

## **Product datasheet for SC309029**

## HLAG (HLA-G) (NM 002127) Human Untagged Clone

**Product data:** 

**Product Type:** Expression Plasmids

Product Name: HLAG (HLA-G) (NM\_002127) Human Untagged Clone

Tag: Tag Free

Symbol: HLAG

Synonyms: MHC-G

Mammalian Cell None

Selection:

Vector: pCMV6-XL5

E. coli Selection: Ampicillin (100 ug/mL)

Fully Sequenced ORF: >OriGene sequence for NM\_002127 edited

ATGGTGGTCATGGCGCCCCGAACCCTCTTCCTGCTGCTCTCGGGGGCCCTGACCCTGACC GAGACCTGGGCGGGCTCCCACTCCATGAGGTATTTCAGCGCCGCCGTGTCCCGGCCCGGC CGCGGGGAGCCCCGCTTCATCGCCATGGGCTACGTGGACGACACGCAGTTCGTGCGGTTC CCGGAGTATTGGGAAGAGGAGACACGGAACACCAAGGCCCACGCACAGACTGACAGAATG AACCTGCAGACCCTGCGCGGCTACTACAACCAGAGCGAGGCCAGTTCTCACACCCTCCAG TGGATGATTGGCTGCGACCTGGGGTCCGACGGACGCCTCCTCCGCGGGTATGAACAGTAT GCCTACGATGGCAAGGATTACCTCGCCCTGAACGAGGACCTGCGCTCCTGGACCGCAGCG GACACTGCGGCTCAGATCTCCAAGCGCAAGTGTGAGGCGGCCAATGTGGCTGAACAAAGG AGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCACAGATACCTGGAGAACGGGAAG GAGATGCTGCAGCGCGCGGACCCCCCAAGACACACGTGACCCACCACCCTGTCTTTGAC TATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCATACTGACC TGGCAGCGGGATGGGAGGACCAGACCCAGGACGTGGAGCTCGTGGAGACCAGGCCTGCA GGGGATGGAACCTTCCAGAAGTGGGCAGCTGTGGTGGTGCCTTCTGGAGAGGAGCAGAGA TACACGTGCCATGTGCAGCATGAGGGGCTGCCGGAGCCCCTCATGCTGAGATGGAAGCAG TCTTCCCTGCCCACCATCCCCATCATGGGTATCGTTGCTGGCCTGGTTGTCCTTGCAGCT 

Restriction Sites: Please inquire

ACCN: NM\_002127

Insert Size: 1000 bp



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## HLAG (HLA-G) (NM\_002127) Human Untagged Clone - SC309029

**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:** The open reading frame of this TrueClone was fully sequenced and found to be a perfect

match to the protein associated to this reference.

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: <u>NM 002127.3</u>, <u>NP 002118.1</u>

6p22.1

 RefSeq Size:
 1840 bp

 RefSeq ORF:
 1017 bp

 Locus ID:
 3135

 UniProt ID:
 P17693

Cytogenetics:

**Protein Families:** Transmembrane

**Protein Pathways:** Allograft rejection, Antigen processing and presentation, Autoimmune thyroid disease, Cell

adhesion molecules (CAMs), Endocytosis, Graft-versus-host disease, Natural killer cell

mediated cytotoxicity, Type I diabetes mellitus, Viral myocarditis

Gene Summary: HLA-G belongs to the HLA class I heavy chain paralogues. This class I molecule is a

heterodimer consisting of a heavy chain and a light chain (beta-2 microglobulin). The heavy chain is anchored in the membrane. HLA-G is expressed on fetal derived placental cells. The heavy chain is approximately 45 kDa and its gene contains 8 exons. Exon one encodes the leader peptide, exons 2 and 3 encode the alpha1 and alpha2 domain, which both bind the peptide, exon 4 encodes the alpha3 domain, exon 5 encodes the transmembrane region, and

exon 6 encodes the cytoplasmic tail. [provided by RefSeq, Jul 2008]

Transcript Variant: This variant (2) differs in the 5' UTR and coding sequence compared to variant 1. The resulting isoform (2) is shorter at the N-terminus 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.