

Product datasheet for **SC328751**

BRUNOL6 (CELF6) (NM_001172684) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	BRUNOL6 (CELF6) (NM_001172684) Human Untagged Clone
Tag:	Tag Free
Symbol:	BRUNOL6
Synonyms:	BRUNOL6
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC328751 representing NM_001172684. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTT TAGTGAACCGTCAGAATTTTGT AATACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCC GCGATCGCC
ATGGCCGCGCGCCGGGAGGGTCAGCGCAGCCCGCTGGCCCCGGCCCGCCTGGGTTTCAGCACCCGG
GACAGCGCGCTCGGCATGAGCGGGCTAAACCCCGTCCC GCCGTACCCATGAAGGACCACGACGCCATC
AAGCTCTTCGTGGGGCAGATCCC GCGGGCTTGGACGAGCAGGACCTCAAGCCGCTGTTCGAGGAGTTC
GGCCGCATCTACGAGCTACGGTCTGAAGGACC GGCTCACCGCCTCCACAAAGCTGTGCCTTCCTC
ACCTACTGCGCCCGGACTCTGCTCTCAAGGCCAGAGTGC ACTGCACGAGCAGAAGACCCTGCCAGGG
ATGAATCGTCCGATCCAAGTGAAGCCAGCTGCCAGTGAGGGCCGAGGAGAGGACC GAAAGCTGTTTGTG
GGGATGCTGGGCAAGCAGCAGGGTGAGGAGGACGTCAGACGCCTGTTCCAGCCCTTTGGCCACATCGAG
GAGTGCACGGTCTCGGAGTCTTGACGGCACCAGTAAAGGCTGTGCCTTTGTGAAGTTCGGGAGTCAA
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CAGGCGGCCCTGCTGGCGGGCACAGGGCCAGGCCTAGGCCGGTGGCGGCAGTGGCGGCCAGATG
CAACACGTGGCGGCCTTTAGCTGGTAGCTGCGCCTCTGTTGCCGCGGCAGCAGCCAAC TCCCCGCTG
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CCCCAGACCAATGGCCAGCCGGGCTCCGACACGCTCTACAATAACGGGCTCTCCCCTTATCCAGCCAG
AGCCCCGCGTGGCTGACCCCTGCAGCAGGCCTACGCTGGGATGCACCACTACG CAGGCCCCGAAGGC
TGTAACCTCTTCACTATCACCTGCCTCAGGAGTTTGGTATGCGGAACTCATA CAGACATTCTGCC
TTTGGAGCCGTTGCTCTGCTAAAGTCTTTGTGGATCGAGCCACCAACCAGAGCAAGTGT TTTGGGTTT
GTTAGTTTGGACAATCCAAGTGTGCCAGACTGCTATT CAGGCGATGAATGGCTTTCAAATTGGCATG
AAGAGGCTCAAGGTCCAGCTAAAGCGGCCAAGGATGCCAACCGCCTTACTGA
ACGGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGCGC
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Restriction Sites:	Sgfl-Mlul
ACCN:	NM_001172684
Insert Size:	1365 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 style="list-style-type: none">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_001172684.1
RefSeq Size:	3081 bp
RefSeq ORF:	1365 bp
Locus ID:	60677
UniProt ID:	Q96J87
Cytogenetics:	15q23
MW:	47.6 kDa
Gene Summary:	<p>Members of the CELF/BRUNOL protein family contain two N-terminal RNA recognition motif (RRM) domains, one C-terminal RRM domain, and a divergent segment of 160-230 aa between the second and third RRM domains. Members of this protein family regulate pre-mRNA alternative splicing and may also be involved in mRNA editing, and translation. Multiple alternatively spliced transcript variants encoding different isoforms have been identified in this gene. [provided by RefSeq, Feb 2010]</p> <p>Transcript Variant: This variant (2) lacks an in-frame coding exon, as compared to variant 1. The resulting isoform (2) lacks an internal segment, as 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.</p>