

Product datasheet for SC330202

HLA-DQB1 (NM_001243962) Human Untagged Clone

Product data:

Product Type: Expression Plasmids
Product Name: HLA-DQB1 (NM_001243962) Human Untagged Clone
Tag: Tag Free
Symbol: HLA-DQB1
Synonyms: CELIAC1; HLA-DQB; IDDM1
Vector: pCMV6-Entry (PS100001)
Fully Sequenced ORF: >SC330202 representing NM_001243962.
 Blue=Insert sequence Red=Cloning site Green=Tag(s)

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ATGCTCTGGAAAAAGGCTTTGCGGATCCCCGAGGCTTCGGGCAGCAACTGTGACCTTGATGCTGTCG
ATGCTGAGCACCCAGTGGCTGAGGGCAGAGACTCTCCGAGGATTTCTGTGTACCAAGTTAAGGGCATG
TGCTACTTCACCAACGGGACAGAGCGCTGCGTCTTGAGCAGAAGCATCTATAACCGAGAAGAGATC
GTGCGCTTCGACAGCGACGTGGGGGAGTCCGGGCGGTGACGCTGCTGGGGCTGCCTGCCGCCGAGTAC
TGAACAGCCAGAAGGACATCCTGGAGAGGAAACGGGCGGCGGTGACAGGGTGTGCAGACACAACACTAC
CAGTTGGAGCTCCGCACGACCTTGACGCGCGAGTGGAGCCACAGTGACCATCTCCCCATCCAGGACA
GAGGCCCTCAACCACCACAACCTGCTGGTCTGCTCGGTGACAGATTTCTATCCAGCCAGATCAAAGTC
CGGTGGTTTCGGAATGACCAGGAGGAGACAGCTGGCGTTGTGTCCACCCCTTATTAGGAATGGTGAC
TGGACCTTCAGATCCTGGTGATGCTGGAATGACTCCCCAGCGTGGAGACGTCTACACCTGCCACGTG
GAGCACCCAGCTCCAGAGCCCATCACCGTGGAGTGGCGGGCTCAATCTGAATCTGCCAGAGCAAG
ATGCTGAGTGGCATTGGAGGCTTCGTGCTGGGGCTGATCTTCTCGGGCTGGGCCTTATCATCCATCAC
AGGAGTCAGAAAGGGCTCCTGCAC
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Restriction Sites: SgfI-MluI

ACCN: NM_001243962

Insert Size: 786 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).

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).


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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:	<u>NM_001243962.1</u>
RefSeq Size:	1638 bp
RefSeq ORF:	786 bp
Locus ID:	3119
UniProt ID:	<u>P01920</u>
Cytogenetics:	6p21.32
Protein Families:	Transmembrane
Protein Pathways:	Allograft rejection, Antigen processing and presentation, Asthma, Autoimmune thyroid disease, Cell adhesion molecules (CAMs), Graft-versus-host disease, Systemic lupus erythematosus, Type I diabetes mellitus, Viral myocarditis
MW:	29.7 kDa
Gene Summary:	<p>HLA-DQB1 belongs to the HLA class II beta chain paralogs. This class II molecule is a heterodimer consisting of an alpha (DQA) and a beta chain (DQB), both anchored in the membrane. It plays a central role in the immune system by presenting peptides derived from extracellular proteins. Class II molecules are expressed in antigen presenting cells (APC: B lymphocytes, dendritic cells, macrophages). The beta chain is approximately 26-28 kDa and it contains six exons. Exon 1 encodes the leader peptide, exons 2 and 3 encode the two extracellular domains, exon 4 encodes the transmembrane domain and exon 5 encodes the cytoplasmic tail. Within the DQ molecule both the alpha chain and the beta chain contain the polymorphisms specifying the peptide binding specificities, resulting in up to four different molecules. Typing for these polymorphisms is routinely done for bone marrow transplantation. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2011]</p> <p>Transcript Variant: This variant (3) has the same exon combination as variant 1 but represents the DQB1*02:01:01:01 allele of the HLA-DQB1 gene, as represented in the alternate locus group ALT_REF_LOCI_2 of the reference genome. It encodes isoform 1. Sequence Note: The RefSeq transcript and protein were derived from genomic sequence to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.</p>