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# Product datasheet for SC323644

## IRAK4 (NM_016123) Human Untagged Clone

### Product data:

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|---|---|
| **Product Type:** | Expression Plasmids |
| **Product Name:** | IRAK4 (NM_016123) Human Untagged Clone |
| **Tag:** | Tag Free |
| **Symbol:** | IRAK4 |
| **Synonyms:** | IMD67; IPD1; IRAK-4; NY-REN-64; REN64 |
| **Mammalian Cell Selection:** | None |
| **Vector:** | pCMV6-XL5 |
| **E. coli Selection:** | Ampicillin (100 ug/mL) |
| **Fully Sequenced ORF:** | >NCBI ORF sequence for NM_016123, the custom clone sequence may differ by one or more nucleotides |

ATGAACAAACCCATAACACCATCAACATATGTGCGCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAG
ATTTTATTGATCCTCAAGAAGGATGGAAGAAGTTAGCTGTAGCTATTAAAAAACCATCTGGTGATGATAG
ATACAATCAGTTTCACATAAGGAGATTTGAAGCATTACTTCAAACTGGAAAAAGTCCCACTTCTGAATTA
CTGTTTGACTGGGGCACCACAAATTGCACAGTTGGTGATCTTGTGGATCTTTTGATCCAAAATGAATTTT
TTGCTCCTGCGAGTCTTTTGCTCCCAGATGCTGTTCCCAAAACTGCTAATACACTACCTTCTAAAGAAGC
TATAACAGTTCAGCAAAAACAGATGCCTTTCTGTGACAAAGACAGGACATTGATGACACCTGTGCAGAAT
CTTGAACAAAGCTATATGCCACCTGACTCCTCAAGTCCAGAAAATAAAAGTTTAGAAGTTAGTGATACAC
GTTTTCACAGTTTTTCATTTTATGAATTGAAGAATGTCACAAATAACTTTGATGAACGACCCATTTCTGT
TGGTGGTAATAAAATGGGAGAGGGAGGATTTGGAGTTGTATATAAAGGCTACGTAAATAACACAACTGTG
GCAGTGAAGAAGCTTGCAGCAATGGTTGACATTACTACTGAAGAACTGAAACAGCAGTTTGATCAAGAAA
TAAAAGTAATGGCAAAGTGTCAACATGAAAACTTAGTAGAACTACTTGGTTTCTCAAGTGATGGAGATGA
CCTCTGCTTAGTATATGTTTACATGCCTAATGGTTCATTGCTAGACAGACTCTCTTGCTTGGATGGTACT
CCACCACTTTCTTGGCACATGAGATGCAAGATTGCTCAGGGTGCAGCTAATGGCATCAATTTTCTACATG
AAAATCATCATATTCATAGAGATATTAAAAGTGCAAATATCTTACTGGATGAAGCTTTTACTGCTAAAAT
ATCTGACTTTGGCCTTGCACGGGCTTCTGAGAAGTTTGCCCAGACAGTCATGACTAGCAGAATTGTGGGA
ACAACAGCTTATATGGCACCAGAAGCTTTGCGTGGAGAAATAACACCCAAATCTGATATTTACAGCTTTG
GTGTGGTTTTACTAGAAATAATAACTGGACTTCCAGCTGTGGATGAACACCGTGAACCTCAGTTATTGCT
AGATATTAAAGAAGAAATTGAAGATGAAGAAAAGACAATTGAAGATTATATTGATAAAAAGATGAATGAT
GCTGATTCCACTTCAGTTGAAGCTATGTACTCTGTTGCTAGTCAATGTCTGCATGAAAAGAAAAATAAGA
GACCAGACATTAAGAAGGTTCAACAGCTGCTGCAAGAGATGACAGCTTCTTAA



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**5' Read Nucleotide Sequence:**

>OriGene 5' read for mutant NM_016123 unedited
ACCGCCCGTTGAGCAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTCGTTTAGTGA
ACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGCGAATTCGGCACGAGGGTTCTTCTGTCGC
CGGCTTCAGCAGCCCGCGCCCGGGCAGGAATAGAAGATGAACAAACCCATAACACCATCAACATATGTGC
GCTGCCTCAATGTTGGACTAATTAGGAAGCTGTCAGATTTTATTGATCCTCAAGAAGGATGGAAGAAGTT
AGCTGTAGCTATTAAAAAACCATCTGGTGATGATAGATACAATCAGTTTCACATAAGGGAGATTTGAAGC
ATTACTTCAAACTGGAAAAAGTCCCCACTTCTGATTTACTGTTTGACTGGGGGCACCACCAATTGTGCAC
AGTTGGTGTAATCTTTGTGGGGATCTTTTGAGATCCCAAAATGAAATTTTTTGCTTCCGCGCGATCTCTT
TGGCTCCAGAAATGCCTGGTTCCCAAAACTGCTAAACCACTACTTCTCTAAGAAAAGCTAAAACAGTCCG
ACCAAAAACAATGGCCTTTTCTGTGACAGACACGAGAATTGGGGCACCCTCGGTCGAAAACTTTTACAAA
AGCTATTATACCCCACCCGCACCCCCAATGCCCGAAAAAAAAAGTTTTAAAATTTTAGGGATACCGTTTT
ACACGATTTTTCATTTTTAAAATGTGAAAAAAGTGCCAAAAAACATTTTTGGAAAAACCACCCTTTGTGG
GTGGTGGATATAAAATGAAAAGAGAATATTTTGTTGTTTTAAAGGGGCCTCATACACACTGTGGTGGGGG
AGACATGCTGCACGGTTGTATACTACTGCGAATGAGCACCGTTGTTTCTAAAAAAAAATGGCGAGAGTGT
GCCGAGAACACTTGACACTCCGTTGTCACTGATGAGAGACACACCGCTACTATAGTTATATCCCCGCGTG
TTGTCCG

**Kinase Domain Sequence:**

>SC323644 kinase domain raw sequence. By performing BLASTX analysis with this sequence against NCBI refernce protein database, you can confirm the presence of the kinase-deficient mutation
CMCTTCTGTTGGTGGTATAAATGGGAGAGGGAGGATTTGGAGTTGTATATAAAGGCTACGTAAATAACAC
AACTGTGGCAGTGATGAAGCTTGCAGCAATGGTTGACATTACTACTGAAGAACTGAAACAGCAGTTTGAT
CAAGAAATAAAAGTAATGGCAAAGTGTCAACATGAAAACTTAGTAGAACTACTTGGTTTCTCAAGTGATG
GAGATGACCTCTGCTTAGTATATGTTTACATGCCTAATGGTTCAT

**Restriction Sites:** Please inquire

**ACCN:** NM_016123

**Insert Size:** 3000 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:** This kinase-deficient mutant clone was generated by created by site-directed mutagenesis from the corresponding wild-type clone. See details in "Application of active and kinase-deficient kinome collection for identification of kinases regulating hedgehog signaling." Cell. 2008 May p536-548.

**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_016123.1, NP_057207.1

| | |
|---|---|
| **RefSeq Size:** | 2817 bp |
| **RefSeq ORF:** | 1383 bp |
| **Locus ID:** | 51135 |
| **UniProt ID:** | Q9NWZ3 |
| **Cytogenetics:** | 12q12 |
| **Domains:** | DEATH, pkinase, TyrKc, S_TKc |
| **Protein Families:** | Druggable Genome, Protein Kinase |
| **Protein Pathways:** | Apoptosis, Neurotrophin signaling pathway, Toll-like receptor signaling pathway |
| **Gene Summary:** | This gene encodes a kinase that activates NF-kappaB in both the Toll-like receptor (TLR) and T-cell receptor (TCR) signaling pathways. The protein is essential for most innate immune responses. Mutations in this gene result in IRAK4 deficiency and recurrent invasive pneumococcal disease. Multiple transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Aug 2011]<br>Transcript Variant: This variant (2) differs in the 5' UTR compared to variant 1. Variants 1, 2, and 13 all encode the same 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. |