



Monoclonal Sequencing Report

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Project Name:

Protein Production Code Number:

PO Number:

Your main Fusion Representative: Richard Buick

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Start Date:

Completion Date:

Proposed plan for client:

Monoclonal sequencing of cell line XXX

Name person(s) responsible at this stage:

Experimental Report

mRNA was extracted from the hybridoma cell pellets on xx/xx/xx. Total RNA was extracted from the pellets using Fusion Antibodies Ltd in-house RNA extraction protocol.

RT-PCR

cDNA was created from the RNA by reverse-transcription with an oligo(dT) primer. PCR reactions using variable domain primers to amplify both the VH and VL regions of the monoclonal antibody DNA giving the following bands:

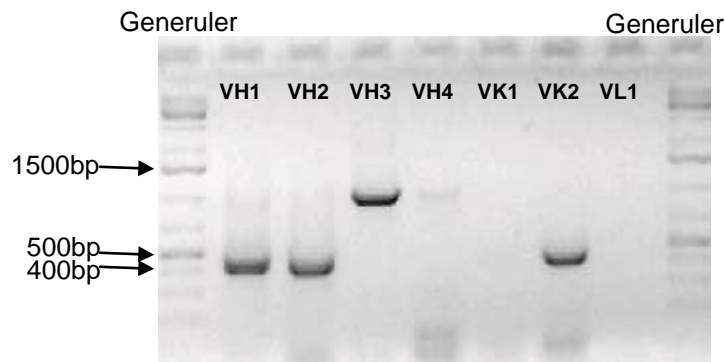


Figure 1: PCR using several combinations of Ig variable domain primers

The VH and VL products were cloned into the Invitrogen sequencing vector pCR2.1 and transformed into TOP10 cells and screened by PCR for positive transformants. Selected colonies were picked and analyzed by DNA sequencing on an ABI3130xl Genetic Analyzer, the result may be seen below.

Sequencing Results

Heavy Chain Alignment (V_H underlined)

		1	50
VH5-8	(1)	MYLGLSCVFIVFLN <u>GVQSEVKLEESGGGLVQ</u> PGGSMKLSCAASGFIFSD	
VH5-3	(1)	MYLGLSCVFIVFLN <u>GVQSEVKLEESGGGLVQ</u> PGGSMKLSCAASGFIFSD	
VH4-8	(1)	MYLGLSCVFIVFLN <u>SVQSEVKLEESGGGLVQ</u> PGGSMKLSCAASGFIFSD	
VH4-7	(1)	MYLGLSCVFIVFLN <u>GVQSEVKLEESGGGLVQ</u> PGGSMKLSCAASGFIFSD	
VH4-6	(1)	MYLGLSCVFIVFLN <u>GVQSEVKLEESGGGLVQ</u> PGGSMKLSCAASGFIFSD	
VH4-5	(1)	MYLGLSCVFIVFLN <u>GVQSEVKLEESGGGLVQ</u> PGGSMKLSCAASGFIFSD	
VH4-3	(1)	MYLGLSCVFIVFLN <u>GVQSEVKLEESGGGLVQ</u> PGGSMKLSCAASGFIFSD	
Consensus	(1)	MYLGLSCVFIVFLN <u>GVQSEVKLEESGGGLVQ</u> PGGSMKLSCAASGFIFSD	
		51	100
VH5-8	(51)	AWMDWVRQSP <u>PEKGLEWVAEIRSKANNHATYYAESV</u> KGRFTISRDDSKSSV	
VH5-3	(51)	AWMDWVRQSP <u>PEKGLEWVAEIRSKANNHATYYAESV</u> KGRFTISRDDSKSSV	
VH4-8	(51)	AWMDWVRQSP <u>PEKGLEWVAEIRSKANNHATYYAESV</u> KGRFTISRDDSKSSV	
VH4-7	(51)	AWMDWVRQSP <u>PEKGLEWVAEIRSKANNHATYYAESV</u> KGRFTISRDDSKSSV	
VH4-6	(51)	AWMDWVRQSP <u>PEKGLEWVAEIRSKANNHATYYAESV</u> KGRFTISRDDSKSSV	
VH4-5	(51)	AWMDWVRQSP <u>PEKGLEWVAEIRSKANNHATYYAESV</u> KGRFTISRDDSKSSV	
VH4-3	(51)	AWMDWVRQSP <u>PEKGLEWVAEIRSKANNHATYYAESV</u> KGRFTISRDDSKSSV	
Consensus	(51)	AWMDWVRQSP <u>PEKGLEWVAEIRSKANNHATYYAESV</u> KGRFTISRDDSKSSV	
		101	150
VH5-8	(101)	YLQMNSLRAEDTGIYYCTRDFDSWGQGTTLTVSSAKTT <u>PP</u> PPVYPLAPGSL	
VH5-3	(101)	YLQMNSLRAEDTGIYYCTRDFDSWGQGTTLTVSSAKTT <u>PP</u> PPVYPLAPGSL	
VH4-8	(101)	YLQMNSLRAEDTGIYYCTRDFDSWGQGTTLTVSSAKTT <u>PPSVF</u> PPLA----	
VH4-7	(101)	YLQMNSLRAEDTGIYYCTRDFDSWGQGTTLTVSSAKTT <u>PPSVF</u> PPLA----	
VH4-6	(101)	YLQMNSLRAEDTGIYYCTRDFDSWGQGTTLTVSSAKTT <u>PPSVF</u> PPLA----	
VH4-5	(101)	YLQMNSLRAEDTGIYYCTRDFDSWGQGTTLTVSSAKTT <u>LP</u> SVFPLA----	
VH4-3	(101)	YLQMNSLRAEDTGIYYCTRDFDSWGQGTTLTVSSAKTT <u>PPSVF</u> PPLA----	
Consensus	(101)	YLQMNSLRAEDTGIYYCTRDFDSWGQGTTLTVSSAKTT <u>PPSVF</u> PPLA	

Key to amino acid shading:

Black	non-similar residues
Blue on cyan	consensus residue derived from a block of residues at a given position
Black on green	residues similar in structure to consensus residue or each other when no consensus found
Red on yellow	consensus residue derived from a completely conserved residue at a given position
Green	residue weakly similar to consensus residue at given position

VH Consensus Sequence:

EVKLEESGGGLVQPGGSMKLSCAASGFIFSDAWMDWVRQSPEKGLEWVAEIRS
 KANNHATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTRDFDSWGQ
 GTTLTVSS

VH CDR Annotation (IMGT System)

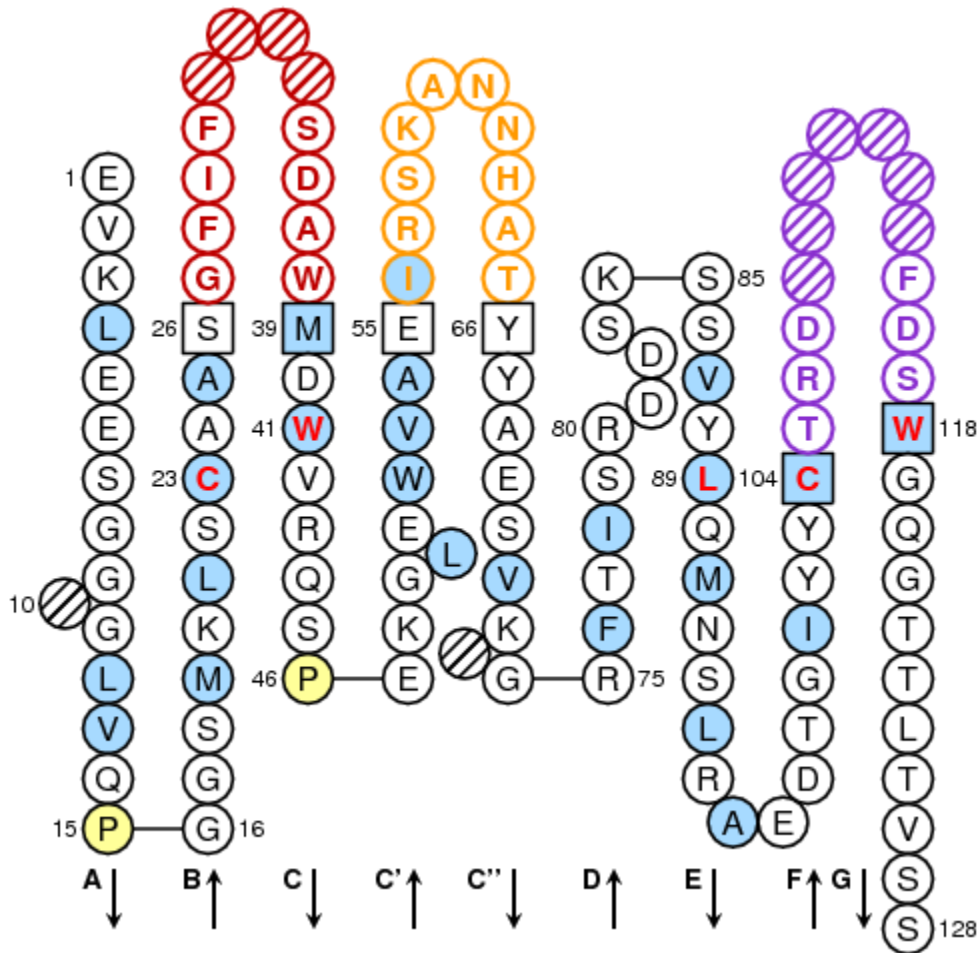


Figure 2: Graphical representation of the CDR loops.

Ref: Lefranc, M.-P. et al., Dev. Comp. Immunol., 27, 55-77 (2003) [PMID: 12477501](https://pubmed.ncbi.nlm.nih.gov/12477501/)

Key to amino acid shading:

Blue shaded circles are hydrophobic (non-polar) residues in frameworks 1-3 at sites that are hydrophobic in the majority of antibodies.

Yellow shaded circles are proline residues

Squares are key residues at the start and end of the CDR

Red amino acids in the framework are structurally conserved amino acids

VH CDR Identification by Kabat Numbering System

CDR H1

FIFSDAWMD

(DNA sequence: TTCATTTTTAGTGACGCCTGGATGGAC)

CDR H2

IRSKANNHATYYAESVKG

(DNA sequence:

ATTAGAAGCAAAGCTAACAATCATGCAACATACTATGCTGAGTCTGTGAAAG
GG)

CDR H3

DFDS

(DNA sequence: GACTTTGACTCC)

Light Chain Alignment (V_L underlined)

		1	50
VL3-8	(1)	MVL <u>MLLLL</u> LWVSGTCGDIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTR	
VL3-5	(1)	MVL <u>MLLLL</u> LWVSGTCGDIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTR	
VL3-7	(1)	MVL <u>MLLLL</u> LWVSGTCGDIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTR	
VL3-4	(1)	MVL <u>MLLLL</u> LWVSGTCGDIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTR	
VL3-3	(1)	MVL <u>MLLLL</u> LWVSGTCGDIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTR	
VL3-2	(1)	MVL <u>MLLLL</u> LWVSGTCGDIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTR	
VL3-1	(1)	MVL <u>MLLLL</u> LWVSGTCGDIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTR	
Consensus	(1)	MVL <u>MLLLL</u> LWVSGTCGDIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTR	
		51	100
VL3-8	(51)	KNYLAWYQQKPGQSPKLL <u>I</u> YWASSRESGVPDRFTGSGSGTDFTLT <u>I</u> SSVQ	
VL3-5	(51)	KNYLAWYQQKPGQSPKLL <u>I</u> YWASSRESGVPDRFTGSGSGTDFTLT <u>I</u> SSVQ	
VL3-7	(51)	KNYLAWYQQKPGQSPKLL <u>I</u> YWASSRESGVPDRFTGSGSGTDFTLT <u>I</u> SSVQ	
VL3-4	(51)	KNYLAWYQQKPGQSPKLL <u>I</u> YWASSRESGVPDRFTGSGSGTDFTLT <u>I</u> SSVQ	
VL3-3	(51)	KNYLAWYQQKPGQSPKLL <u>I</u> YWASSRESGVPDRFTGSGSGTDFTLT <u>I</u> SSVQ	
VL3-2	(51)	KNYLAWYQQKPGQSPKLL <u>I</u> YWASSRESGVPDRFTGSGSGTDFTLT <u>I</u> SSVQ	
VL3-1	(51)	KNYLAWYQQKPGQSPKLL <u>I</u> YWASSRESGVPDRFTGSGSGTDFTLT <u>I</u> SSVQ	
Consensus	(51)	KNYLAWYQQKPGQSPKLL <u>I</u> YWASSRESGVPDRFTGSGSGTDFTLT <u>I</u> SSVQ	
		101	150
VL3-8	(101)	AEDLAVYYCKQSYNLRRTFGGGTKLEIKRADAAPT <u>V</u> SIFPPSSEQLTSGGA	
VL3-5	(101)	AEDLAVYYCKQSYNLRRTFGGGTKLEIKRADAAPT <u>V</u> SIFPPSSEQLTSGGA	
VL3-7	(101)	AEDLAVYYCKQSYNLRRTFGGGTKLEIKRADAAPT <u>V</u> SIFPPSSEQLTSGGA	
VL3-4	(101)	AEDLAVYYCKQSYNLRRTFGGGTKLEIKRADAAPT <u>V</u> SIFPPSSEQLTSGGA	
VL3-3	(101)	AEDLAVYYCKQSYNLRRTFGGGTKLEIKRADAAPT <u>V</u> SIFPPSSEQLTSGGA	
VL3-2	(101)	AEDLAVYYCKQSYNLRRTFGGGTKLEIKRADAAPT <u>V</u> SIFPPSSEQLTSGGA	
VL3-1	(101)	AEDLAVYYCKQSYNLRRTFGGGTKLEIKRADAAPT <u>V</u> SIFPPSSEQLTSGGA	
Consensus	(101)	AEDLAVYYCKQSYNLRRTFGGGTKLEIKRADAAPT <u>V</u> SIFPPSSEQLTSGGA	
		151	162
VL3-8	(151)	SVVCFLN <u>N</u> FYPK	
VL3-5	(151)	SVVCFLN <u>N</u> FYPK	
VL3-7	(151)	SVVCFLN <u>N</u> FYPK	
VL3-4	(151)	SVVCFLN <u>N</u> FYPK	
VL3-3	(151)	SVVCFLN <u>N</u> FYPK	
VL3-2	(151)	SVVCFLN <u>N</u> FYPK	
VL3-1	(151)	SVVCFLN <u>N</u> FYPK	
Consensus	(151)	SVVCFLN <u>N</u> FYPK	

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Black on green	residues similar in structure to consensus residue or each other when no consensus found
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Green	residue weakly similar to consensus residue at given position

VL Consensus Sequence

DIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTRKNYLAWYQQKPGQSPKLLI
 YWASSRESGVPDRFTGSGSGTDFLTITSSVQAEDLAVYYCKQSYNLRITFGGGTK
 LEIKR

VL CDR Annotation (IMGT System)

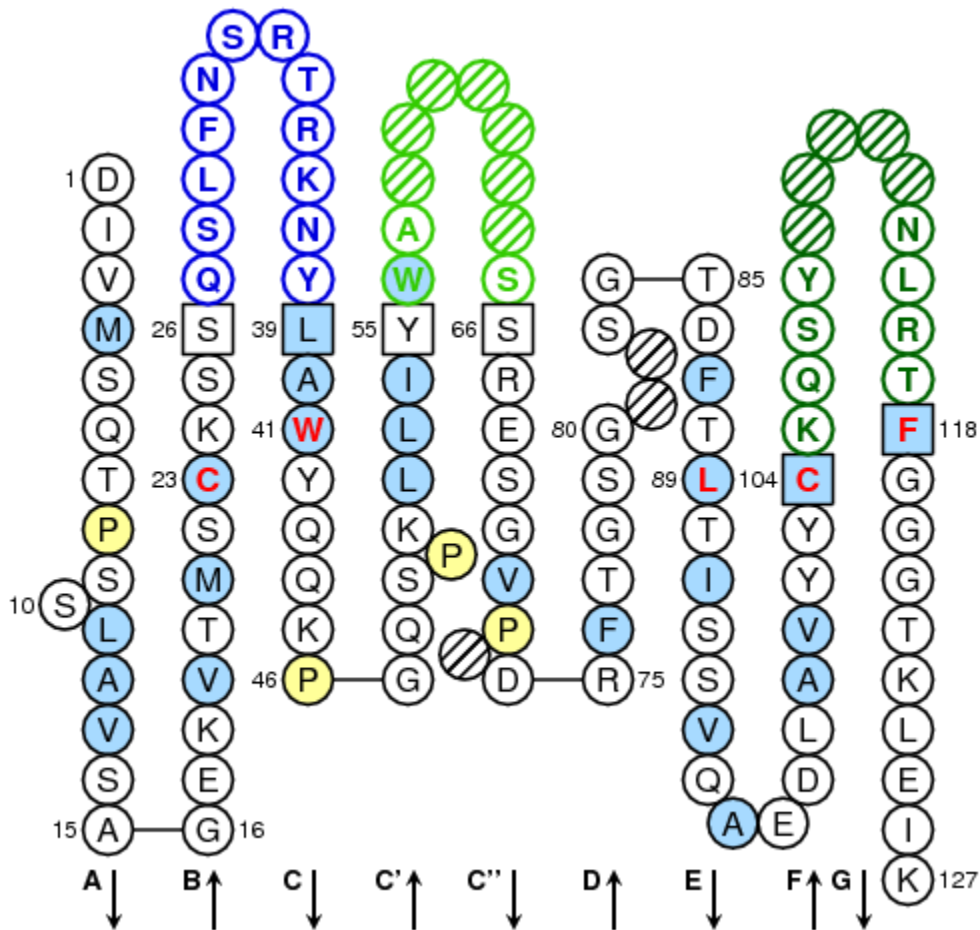


Figure 3: Graphical representation of the CDR loops.

Ref: Lefranc, M.-P. et al., Dev. Comp. Immunol., 27, 55-77 (2003) [PMID: 12477501](https://pubmed.ncbi.nlm.nih.gov/12477501/)

Key to amino acid shading:

Blue shaded circles are hydrophobic (non-polar) residues in frameworks 1-3 at sites that are hydrophobic in the majority of antibodies.

Yellow shaded circles are proline residues

Squares are key residues at the start and end of the CDR

Red amino acids in the framework are structurally conserved amino acids

CDR Identification by Kabat Numbering System

CDR L1

KSSQSLFNSRTRKNYLA

(DNA sequence:

AAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCGAAAGAACTACTTGGCT)

CDR L2

WASSRES

(DNA sequence: TGGGCATCCAGTAGGGAATCT)

CDR L3

KQSYNLRT

(DNA sequence: AAGCAATCTTATAATCTTCGGACG)

Appendix

VH Sequencing Results

VH4-3

DNA Sequence:

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCA
TGAAACTCTCTTGTGCTGCCTCTGGATTCATTTTTAGTGACGCCTGGATGGAC
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGAA
GCAAAGCTAACAATCATGCAACATACTATGCTGAGTCTGTGAAAGGGAGGTT
CACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAGC
TTAAGAGCTGAAGACACTGGCATTATTTACTGTACCAGGGACTTTGACTCCTG
GGCCAAGGCACCACTCTCACAGTCTCCTCA

AA Sequence:

EVKLEESGGGLVQPGGSMKLSCAASGFIFSDAWMDWVRQSPEKGLEWVAEIRS
KANNHATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTRDFDSWGQ
GTTLTVSS

VH4-5

DNA Sequence:

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCA
TGAAACTCTCTTGTGCTGCCTCTGGATTCATTTTTAGTGACGCCTGGATGGAC
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGAA
GCAAAGCTAATAATCATGCAACATACTATGCTGAGTCTGTGAAAGGGAGGTT
CACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAGC
TTAAGAGCTGAAGACACTGGCATTATTTACTGTACCAGGGACTTTGACTCCTG
GGCCAAGGCACCACTCTCACAGTCTCCTCA

AA Sequence:

EVKLEESGGGLVQPGGSMKLSCAASGFIFSDAWMDWVRQSPEKGLEWVAEIRS
KANNHATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTRDFDSWGQ
GTTLTVSS

VH4-6

DNA Sequence:

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCA
TGAAACTCTCTTGTGCTGCCTCTGGATTCATTTTTAGTGACGCCTGGATGGAC
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGAA
GCAAAGCTAATAATCATGCAACATACTATGCTGAGTCTGTGAAAGGGAGGTT
CACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAGC
TTAAGAGCTGAAGACACTGGCATTATTACTGTACCAGGGACTTTGACTCCTG
GGCCAAGGCACCACTCTCACAGTCTCCTCA

AA Sequence:

EVKLEESGGGLVQPGGSMKLSCAASGFIFSDAWMDWVRQSPEKGLEWVAEIRS
KANNHATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTRDFDSWGQ
GTTLTVSS

VH4-7

DNA Sequence:

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCA
TGAAACTCTCTTGTGCTGCCTCTGGATTCATTTTTAGTGACGCCTGGATGGAC
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGAA
GCAAAGCTAATAATCATGCAACATACTATGCTGAGTCTGTGAAAGGGAGGTT
CACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAGC
TTAAGAGCTGAAGACACTGGCATTATTACTGTACCAGGGACTTTGACTCCTG
GGCCAAGGCACCACTCTCACAGTCTCCTCA

AA Sequence:

EVKLEESGGGLVQPGGSMKLSCAASGFIFSDAWMDWVRQSPEKGLEWVAEIRS
KANNHATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTRDFDSWGQ
GTTLTVSS

VH4-8

DNA Sequence:

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCA
TGAAACTCTCTTGTGCTGCCTCTGGATTCATTTTTAGTGACGCCTGGATGGAC
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGAA
GCAAAGCTAATAATCATGCAACATACTATGCTGAGTCTGTGAAAGGGAGGTT
CACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAGC
TTAAGAGCTGAAGACACTGGCATTATTACTGTACCAGGGACTTTGACTCCTG
GGCCAAGGCACCACTCTCACAGTCTCCTCA

AA Sequence:

EVKLEESGGGLVQPGGSMKLSCAASGFIFSDAWMDWVRQSPEKGLEWVAEIRS
KANNHATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTRDFDSWGQ
GTTLTVSS

VH5-3

DNA Sequence:

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCA
TGAAACTCTCTTGTGCTGCCTCTGGATTCATTTTTAGTGACGCCTGGATGGAC
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGAA
GCAAAGCTAATAATCATGCAACATACTATGCTGAGTCTGTGAAAGGGAGGTT
CACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAGC
TTAAGAGCTGAAGACACTGGCATTATTACTGTACCAGGGACTTTGACTCCTG
GGCCAAGGCACCACTCTCACAGTCTCCTCA

AA Sequence:

EVKLEESGGGLVQPGGSMKLSCAASGFIFSDAWMDWVRQSPEKGLEWVAEIRS
KANNHATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTRDFDSWGQ
GTTLTVSS

VH5-8

DNA Sequence:

GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCA
TGAAACTCTCTTGTGCTGCCTCTGGATTCATTTTTAGTGACGCCTGGATGGAC
TGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGAA
GCAAAGCTAATAATCATGCAACATACTATGCTGAGTCTGTGAAAGGGAGGTT
CACCATCTCAAGAGATGATTCCAAAAGTAGTGTCTACCTGCAAATGAACAGC
TTAAGAGCTGAAGACACTGGCATTATTACTGTACCAGGGACTTTGACTCCTG
GGCCAAGGCACCACTCTCACAGTCTCCTCA

AA Sequence:

EVKLEESGGGLVQPGGSMKLSCAASGFIFSDAWMDWVRQSPEKGLEWVAEIRS
KANNHATYYAESVKGRFTISRDDSKSSVYLQMNSLRAEDTGIYYCTRDFDSWGQ
GTTTLTVSS

VL Sequencing Results

VL3-1

DNA Sequence:

GACATTGTGATGTCACAGACTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGA
AGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCG
AAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
CTGATCTACTGGGCATCCAGTAGGGAATCTGGGGTCCCTGATCGCTTCACAG
GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA
AGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCCGGTG
GCGGCACCAAGCTGGAAATCAAACGG

AA Sequence:

DIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTRKNYLAWYQQKPGQSPKLLI
YWASSRESGVPDRFTGSGSGTDFLTISVQAEDLAVYYCKQSYNLRFTGGGTK
LEIKR

VL3-2

DNA Sequence:

GACATTGTGATGTCACAGACTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGA
AGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCG
AAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
CTGATCTACTGGGCATCCAGTAGGGAATCTGGGGTCCCTGATCGCTTCACAG
GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA
AGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCCGGTG
GCGGCACCAAGCTGGAAATCAAACGG

AA Sequence:

DIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTRKNYLAWYQQKPGQSPKLLI
YWASSRESGVPDRFTGSGSGTDFLTISVQAEDLAVYYCKQSYNLRFTGGGTK
LEIKR

VL3-3

DNA Sequence:

GACATTGTGATGTCACAGACTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGA
AGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCG
AAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
CTGATCTACTGGGCATCCAGTAGGGAATCAGGGGTCCCTGATCGCTTCACAG
GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA
AGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCCGGTG
GCGGCACCAAGCTGGAAATCAAACGG

AA Sequence:

DIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTRKKNYLAWYQQKPGQSPKLLI
YWASSRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTEFGGK
LEIKR

VL3-4

DNA Sequence:

GACATTGTGATGTCACAGACTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGA
AGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCG
AAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
CTGATCTACTGGGCATCCAGTAGGGAATCTGGGGTCCCTGATCGCTTCACAG
GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA
AGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCCGGTG
GCGGCACCAAGCTGGAAATCAAACGG

AA Sequence:

DIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTRKKNYLAWYQQKPGQSPKLLI
YWASSRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYNLRTEFGGK
LEIKR

VL3-5

DNA Sequence:

GACATTGTGATGTCACAGACTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGA
AGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCG
AAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
CTGACCTACTGGGCATCCAGTAGGGAATCTGGGGTCCCTGATCGCTTCACAG
GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA
AGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCCGGTG
GCGGCACCAAGCTGGAAATCAAACGG

AA Sequence:

DIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTRKNYLAWYQQKPGQSPKLLT
YWASSRESGVPDRFTGSGSGTDFLTISSVQAEDLAVYYCKQSYNLRFTFGGGTK
LEIKR

VL3-7

DNA Sequence:

GACATTGTGATGTCACAGACTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGA
AGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCG
AAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
CTGATCTACTGGGCATCCAGTAGGGAATCTGGGGTCCCTGATCGCTTCACAG
GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA
AGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCCGGTG
GCGGCACCAAGCTGGAAATCAAACGG

AA Sequence:

DIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTRKNYLAWYQQKPGQSPKLLI
YWASSRESGVPDRFTGSGSGTDFLTISSVQAEDLAVYYCKQSYNLRFTFGGGTK
LEIKR

VL3-8

DNA Sequence:

GACATTGTGATGTCACAGACTCCATCCTCCCTGGCTGTGTCAGCAGGAGAGA
AGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGTTCAACAGTAGAACCCG
AAAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
CTGATCTACTGGGCATCCAGTAGGGAATCTGGGGTCCCTGATCGCTTCACAG
GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTGTGCAGGCTGA
AGACCTGGCAGTTTATTACTGCAAGCAATCTTATAATCTTCGGACGTTCCGGTG
GCGGCACCAAGCTGGAAATCAAACGG

AA Sequence:

DIVMSQTPSSLAVSAGEKVTMSCKSSQSLFNSRTRKNYLAWYQQKPGQSPKLLI
YWASSRESGVPDRFTGSGSGTDFLTISVQAEDLAVYYCKQSYNLRFTFGGGTK
LEIKR