

Product datasheet for **SC328552**

BRUNOL6 (CELF6) (NM_001172685) Human Untagged Clone

Product data:

Product Type:	Expression Plasmids
Product Name:	BRUNOL6 (CELF6) (NM_001172685) Human Untagged Clone
Tag:	Tag Free
Symbol:	CELF6
Synonyms:	BRUNOL6
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC328552 representing NM_001172685. Blue=Insert sequence Red=Cloning site Green=Tag(s)

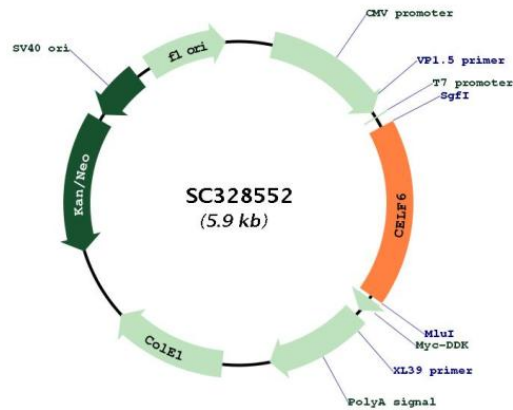
GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCC**GCGATCGCC**
ATGAATCGTCCGATCCAAGTGAAGCCAGCTGCCAGTGAGGGCCGAGGAGAGGACCGAAAGCTGTTTGTG
GGGATGCTGGGCAAGCAGCAGGGTGAGGAGGACGTGACACGCCTGTTCCAGCCCTTTGGCCACATCGAG
GAGTGCACGGTCTCGGGAGTCTGACGGCACCAGTAAAGGCTGTGCCTTTGTGAAGTTCGGGAGTCAA
GGGGAAGCTCAGGCGCCATCCGGGTCTGCACGGCAGCCGACCATGGCGGGCCCTCGTCCAGCCTC
GTGGTCAAGCTGGCGGACACCGACCGGGAGCGCGCTGCGGCGGATGCAGCAGATGGCCGGCCACCTG
GGCGCCTTCCACCCCGCCACTGCCGCTAGGGGCTGCGGCGCCTACACCACGGCGATCCTGCAGCAC
CAGGCGGCCCTGCTGGCGCGGCACAGGGCCAGGCCTAGGCCCGGTGGCGGCAGTGGCGGCCAGATG
CAACACGTGGCGGCTTTAGCCTGGTAGCTGCGCCTCTGTTGCCCGGGCAGCCAACTCCCCGCTGGC
AGCGGCCCTGGCACCCCTCCCAGGTCTTCCGGCGCCCATCGGGGTCAATGGATTCCGGCCCTGACCCCC
CAGACCAATGGCCAGCCGGGCTCCGACACGCTCTACAATAACGGGCTCTCCCTTATCCAGCAGCCTAT
CCGTCGGCCTATGCCCAAGTGAACCTTTTCCAGCAGCCTTCAGCCCTGCCCCAGCAGCAGAGA
GAAGGCCCGAAGGCTGTAACCTTTTCACTATCACCTGCCTCAGGAGTTTGGTATGCGGAACTCATA
CAGACATTCCTGCCCTTTGGAGCCGTTGTCTCTGCTAAAGTCTTTGTGGATCGAGCCACCAACCAGAGC
AAGTGTGTTGGT
TTTCAAATTGGCATGAAGAGGCTCAAGGTCCAGCTAAAGCGGCCCAAGGATGCCAACCGGCCCTTACTGA

ACGCGTACGCGGCCGCTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC

Restriction Sites: SgfI-MluI



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Plasmid Map:


ACCN: NM_001172685

Insert Size: 1035 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:

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_001172685.1](#)

RefSeq Size: 2854 bp

RefSeq ORF: 1035 bp

Locus ID: 60677

UniProt ID: [Q96J87](#)

Cytogenetics: 15q23

MW: 36.2 kDa

Gene Summary: 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]

Transcript Variant: This variant (3) has an alternate 5' sequence, which results in a downstream AUG start codon, and lacks an in-frame coding exon, as compared to variant 1. The resulting isoform (3) has a shorter N-terminus and 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.