

## Product datasheet for SC325616

### NEIL2 (NM\_001135748) Human Untagged Clone

#### Product data:

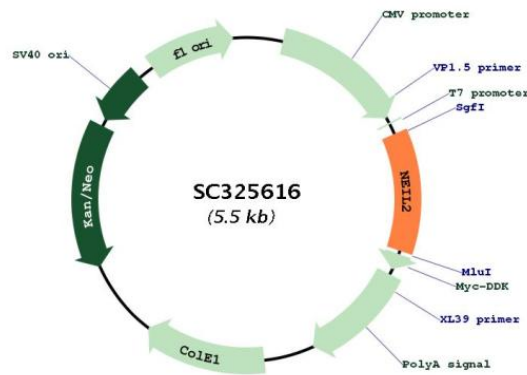
Product Type:	Expression Plasmids
Product Name:	NEIL2 (NM_001135748) Human Untagged Clone
Tag:	Tag Free
Symbol:	NEIL2
Synonyms:	NEH2; NEI2
Mammalian Cell Selection:	Neomycin
Vector:	pCMV6-Entry (PS100001)
E. coli Selection:	Kanamycin (25 ug/mL)
Fully Sequenced ORF:	>SC325616 representing NM_001135748. Blue=Insert sequence Red=Cloning site Green=Tag(s)

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GCTCGTTTAGTGAACCGTCAGAATTTTGTAAACGACTCACTATAGGGCGCCGGGAATTCGTCGACTG
GATCCGGTACCGAGGAGATCTGCCGCCGCGATCGCC
ATGCCAGAAGGGCCGTTGGTGAGGAAATTTACCATTGGTCTCCCCCTTGTGGGTCAGCAGGTGGTC
AAGACAGGGGGCAGCAGTAAGAAGCTACAGCCCGCCAGCCTGCAGTCTGTGGCTCCAGGACACCCAG
GTGAGGTTGGTCTGCACTTTGGTGGTGGTGGCTTCTGGCATTATAATTGTCAGTTGTCTGGAGC
TCTTCCCCAGTGGTCACACCCACCTGTGACATCTGTCTGAGAAGTCCATCGAGGACAAGCCTTAGAA
GCTCTAGGCCAGGCTCAGCCTGTCTGCTATACACTGCTGGACCAGAGATACTTCTCAGGGCTAGGGAAC
ATCATTAAAGAATGAAGCCTTGTACAGAGCTGGGATCCATCCCCTTCTCTCGGTTGAGTCTGAGTGCC
TCGCGTCCGGGAGGTCCTGGTGGATCACGTGGTGGAGTTCAGTACAGCCTGGCTGCAGGGCAAGTTCCAA
GGCAGACCCGACACACAGGTCTACCAGAAAGAAGCAGTGCCTGCTGGCCACCAGGTCATGAAGGAG
GCGTTTGGGCCGAAGATGGGTTACAGAGGCTCACCTGGTGGTGGCCGAGTCCAGCCCAAGTTGTCA
GAGGAGCCAGAGCAGTCCAGTTCTCTAA
ACGCGTACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCTGGAT
TACAAGGATGACGACGATAAGGTTTAAACGGCCGGC
```

Restriction Sites: SgfI-MluI



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**Plasmid Map:**


**ACCN:** NM\_001135748

**Insert Size:** 651 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\\_001135748.1](#)

RefSeq Size:	2016 bp
RefSeq ORF:	651 bp
Locus ID:	252969
UniProt ID:	<a href="#">Q969S2</a>
Cytogenetics:	8p23.1
Protein Families:	Druggable Genome
Protein Pathways:	Base excision repair
MW:	24.1 kDa

**Gene Summary:** This gene encodes a member of the Fpg/Nei family of DNA glycosylases. These glycosylases initiate the first step in base excision repair by cleaving oxidatively damaged bases and introducing a DNA strand break via their abasic site lyase activity. This enzyme is primarily associated with DNA repair during transcription and acts preferentially on cytosine-derived lesions, particularly 5-hydroxyuracil and 5-hydroxycytosine. It contains an N-terminal catalytic domain, a hinge region, and a C-terminal DNA-binding domain with helix-two-turn-helix and zinc finger motifs. This enzyme interacts with the X-ray cross complementing factor 1 scaffold protein as part of a multi-protein DNA repair complex. A pseudogene of this gene has been identified. [provided by RefSeq, Mar 2017]

Transcript Variant: This variant (4) differs in the 5' UTR and lacks an alternate exon compared to variant 1. The encoded isoform (c) has the same N- and C-termini but is shorter compared to isoform a. 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.