

# Product datasheet for SC325835

## RBFOX1 (NM\_001142333) Human Untagged Clone

### **Product data:**

#### OriGene Technologies, Inc.

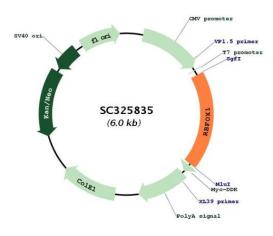
9620 Medical Center Drive, Ste 200 Rockville, MD 20850, US Phone: +1-888-267-4436 https://www.origene.com techsupport@origene.com EU: info-de@origene.com CN: techsupport@origene.cn

Product Type:	Expression Plasmids
Product Name:	RBFOX1 (NM_001142333) Human Untagged Clone
Tag:	Tag Free
Symbol:	RBFOX1
Synonyms:	2BP1; A2BP1; FOX-1; FOX1; HRNBP1
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC325835 representing NM_001142333. Blue=Insert sequence <mark>Red</mark> =Cloning site Green=Tag(s)
	GCTCGTTTAGTGAACCGTCAGAATTTTGTAATACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCCGCCGCGCGCCCCGCGCCCCCTGACAAATGGCTCAGCCTTACGCTTCGGCCCAGTTTGCTCCCCGCGAACGGTATCACCGGCGGAATACACGGGCCCCTCATCCCCACCCCGCGCCAGAGTACACAGGCCAGACCACGGTTCCCGAGCACACATTAAACCTGTACCCTCCCGCCCACCCCGCGCCAGAGTACACAGGCCAGACCACGGTTCCCGAGCACACATTAAACCTGTACCCTCCCGCCCAGACGCACTCCGAGCAGAGCCCGGCGGACACGAGCCCCAGACCGTCTGGCACCGCCACACAAGCAGATGACGCAGCACCGACGGATGGCCAGCCCCAGACACAACCTTCTGGAAAACACGGAAAACAAGTCTCAGCCCAAGCGGCTGCATGTCTCCAATATCCCCTTCAGGACACACCTTCTGGAAACACGGAAAACAAGTTTGGTCAATTTGGTAAAATCTTAGATGTTGAAATTATTTTTAATGAGCGAGGCTCAAAGGGATTTGGTTTCGTAACTTTCGAAAATAGTGCCGATGCGGACAGGGCGAGGAGAAATTACACGGCACCGTGGTAGAGGGCCGTAAAATCGAGGTAAATAATGCCACAGCACGTGTAATGACAAATAAAAAGACCGTCAACCCTTATACAAATGGCTGGAAATTGAATCCAGTTGTGGGGTGCAGTCTACAGTCCCGGACCTGCGAGGCGCGCCGCGGCGCCCCCGGCCCCCGGCCCCCGGCCCCC
Restriction Sites:	Sgfl-Mlul



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#### Plasmid Map:



ACCN:	NM_001142333
Insert Size:	1113 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 TrueClone is provided through our Custom Cloning Process that includes sub-cloning into OriGene's pCMV6 vector and full sequencing to provide a non-variant match to the expected reference without frameshifts, and is delivered as lyophilized plasmid DNA.
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:	<ol> <li>Centrifuge at 5,000xg for 5min.</li> <li>Carefully open the tube and add 100ul of sterile water to dissolve the DNA.</li> <li>Close the tube and incubate for 10 minutes at room temperature.</li> <li>Briefly vortex the tube and then do a quick spin (less than 5000xg) to concentrate the liquid at the bottom.</li> <li>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.</li> </ol>
RefSeq:	<u>NM 001142333.1</u>
RefSeq Size:	4694 bp
RefSeq ORF:	1113 bp
Locus ID:	54715
UniProt ID:	<u>Q9NWB1</u>

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	RBFOX1 (NM_001142333) Human Untagged Clone – SC325835
Cytogenetics:	16p13.3
MW:	40 kDa
Gene Summary:	The Fox-1 family of RNA-binding proteins is evolutionarily conserved, and regulates tissue- specific alternative splicing in metazoa. Fox-1 recognizes a (U)GCAUG stretch in regulated exons or in flanking introns. The protein binds to the C-terminus of ataxin-2 and may contribute to the restricted pathology of spinocerebellar ataxia type 2 (SCA2). Ataxin-2 is the product of the SCA2 gene which causes familial neurodegenerative diseases. Fox-1 and ataxin-2 are both localized in the trans-Golgi network. Several alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Nov 2011]
	Transcript Variant: This variant (5) differs in the 5' UTR and has multiple coding region differences compared to variant 1. The resulting isoform (5) has a shorter and distinct N- terminus and other internal differences compared to isoform 1. Sequence Note: This RefSeq record was created from transcript and genomic sequence data because no single transcript was available for the full length of the gene. The extent of this transcript is supported by

transcript alignments.

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