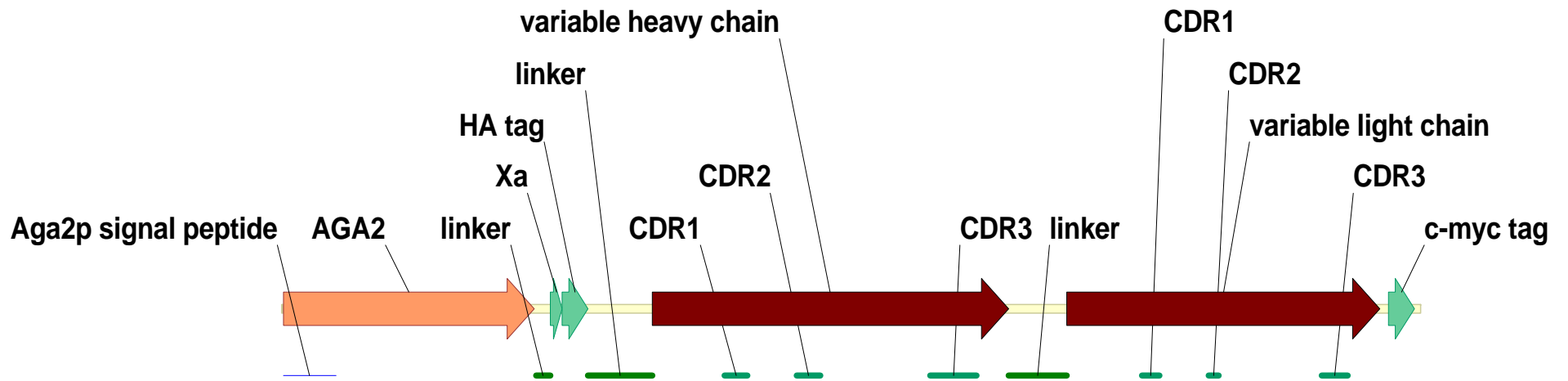


HL4-MG (pPNL6)



HL4-MG (pPNL6)

1176 bp

HL4-MG (pPNL6)

Aga2p signal peptide

AGA2

+1 M Q L L R C F S I F S V I A S V L A Q E L T T I C E Q I P S P T L E
 1 ATGCAGTTAC TTCGCTGTTT TTCAATATTT TCTGTTATTG CTTAGTTTT AGCACAGGAA CTGACAAC TA TATGCGAGCA AATCCCCTCA CCAACTT TAG
 TACGTCAATG AAGCGACAAA AAGTTATAAA AGACAATAAC GAAGTCAAAA TCGTGTCTT GACTGTTGAT ATACGCTCGT TTAGGGGAGT GGTGAAATC

AGA2

+1 E S T P Y S L S T T T I L A N G K A M Q G V F E Y Y K S V T F V S N
 101 AATCGACGCC G TACTCTTG TCAACGACTA CTATTTTGGC CAACGGGAAG GCAATGCAAG GAGTTTTTGA ATATTACAAA TCAGTAACGT TTGTGAGTAA
 TTAGCTGCGG CATGAGAAAC AGTTGCTGAT GATAAAACCG GTTGCCCTTC CGTTACGTTC CTCAAAAAC TATAATGTTT AGTCATTGCA AACAGTCATT

AGA2

Xa

HA tag

+1 N C G S H P S T T S K G S P I N T Q Y V F K D N S S T I E G R Y P Y
 201 TTGCGGTTCT CACCCCTCAA CAACTAGCAA AGGCAGCCCC ATAAACACAC AGTATGTTTT TAAGGACAAT AGCTCGACGA TTGAAGGTAG ATACCCATAC
 AACGCCAAGA GTGGGGAGTT GTTGATCGTT TCCGTCGGGG TATTTGTGTG TCATACAAA ATTCCGTGTA TCGAGCTGCT AACTTCCATC TATGGGTATG

linker

HA tag

variable heavy chain

+1 D V P D Y A L Q A S G G G G S G G G G S G G G G S A S Q V Q L V E S
 301 GACGTTCCAG ACTACGCTCT GCAGGCTAGT GGTGGTGGTG GTTCTGGTGG TGGTGGTTCT GGTGGTGGTG GTTCTGCTAG CCAGGTGCAG CTGGTGGAGT
 CTGCAAGGTC TGATGCGAGA CGTCCGATCA CCACCACCAC CAAGACCACC ACCACCAAGA CCACCACCAC CAAGACGATC GGTCCACGTC GACCACCTCA

linker

variable heavy chain

CDR1

+1 S E G G L V Q P G G S L R L S C A A S G F T F S S Y E M N W V R Q A
 401 CTGAGGGAGG CTTGGTACAG CCTGGAGGGT CCCTGAGACT CTCCTGTGCA GCCTCTGGAT TCACCTTCAG TAGTTATGAA ATGAACTGGG TCCGCCAGGC
 GACTCCCTCC GAACCATGTC GGACTCCCA GGGACTCTGA GAGGACACGT CGGAGACCTA AGTGAAGTC ATCAATACTT TACTTGACCC AGCGGTCCG

variable heavy chain

CDR2

+1 A P G K G L E W V S R I D G D G S S T N Y A D S V K G R F T I S R D
 501 TCCAGGTAAG GGGCTGGAGT GGGTCTCACG TATTGATGGT GATGGGAGCA GCACAAACTA CGCGGACTCC GTGAAGGGCC GATTCACCAT CTCCAGAGAC
 AGGTCCATC CCCGACCTCA CCCAGAGTGC ATAACTACCA CTACCCTCGT CGTGTGTTGAT GCGCCTGAGG CACTTCCCGG CTAAGTGGTA GAGGTCTCTG

variable heavy chain

CDR3

+1 N A K S T L Y L Q M N S L R A E D T A V Y Y C T R A R Y F G S V S P
 601 AACGCCAAGA GCACGCTGTA TCTGCAAATG AATAGTCTGA GAGCCGAGGA CACGGCTGTG TATTACTGTA CAAGGGCCAG ATACTTTGGT TCGGTGAGCC
 TTGCGGTTCT CGTGCGACAT AGACGTTTAC TTATCAGACT CTCGGCTCCT GTGCCGACAC ATAATGACAT GTTCCCGGTC TATGAAACCA AGCCACTCGG

