

Product datasheet for MC228355

Foxp1 (NM_001197322) Mouse Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	Foxp1 (NM_001197322) Mouse Untagged Clone
Tag:	Tag Free
Symbol:	Foxp1
Synonyms:	3110052D19Rik; 4932443N09Rik; AI461938; AW494214
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Cell Selection:	Neomycin

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This product is to be used for laboratory only. Not for diagnostic or therapeutic use.

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Fully Sequenced ORF: >MC228355 representing NM_001197322
Red=Cloning site Blue=ORF Orange=Stop codon

TTTTGTAATACGACTCACTATAGGGCGCCGGATTCTGACTGGATCCGTACCGAGGAGATCTGCC
GCCGCGATCGCC

ATGATGACACCTCAGTTATCACTCCTAACAAATGCAGCAGATCCTCCAGCAGCAGGTGCTGAGCCCC
AGCAGCTCAGGTTCTCCTCAGCAGCAGCAGGCCCTATGTTAACAGCAGCTTAAGAATTATAA
AAAACAACAGGAACAGTTGAGCTTCAACTCTCCAACAGCAACATGCTGGAAAACAGCCGAAAGAGCAG
CAGCAGGTGGCTACCCAGCAGTTGGCTTCCAGCAGCAGCTCTCAGATGCAGCAGCTGCAGCAGCAG
ACCTCTTGCTCTCCAGGCCAAGGCCTTAACAATTAGCCGGGCAGCCTGCCCTCCCTCCAACC
CCTCGCTCAAGGCATGATTCCAACGGAACCTGAGCAGCTGGAAAAGAAGTGACAAGTGCCCACACTGCA
GAGGAAACCACAAGCAGCAACCACAGCAGCCTAGACCTGACCAGCACATGTGTCGTCCCTGGCACCT
CCAAGTCCTCCCTAACATCATGAACCCGATGCCCTACCAATGGACAGCTCTGGTCCACACTCCAAAAG
GGAAAGCTTGTCCCAGGAGCACCCCCACAGCCACCCCTCTATGGACATGGTATGCAAGTGGCA
GGCTGTGAGGCGGTTGTGACGACTTCCAGCCTTCTAAACATCTAACAGTGAGCATGCGCTGGACG
ATAGAAGCACAGCTCAATGTAGAGTACAATGCAGGTTGACAGCAGTTAGAGCTACAGCTTGTCAAAGA
CAAAGAGCGCCTGCAAGCCATGATGACCCACCTGCATGTGAAGTCTACAGAACCCAAAGCTGCCCTCAG
CCCTGAATCTGTATCAAGTGTACCCCTCCAAGTGTGCTCAGAGGCTTCTCACAGAGCTTACCTC
ATACTCCAACACCCCCACCGCCCCCTGACTCTGTACCCAAGGGCCCTCGTCATCACCACCCAG
CATGCACACGGTGGGACCTATCCGAGGGTACTCAGACAATACAACGTGCCATTCTCAGCAGAT
ATTGCGAGAACAAAGAATTATAAGAACGCGGAAGTTAGACCACATTACATATGCATTTAATCA
GGCAGGCCATTCTGAATCTCAGAAAAGCAGCTAACACTAAACGAAATCTATAACTGGTCACACGAAT
GTTGCTTACTTCCAGCAGCTGACGCACTGCAGCCACGTGGAAGAATGAGCTGCGTCATAATTTAGTCTCCACAAG
TGTTTGTGCGAGTAGAGAACGTTAAGGGGAGTATGGACAGTGGATGAAGTAGAGTTCCAAAACGGA
GGCCACAAAAGATCAGTGGTAACCCTCCCTATTAAAAACATGCAGAGCAGGCCAGCCTACTGCACACC
TCTCAATGCAGCTTACAGGCTTCATGGCTGAGAATAGTACCTCTGTACACTACCGCTTCCATGGGA
AATCCCACCTGGGAGCCTGGCAGTGCATCCGGAGGAGCTGAACGGGGCATGGAGCACACCAACA
GCAACGAGAGTGACAGCAGTCCAGGAGTCCAGTGCACCGTGTGACCCCATACAGTCAAAGAAGA
ACCCCTGACCCCGAGGAAGCTGAAGGCCCTGTCTTAGTGACAACAGCAACACAGTCCAGATTT
GACCATGACAGAGATTACGAAGACGAACCAAGTAAATGAGGACATGGAGTGA

ACCGTACGCGCCGCTGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGATT
ACAAGGATGACGACGATAAGGTTAA

Restriction Sites: Sgfl-Mlul

ACCN: NM_001197322

Insert Size: 1731 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_001197322.1](#), [NP_001184251.1](#)

RefSeq Size: 6649 bp

RefSeq ORF: 1731 bp

Locus ID: 108655

UniProt ID: [P58462](#)

Cytogenetics: 6 D3

Gene Summary:	<p>Transcriptional repressor. Can act with CTBP1 to synergistically repress transcription but CTPBP1 is not essential (PubMed:11358962, PubMed:14701752). Plays an important role in the specification and differentiation of lung epithelium. Acts cooperatively with FOXP4 to regulate lung secretory epithelial cell fate and regeneration by restricting the goblet cell lineage program; the function may involve regulation of AGR2 (PubMed:11358962, PubMed:22675208). Essential transcriptional regulator of B-cell development (PubMed:16819554). Involved in regulation of cardiac muscle cell proliferation (PubMed:20713518). Involved in the columnar organization of spinal motor neurons. Promotes the formation of the lateral motor neuron column (LMC) and the preganglionic motor column (PGC) and is required for respective appropriate motor axon projections. The segment-appropriate generation of spinal chord motor columns requires cooperation with other Hox proteins (PubMed:18667151, PubMed:18662545). Can regulate PITX3 promoter activity; may promote midbrain identity in embryonic stem cell-derived dopamine neurons by regulating PITX3 (PubMed:20175877). Negatively regulates the differentiation of T follicular helper cells T(FH)s (PubMed:24859450). Involved in maintenance of hair follicle stem cell quiescence; the function probably involves regulation of FGF18 (PubMed:23946441). Represses transcription of various pro-apoptotic genes and cooperates with NF-kappa B-signaling in promoting B-cell expansion by inhibition of caspase-dependent apoptosis. Binds to CSF1R promoter elements and is involved in regulation of monocyte differentiation and macrophage functions; repression of CSF1R in monocytes seems to involve NCOR2 as corepressor. Involved in endothelial cell proliferation, tube formation and migration indicative for a role in angiogenesis; the role in neovascularization seems to implicate suppression of SEMA5B. Can negatively regulate androgen receptor signaling (By similarity).</p> <p>[UniProtKB/Swiss-Prot Function]</p> <p>Transcript Variant: This variant (3) differs in the 5' UTR and coding sequence compared to variant 1. The resulting isoform (3) is shorter at the N-terminus compared to isoform 1.</p> <p>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.</p>
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