

## Product datasheet for **MC229384**

### **Abl1 (NM\_001283045) Mouse Untagged Clone**

#### Product data:

**Product Type:** Expression Plasmids  
**Product Name:** Abl1 (NM\_001283045) Mouse Untagged Clone  
**Tag:** Tag Free  
**Symbol:** Abl1  
**Synonyms:** Abl; AI325092; c-Abl; E430008G22Rik  
**Vector:** pCMV6-Entry (PS100001)  
**E. coli Selection:** Kanamycin (25 ug/mL)  
**Cell Selection:** Neomycin  
**Fully Sequenced ORF:** >MC229384 representing NM\_001283045  
**Red=Cloning site Blue=ORF Orange=Stop codon**

TTTTGTAATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCC  
GCC**CGGATCGCC**

ATGTCACAAGGTGGACCTACCCAAGTGCCGCTACAAAGGGATCCCGCTCTACCATTTATGGAAGCCC  
TGCAGAGGCCAGTGGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAGCAGCTCGATGGAAGCTCCAAGGA  
AAACCTTCTTGCTGGGCCAGTAAAATGACCCCAACCTTTTTGTGGCACTCTATGATTTGTGGCCAGT  
GGAGATAACACTCTCAGCATCACTAAAGGTGAAAAGCTCCGGGTCTTGGGTATAATCACAAATGGGGAAT  
GGTGTGAAGCCAAACGAAAAATGGCCAAGGATGGGTCCCAAGCAACTACATCACCCCGTCAACAGCCT  
GGAGAAACATTCTGGTATCATGGCCCTGTATCTCGGAATGCTGCTGAGTATCTGCTGAGCAGCGGAATC  
AACGGCAGCTTCTTAGTGCGGGAGAGTGAGAGTAGCCCTGGCCAGAGATCCATCTCGCTGCGGTATGAAG  
GGAGGGTGTACCACTACAGGATCAACTGCCTCTGATGGCAAGCTGTACGTGTCCTCCGAGAGCCGCTT  
CAACTCTGGCTGAGTTAGTTCACCATCACTCCACGGTGGCTGATGGCCTCATCACCACACTCCACTAC  
CCAGCTCCAAGCGCAACAAGCCCACTATCTACGGTGTGTCCCCAACTACGACAAGTGGGAAATGGAGC  
GCACCGACATCACCATGAAGCACAAGTTGGGTGGAGGCCAGTACGGGGAGGTGTACGAGGGCGTTTGGAA  
GAAGTACAGCCTCACTGTGGCCGTGAAGACCTTGAAGGAGGACACCATGGAGGTGGAGGATTCCTGAAG  
GAAGCGCGGTGATGAAGGAGATCAAACACCCTAACCTGGTGCAGCTGCTAGGGGTGTGTACCCGGGAAC  
CACCATTCTACATAATCACTGAGTTCATGACCTATGGGAACCTGCTGGACTACCTGAGGGAGTGAACCG  
GCAGGAGGTGAGCGCCGTGACTGCTCTACATGGCCACACAGATCTCATCAGCCATGGAGTACTTGGAG  
AAGAAGAACTTCATCCACAGAGACCTTGTGCCCCGAACTGCCTGGTAGGGGAAAACCACTTGGTGAAGG  
TGGCTGATTTGGCTGAGCAGTTGATGACAGGGGACACCTACACGGCCATGCTGGAGCCAAATTC  
CATCAAATGGACGCACCTGAGAGCCTGGCCTACAACAAGTTCTCCATCAAGTCGGACGTGTGGCATT  
GGAGTATTGCTCTGGGAGATTGCTACCTATGGCATGTCACCTTACCCGGGAATTGACCTGTCTCAGTTT  
ATGAGCTGCTGGAAAAGACTACCGCATGGAGCGCCCTGAAGGCTGCCCGGAGAAGGTCTACGAGCTCAT  
GCGAGCATGTTGGCAGTGAACCCCTCTGACCGGCCCTCCTTTGCTGAAATCCACCAAGCCTTTGAAACC  
ATGTTCCAGGAATCCAGTATCTCAGATGAGGTGGAGAAGGAGCTGGGAAACGAGGCACGAGAGGAGGTG



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CTGGGAGTATGCTGCAGGCCCCAGAGCTGCCACCAAGACCAGAACCTGCAGGAGAGCAGCTGAGCAGAA
AGATGCGCCTGACACCCCTGAGCTGCTCCACACGAAGGGCCTGGGAGAAAAGCGATGCACTGGACAGTGAG
CCTGCTGTATCGCCACTGCTTCTCGGAAAAGAGCGGGGCCCCAGACGGCAGCCTAAATGAAGATGAGC
GCCTTCTCCCCAGAGACAGAAAAGACCACTGTTACAGCGCTTTGATCAAGAAGAAGAAGAAAATGGCGCC
GACGCCCCCTAAGCGCAGCAGTTCCTCCGAGAGATGGATGGCCAGCCAGACCCGAGAGGGGCTAGTGAG
GATGACAGCAGGGAACCTGCAATGGACCACCAGCTCTCACCTCAGACGCAGCAGAGCCTACCAAGTCCC
CAAAGGCCAGCAATGGGGCTGGCGTCCCTAATGGAGCCTTCCGGGAGCCGGCAACTCAGGCTCCGTTTC
TCCCCACATGTGAAAAAGTCCAGCACACTGACCGGGAGCCGCCTGGCTGCTGCCGAAGAGGAGAGCGGC
ATGAGCTCCAGTAAGCGCTTCTGCGTTCTTGTTGCGCCTCCTGCATGCCCCATGGGGCAAGGGACACAG
AGTGGCGGTGGTACGCTGCCTCGAGACTGCCGTCTGCTGGCAAGCAGTTTACTCATCCACCTTTGG
AGGGCACAAAAGCGAAAAGCCAGCTCTGCCTCGGAAAACGCACCAGTGAGAGCAGGTCTGAGCAGGTGGCC
AAAAGCACGGCGATGCCCCCTCCCGGCTGGTGAAGAAGAACGAGGAGGCTGCTGAAGAAGGCTTCAAAG
ACACAGAAATCCAGCCCTGGCTCCAGCCCTCCAGCTTGACTCCCAAACCTCTCCGACGGCAGGTCACTGC
CTCTCCTTCTCTGGCCTCTCTACAAGGAAGAGGCCACCAAGGGCAGTGCCCTCAGGCATGGGGACTCCG
GCCACTGCAGAGCCAGCACCCCCAGCAACAAAGTGGGCCTCAGCAAGGCCTCCTCTGAGGAGATGCGCG
TAAGGAGGCACAAGCACAGCTCGGAGTCCCAGGGAGAGACAAGGGGCGACTGGCTAAGCTCAAGCCTGC
CCCGCCGCTCCTCTGCCTGCACAGGAAAAGCAGGCAAGCCCGCACAGAGCCCCAGCCAAGAGGGCCGGG
GAGGCAGGGGGGCCACAAAAGACAAAATGCACGAGTCTGGCTATGGATGTGTGAACACTGACCCACCA
AGGCCGGCCACCTGGAGAAGGACTGAGAAAGCCTGTGCCCCATCTGTGCCAAAGCCCCAGTCGACGGC
TAAGCCTCCAGGGACTCCACCAGCCCGGTCTCCACCCCTCCACAGCACCAGCTCCTTACCCCTGGCT
GGGGACCAGCAGCCATCTTCTGCCGCTTATCCCCCTCATATCAACCCGTGTGTCTTTAGGAAGACC
GCCAGCCGCCAGAGCGCATTGCCAGTGGCACCATCACCAAGGGTGTGGTTCTGGACAGTACTGAGGCCCT
GTGCCTTGCCATCTCCCGAACTCAGAGCAGATGGCCAGCCACAGTGTACTGGAGGCTGGCAAGAAC
CTGTACACTTTTCTGTGTGAGCTATGTGGACTCTATCCAGCAGATGAGGAACAAGTTTGCCTTCCGTGAGG
CTATCAACAAGCTGGAGAGCAACCTCCGAGAGCTGCAGATCTGCCTGCCACAGCCTCCAGTGGGCCAGC
TGCCACCAAGACTTCAGCAAGCTGCTCAGCTCTGTGAAGGAGATCAGCGACATTGTCCGGAGGTAG

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**ACGCGT**ACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT  
ACAAGGATGACGACGATAAGGTTTAA

- Restriction Sites:** SgfI-MluI
- ACCN:** NM\_001283045
- Insert Size:** 3357 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:** Clone contains native stop codon, and expresses the complete ORF without any c-terminal tag.
- 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\\_001283045.1](#), [NP\\_001269974.1](#)

**RefSeq Size:** 6039 bp

**RefSeq ORF:** 3357 bp

**Locus ID:** 11350

**UniProt ID:** [P00520](#)

**Cytogenetics:** 2 B

**Gene Summary:**

Non-receptor tyrosine-protein kinase that plays a role in many key processes linked to cell growth and survival such as cytoskeleton remodeling in response to extracellular stimuli, cell motility and adhesion, receptor endocytosis, autophagy, DNA damage response and apoptosis. Coordinates actin remodeling through tyrosine phosphorylation of proteins controlling cytoskeleton dynamics like WASF3 (involved in branch formation); ANXA1 (involved in membrane anchoring); DBN1, DBNL, CTTN, RAPH1 and ENAH (involved in signaling); or MAPT and PXN (microtubule-binding proteins). Phosphorylation of WASF3 is critical for the stimulation of lamellipodia formation and cell migration. Involved in the regulation of cell adhesion and motility through phosphorylation of key regulators of these processes such as BCAR1, CRK, CRKL, DOK1, EFS or NEDD9. Phosphorylates multiple receptor tyrosine kinases and more particularly promotes endocytosis of EGFR, facilitates the formation of neuromuscular synapses through MUSK, inhibits PDGFRB-mediated chemotaxis and modulates the endocytosis of activated B-cell receptor complexes. Other substrates which are involved in endocytosis regulation are the caveolin (CAV1) and RIN1. Moreover, ABL1 regulates the CBL family of ubiquitin ligases that drive receptor down-regulation and actin remodeling. Phosphorylation of CBL leads to increased EGFR stability. Involved in late-stage autophagy by regulating positively the trafficking and function of lysosomal components. ABL1 targets to mitochondria in response to oxidative stress and thereby mediates mitochondrial dysfunction and cell death. In response to oxidative stress, phosphorylates serine/threonine kinase PRKD2 at 'Tyr-717' (By similarity). ABL1 is also translocated in the nucleus where it has DNA-binding activity and is involved in DNA-damage response and apoptosis. Many substrates are known mediators of DNA repair: DDB1, DDB2, ERCC3, ERCC6, RAD9A, RAD51, RAD52 or WRN. Activates the proapoptotic pathway when the DNA damage is too severe to be repaired. Phosphorylates TP73, a primary regulator for this type of damage-induced apoptosis. Phosphorylates the caspase CASP9 on 'Tyr-191' and regulates its processing in the apoptotic response to DNA damage. Phosphorylates PSMA7 that leads to an inhibition of proteasomal activity and cell cycle transition blocks. Regulates T-cell differentiation in a TBX21-dependent manner (PubMed:21690296). Phosphorylates TBX21 on tyrosine residues leading to an enhancement of its transcriptional activator activity (PubMed:21690296). [UniProtKB/Swiss-Prot Function]

Transcript Variant: This variant (3) differs in the 5' UTR and coding region, and uses an alternate downstream start codon compared to variant 1. The resulting protein (isoform c) has a shorter and distinct N-terminus compared to isoform a.