

Customer: Your Company
Project: Your Favorite Antigen
Cell Line: Your Hybridoma

Sequencing ID: SEQ###

CONFIDENTIAL

Sequencing Overview

Productive Immunoglobulin Domain Sequence	Reads Aligned to Consensus	V Domain Sequence Q Score >40	Constant Region from Sequence
V _H	≤15	100.0%	IgG1
V _L	≤15	100.0%	Kappa

Recommended Analysis Tools

We recommend the following free online tools for DNA-sequence analysis of immunoglobulin variable regions:

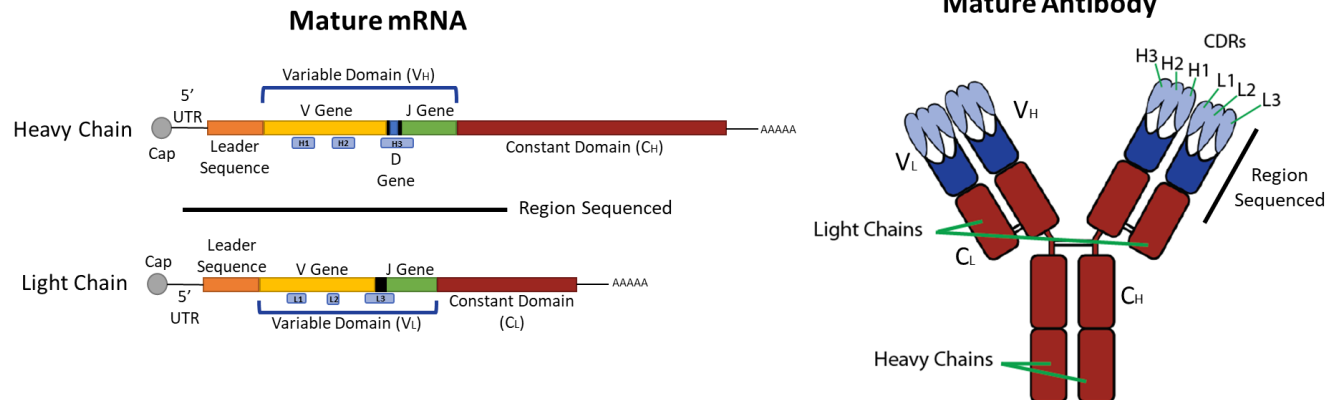
NCBI [Nucleotide BLAST](#)

[IMGT/V-Quest program](#)

NCBI [IgBLAST](#)

Note: Be aware that if you copy sequence directly from this pdf, your text will contain paragraph returns that must be removed prior to BLAST analysis.

Regions Sequenced



Heavy Chain Sequence

DNA Sequence

Leader sequence (underlined) is translated and targets the nascent polypeptide to the endoplasmic reticulum (ER). It is cleaved during translocation into the ER and is not part of the mature antibody.

```
ATGGAAAGGCACTGGATCTTTCTTCTTCTGTTTTAGTAAGTGCAGGTGTCCACTCCgaggttcagctccagcagctctggg
actgtgctggcaaggcctggggctcaggaagatgtcctgcaagactctggctacacattaccagctactggatgactggtaaaacagaggcctggacag
ggtctggaatggataggggctattatcctggaaatagtatactagctacaaccagaagtcaaggccaaggccaaactgactgactgacatccgccagcact
gcctacatggagctcagcagcctgacaaatgaggactctgcggtctattactgtacaagatccgggggtaaccaatattactattctatggactcctggggtcaagg
aacgtcagtcaccgtctcctcag
```

Predicted Protein Sequence (V_H)

Complementarity determining regions (CDRs) are underlined.

```
EVQLQQSGTFLARPGASVKMSCKTSGYTFTSYWMHWVKQRPGQGLEWIGAIYPGNSDTSYNQKFKGKAKLTAVT
SASTAYMELSSLTNEEDSAVYYCTRSGGNQYYYSMDSWGQGTSTVSS
```

Light Chain Sequence

DNA Sequence

Leader sequence is underlined.

```
ATGAAGTCACAGACCCAGGTCTTCGTATTTCTACTGCTCTGTGTGTCTGGTGCTCATGGGagtattgtgatgaccagac
tccaaattcctgctgtttcagcaggagacagggtaccataaacctgcaaggccagtcagattgtgagtaatgatgtagcttggtaccaacagaagtcagggcagc
ctcctaaactgctgatatactatgcatccaatcgctacactggagtcctgatcgcttactggcagtgatagggacggatttcacttccatcagcactgtgacag
gctgaagacctggcagtttattctgtcagcaggattataggtctcccacgttcggtgctgggaccaagctggagctgaaac
```

Predicted Protein Sequence (V_L)

Complementarity determining regions (CDRs) are underlined.

```
DIVMTQTPKFLVLSAGDRVPITCKASQSVSNDVAWYQQKPGQSPKLLIYASSNRYTGVDPDRFTGSGYGTDFFTIST
VQAEDLAVYFCQQDYSSPPFGAGTKLEIK
```

Note: Additional sequence annotation, including 5' UTR, partial constant region, and V/D/J gene identity, are available upon request.

Methods

Total cytoplasmic RNA was isolated from the hybridoma cell line culture (1×10^6 cells). RNA was reverse transcribed into cDNA using isotype-specific antisense primers and SMARTScribe Reverse Transcriptase with a template switch oligonucleotide to capture the 5' end of the mRNA. The resulting V_H and V_L cDNA was amplified by PCR, size confirmed by agarose gel electrophoresis, and sequenced using Oxford nanopore sequencing. A minimum of 15x coverage is required (>99.99% sequence accuracy) and all sequences were analyzed to ensure no process contamination. Additional sequence analysis is available upon request.

Important Notes

To our knowledge, the sequence reported here is accurate.

These results and the information contained in this report are for research use only. They are not intended for diagnostic or therapeutic use.

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