant 1. The encoded isoform (6) is shorter, 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.