SEQUENCE LISTING

SEQ ID NO: 1 (CDR-1-V_L-αvß5)
RCALVM

SEQ ID NO: 2 (CDR-2-V_L-αvß5)
QDIGSD

SEQ ID NO: 3 (CDR-3-V_L-αvß5)
AGYKSYSDDGHG

SEQ ID NO: 4 (CDR-1-V_H-αvß5)
PLRNVWIS

SEQ ID NO: 5 (CDR-2-V_H-αvß5)
CIYTGRDWP

SEQ ID NO: 6 (CDR-3-V_H-αvß5)
ARIVYGGAGYRL

SEQ ID NO: 7 (FR-1-V_L-αvß5)
MDTRAPTQLLGLLLLWLPGA

SEQ ID NO: 8 (FR-2-V_L-αvß5)
TQTPPSVEAAVGGTVTINCQAS

SEQ ID NO: 9 (FR-3-V_L-αvß5)
LAWYQQKPGQPPKLLIYSASSLASGVPSRFKASGSGTQFTLTISDVQCDDAATYSC

SEQ ID NO: 10 (DTM-αvß5)
GLNICTSGSATSCEECLLIHPKCAWCSKEDFGSPRSITSRCDLRANLVKNGCGGEIESPAS
SFHVLRSLPLSSKGSGSAGWDVIQMTPQEIAVNLRPGDKTTFQLQVRQVEDYPVDLYYLMD
LSLSMKDDLDNIRSLGTKLAEEMRKLTSNFRLGFGSFVDKDISPFSYTAPRYQTNPCIGYK
LFPNCVPSFGFRHLLPLTDRVDSFNEEVRKQRVSRNRDAPEGGFDAVLQAAVCKEKIGWRK
DALHLLVFTTDDVPHIALDGKLGGLVQPHDGQCHLNEANEYTASNQMDYPSLALLGEKLAE
NNINLIFAVTKNHYMLYKNFTALIPGTTVEILDGDSKNIIQLIINAYNSIRSKVELSVWDQ
PEDLNLFFTATCQDGVSYPGQRKCEGLKIGDTASFEVSLEARSCPSRHTEHVFALRPVGFR
DSLEVGVTYNCTCGCSVGLEPNSARCNGSGTYVCGLCECSPGYLGTRCECQDGENQSVYQN
LCREAEGKPLCSGRGDCSCNQCSCFESEFGKIYGPFCECDNFSCARNKGVLCSGHGECHCG
ECKCHAGYIGDNCNCSTDISTCRGRDGQICSERGHCLCGQCQCTEPGAFGEMCEKCPTCPD
ACSTKRDCVECLLLHSGKPDNQTCHSLCRDEVITWVDTIVKDDQEAVLCFYKTAKDCVMMF
TYVELPSGKSNLTVLREPECGNTPN

SEQ ID NO: 11 (FR-1-V_H-αvß5)
METGLRWLLLVAVLKGVQCQEQLEESGGGLVQPEGSLTLTCTVSGF

SEQ ID NO: 12 (FR-2-V_H-αvß5)
WVRQAPGKGLEWIG

SEQ ID NO: 13 (FR-3-V_H-αvß5)
YYASWAKGRFTISKSSSTTVTLQMTSLTATDTATYFC

SEQ ID NO: 14 (FR-4-V_H-αvß5)
WGPGTLVTVSS

SEQ ID NO: 15 (V_L-αvß5: CDRs + FRs)
MDTRAPTQLLGLLLLWLPGARCALVMTQTPPSVEAAVGGTVTINCQASQDIGSDLAWYQQK
PGQPPKLLIYSASSLASGVPSRFKASGSGTQFTLTISDVQCDDAATYSCAGYKSYSDDGHG

SEQ ID NO: 16 (V_H-αvß5: CDRs + FRs)
METGLRWLLLVAVLKGVQCQEQLEESGGGLVQPEGSLTLTCTVSGFPLRNVWISWVRQAPG
KGLEWIGCIYTGRDWPYYASWAKGRFTISKSSSTTVTLQMTSLTATDTATYFCARIVYGGA
GYRLWGPGTLVTVSS

SEQ ID NO: 17 (C_L-αvß5)
FGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTTGI
ENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC

SEQ ID NO: 18 (C_H-αvß5)
GQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSG
LYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPK
PKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLP
IAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCM
INGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMH
EALHNHYTQKSISRSPGK

SEQ ID NO: 19 (L-αvß5: CDRs + FRs + C_L)
MDTRAPTQLLGLLLLWLPGA[redacted]TQTPPSVEAAVGGTVTINCQASQDIGSDLAWYQQK
PGQPPKLLIYSASSLASGVPSRFKASGSGTQFTLTISDVQCDDAATYSCAGYKSYSDDGHG
FGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTTGI
ENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC

SEQ ID NO: 20 (H-αvß5: CDRs + FRs + C_H)
METGLRWLLLVAVLKGVQCQEQLEESGGGLVQPEGSLTLTCTVSGF[redacted]WVRQAPG
KGLEWIGCIYTGRDWPYYASWAKGRFTISKSSSTTVTLQMTSLTATDTATYFCARIVYGGA
GYRLWGPGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTL
TNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPP
PELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLR
EQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGP
PREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPT
SEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK

SEQ ID NO: 21 (CDR-1-V_L-αvß5)
AGATGTGCGCTTGTGATG

SEQ ID NO: 22 (CDR-2-V_L-αvß5)
ACATTGGTAGCGAC

SEQ ID NO: 23 (CDR-3-V_L-αvß5)
GCAGGCTATAAAAGTTATAGTGATGATGGTCATGG

SEQ ID NO: 24 (CDR-1-V_H-αvß5)
CCCCTCCGTAATGTCTGGATATCC

SEQ ID NO: 25 (CDR-2-V_H-αvß5)
TGCATTTATACTGGTAGGGATTGG

SEQ ID NO: 26 (CDR-3-V_H-αvß5)
GCGAGAATTGTTTATGGTGGTGCTGGTTATAGATTG

SEQ ID NO: 27 (FR-1-V_L-αvß5)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC

SEQ ID NO: 28 (FR-2-V_L-αvß5)
ACCCAGACTCCACCCTCCGTGGAGGCAGCTGTGGGAGGCACAGTCACCATCAATTGCCAGG
CCAGTCAGG

SEQ ID NO: 29 (FR-3-V_L-αvß5)
TTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATTCTGCATCCA
GTCTGGCATCTGGGGTCCCATCGCGATTCAAAGCCAGTGGATCTGGGACACAGTTCACTCT
CACCATCAGCGACGTGCAGTGTGACGATGCTGCCACTTACTCCTGT

SEQ ID NO: 30 (DTM-αvß5 incl. signal peptide [lower case])

atgccgcgggccccggcgccgctgtacgcctgcctcctggggctctgcgcgctcctgcccc
ggctcgcaGGTCTCAACATATGCACTAGTGGAAGTGCCACCTCATGTGAAGAATGTCTGCT
AATCCACCCAAAATGTGCCTGGTGCTCCAAAGAGGACTTCGGAAGCCCACGGTCCATCACC
TCTCGGTGTGATCTGAGGGCAAACCTTGTCAAAAATGGCTGTGGAGGTGAGATAGAGAGCC
CAGCCAGCAGCTTCCATGTCCTGAGGAGCCTGCCCCTCAGCAGCAAGGGTTCGGGCTCTGC
AGGCTGGGACGTCATTCAGATGACACCACAGGAGATTGCCGTGAACCTCCGGCCCGGTGAC
AAGACCACCTTCCAGCTACAGGTTCGCCAGGTGGAGGACTATCCTGTGGACCTGTACTACC
TGATGGACCTCTCCCTGTCCATGAAGGATGACTTGGACAATATCCGGAGCCTGGGCACCAA
ACTCGCGGAGGAGATGAGGAAGCTCACCAGCAACTTCCGGTTGGGATTTGGGTCTTTTGTT
GATAAGGACATCTCTCCTTTCTCCTACACGGCACCGAGGTACCAGACCAATCCGTGCATTG
GTTACAAGTTGTTTCCAAATTGCGTCCCCTCCTTTGGGTTCCGCCATCTGCTGCCTCTCAC
AGACAGAGTGGACAGCTTCAATGAGGAAGTTCGGAAACAGAGGGTGTCCCGGAACCGAGAT
GCCCCTGAGGGGGGCTTTGATGCAGTACTCCAGGCAGCCGTCTGCAAGGAGAAGATTGGCT
GGCGAAAGGATGCACTGCATTTGCTGGTGTTCACAACAGATGATGTGCCCCACATCGCATT
GGATGGAAAATTGGGAGGCCTGGTGCAGCCACACGATGGCCAGTGCCACCTGAACGAGGCC
AACGAGTACACAGCATCCAACCAGATGGACTATCCATCCCTTGCCTTGCTTGGAGAGAAAT
TGGCAGAGAACAACATCAACCTCATCTTTGCAGTGACAAAAAACCATTATATGCTGTACAA
GAATTTTACAGCCCTGATACCTGGAACAACGGTGGAGATTTTAGATGGAGACTCCAAAAAT
ATTATTCAACTGATTATTAATGCATACAATAGTATCCGGTCTAAAGTGGAGTTGTCAGTCT
GGGATCAGCCTGAGGATCTTAATCTCTTCTTTACTGCTACCTGCCAAGATGGGGTATCCTA
TCCTGGTCAGAGGAAGTGTGAGGGTCTGAAGATTGGGGACACGGCATCTTTTGAAGTATCA
TTGGAGGCCCGAAGCTGTCCCAGCAGACACACGGAGCATGTGTTTGCCCTGCGGCCGGTGG
GATTCCGGGACAGCCTGGAGGTGGGGGTCACCTACAACTGCACGTGCGGCTGCAGCGTGGG
GCTGGAACCCAACAGCGCCAGGTGCAACGGGAGCGGGACCTATGTCTGCGGCCTGTGTGAG
TGCAGCCCCGGCTACCTGGGCACCAGGTGCGAGTGCCAGGATGGGGAGAACCAGAGCGTGT
ACCAGAACCTGTGCCGGGAGGCAGAGGGCAAGCCACTGTGCAGCGGGCGTGGGGACTGCAG
CTGCAACCAGTGCTCCTGCTTCGAGAGCGAGTTTGGCAAGATCTATGGGCCTTTCTGTGAG
TGCGACAACTTCTCCTGTGCCAGGAACAAGGGAGTCCTCTGCTCAGGCCATGGCGAGTGTC
ACTGCGGGGAATGCAAGTGCCATGCAGGTTACATCGGGGACAACTGTAACTGCTCGACAGA
CATCAGCACATGCCGGGGCAGAGATGGCCAGATCTGCAGCGAGCGTGGGCACTGTCTCTGT
GGGCAGTGCCAATGCACGGAGCCGGGGGCCTTTGGGGAGATGTGTGAGAAGTGCCCCACCT
GCCCGGATGCATGCAGCACCAAGAGAGATTGCGTCGAGTGCCTGCTGCTCCACTCTGGGAA
ACCTGACAACCAGACCTGCCACAGCCTATGCAGGGATGAGGTGATCACATGGGTGGACACC
ATCGTGAAAGATGACCAGGAGGCTGTGCTATGTTTCTACAAAACCGCCAAGGACTGCGTCA
TGATGTTCACCTATGTGGAGCTCCCCAGTGGGAAGTCCAACCTGACCGTCCTCAGGGAGCC
AGAGTGTGGAAACACCCCCAAC

SEQ ID NO: 31 (FR-1-V_H-αvß5)

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGG
AGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCCAGCCTGAGGGATCCCTGACACTCACCTG
CACAGTCTCTGGATTC

SEQ ID NO: 32 (FR-2-V_H-αvß5)

TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGA

SEQ ID NO: 33 (FR-3-V_H-αvß5)

CCCTACTACGCGAGCTGGGCGAAAGGCCGATTCACCATTTCCAAGTCCTCGTCGACCACGG
TGACTCTCCAAATGACCAGTCTGACAGCCACGGACACGGCCACATATTTCTGT

SEQ ID NO: 34 (FR-4-V_H-αvß5)
TGGGGCCCAGGCACCCTGGTCACCGTTTCCTCA

SEQ ID NO: 35 (V_L-αvß5: CDRs + FRs)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCA
GATGTGCGCTTGTGATGACCCAGACTCCACCCTCCGTGGAGGCAGCTGTGGGAGGCACAGT
CACCATCAATTGCCAGGCCAGTCAGGACATTGGTAGCGACTTAGCCTGGTATCAGCAGAAA
CCAGGGCAGCCTCCCAAGCTCCTGATCTATTCTGCATCCAGTCTGGCATCTGGGGTCCCAT
CGCGATTCAAAGCCAGTGGATCTGGGACACAGTTCACTCTCACCATCAGCGACGTGCAGTG
TGACGATGCTGCCACTTACTCCTGTGCAGGCTATAAAAGTTATAGTGATGATGGTCATGG

SEQ ID NO: 36 (V_H-αvß5: CDRs + FRs)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGG
AGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCCAGCCTGAGGGATCCCTGACACTCACCTG
CACAGTCTCTGGATTCCCCCTCCGTAATGTCTGGATATCCTGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGATCGGATGCATTTATACTGGTAGGGATTGGCCCTACTACGCGAGCT
GGGCGAAAGGCCGATTCACCATTTCCAAGTCCTCGTCGACCACGGTGACTCTCCAAATGAC
CAGTCTGACAGCCACGGACACGGCCACATATTTCTGTGCGAGAATTGTTTATGGTGGTGCT
GGTTATAGATTGTGGGGCCCAGGCACCCTGGTCACCGTTTCCTCA

SEQ ID NO: 37 (C_L-αvß5)
TTTCGGCGGAGGGACCGAGGTGGTGGTCAAGGGTGATCCAGTTGCACCTACTGTCCTCATC
TTCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATA
AATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCAT
CGAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTG
ACACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCA
CGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG

SEQ ID NO: 38 (C_H-αvß5)
GGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCT
CCACGGTGACCCTGGGCTGCCTGGTCAAAGGGTACCTCCCGGAGCCAGTGACCGTGACCTG
GAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGC
CTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACG
TGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAA
GCCCACGTGCCCACCCCCTGAACTCCTGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGA
GCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGC
CCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCC
ATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCAC
TCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGT
CTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATG
ATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGG
ACAACTACAAGACCACGCCGGCCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAA
GCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCAC
GAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATGA

SEQ ID NO: 39 (L-αvß5: CDRs + FRs + C_L)

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC[redacted]
[redacted]ACCCAGACTCCACCCTCCGTGGAGGCAGCTGTGGGAGGCACAGT
CACCATCAATTGCCAGGCCAGTCAGGACATTGGTAGCGACTTAGCCTGGTATCAGCAGAAA
CCAGGGCAGCCTCCCAAGCTCCTGATCTATTCTGCATCCAGTCTGGCATCTGGGGTCCCAT
CGCGATTCAAAGCCAGTGGATCTGGGACACAGTTCACTCTCACCATCAGCGACGTGCAGTG
TGACGATGCTGCCACTTACTCCTGT[redacted]T
TTCGGCGGAGGGACCGAGGTGGTGGTCAAGGGTGATCCAGTTGCACCTACTGTCCTCATCT
TCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAA
ATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATC
GAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGA
CACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCAC
GACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG

SEQ ID NO: 40 (H-αvß5: CDRs + FRs + C_H)

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGG
AGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCCAGCCTGAGGGATCCCTGACACTCACCTG
CACAGTCTCTGGATTC[redacted]TGGGTCCGCCAGGCTCCAGGG
AAGGGGCTGGAGTGGATCGGATGCATTTATACTGGTAGGGATTGGCCCTACTACGCGAGCT
GGGCGAAAGGCCGATTCACCATTTCCAAGTCCTCGTCGACCACGGTGACTCTCCAAATGAC
CAGTCTGACAGCCACGGACACGGCCACATATTTCTGT[redacted]
[redacted]TGGGGCCCAGGCACCCTGGTCACCGTTTCCTCAGGGCAACCTAAGGCTC
CATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGG
CTGCCTGGTCAAAGGGTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTC
ACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCA
GCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCAC
CAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCACGTGCCCACCC
CCTGAACTCCTGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCA
TGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGA
GGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGG
GAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACT
GGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGA
GAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCT
CCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACC
CTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCAC
GCCGGCCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACG
AGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACC
ACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATGA

SEQ ID NO: 41 (CDR-1-V_L-ß3)
RFAQIVM

SEQ ID NO: 42 (CDR-2-V_L-ß3)
QSIYSY

SEQ ID NO: 43 (CDR-3-V_L-ß3)
QAYSDSYSYDNS

SEQ ID NO: 44 (CDR-1-V_H-ß3)
DFSSDYWMS

SEQ ID NO: 45 (CDR-2-V_H-ß3)
YINVGDGK

SEQ ID NO: 46 (CDR-3-V_H-ß3)
GKDLGL

SEQ ID NO: 47 (FR-1-V_L-ß3)
MDTRAPTQLLGLLLLWLPGA

SEQ ID NO: 48 (FR-2-V_L-ß3)
TQTPASVEAAVGGTVTIKCQAS

SEQ ID NO: 49 (FR-3-V_L-ß3)
LSWFQQKPGQPPNLLIYDASKLASGVPSRFKGSGSGTEFTLTISDLECADAATFYCQS

SEQ ID NO: 50 (ß3-immunogen incl. GST protein [underlined])
MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDG
DVKLTQSMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDF
LSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRI
EAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDGSTRSTSLYKKAGFGGGGSENLYF
QKLLITIHDRKEFAKFEEERARAKWDTANNPLYKEATSTFTNITYRGT

SEQ ID NO: 51 (FR-1-V_H-ß3)
METGLRWLLLVAVLKGVQCQSLEESGGGLVKPGGTLTLTCKASGF

SEQ ID NO: 52 (FR-2-V_H-ß3)
WVRQGPGKGLQWIA

SEQ ID NO: 53 (FR-3-V_H-ß3)
TYYASWAKGRFTISKTSSTTVTLQMTSLAAADTATYFC

SEQ ID NO: 54 (FR-4-V_H-ß3)
WGPGTLVTVSS

SEQ ID NO: 55 (V_L-ß3: CDRs + FRs)
MDTRAPTQLLGLLLLWLPGARFAQIVMTQTPASVEAAVGGTVTIKCQASQSIYSYLSWFQQ
KPGQPPNLLIYDASKLASGVPSRFKGSGSGTEFTLTISDLECADAATFYCQSQAYSDSYSY
DNS

SEQ ID NO: 56 (V_H-ß3: CDRs + FRs)
METGLRWLLLVAVLKGVQCQSLEESGGGLVKPGGTLTLTCKASGFDFSSDYWMSWVRQGPG
KGLQWIAYINVGDGKTYYASWAKGRFTISKTSSTTVTLQMTSLAAADTATYFCGKDLGLWG
PGTLVTVSS

SEQ ID NO: 57 (C_L-ß3)
FGGGTELVVEGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTTGI
ENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC

SEQ ID NO: 58 (C_H-ß3)
GQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSG
LYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPK
PKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLP
IAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCM
INGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMH
EALHNHYTQKSISRSPGK

SEQ ID NO: 59 (L-ß3: CDRs + FRs + C_L)
MDTRAPTQLLGLLLLWLPGA[redacted]TQTPASVEAAVGGTVTIKCQASQSIYSYLSWFQQ
KPGQPPNLLIYDASKLASGVPSRFKGSGSGTEFTLTISDLECADAATFYCQSQAYSDSYSY
DNSFGGGTELVVEGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQT
TGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC

SEQ ID NO: 60 (H-ß3: CDRs + FRs + C_H)
METGLRWLLLVAVLKGVQCQSLEESGGGLVKPGGTLTLTCKASGF[redacted]WVRQGPG
KGLQWIAYINVGDGKTYYASWAKGRFTISKTSSTTVTLQMTSLAAADTATYFCGKDLGLWG
PGTLVTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRT
FPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGG
PSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNS
TIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELS
SRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRG
DVFTCSVMHEALHNHYTQKSISRSPGK

SEQ ID NO: 61 (V_L-CDR-1-ß3)
AGATTTGCCCAAATTGTGATG

SEQ ID NO: 62 (V_L-CDR-2-ß3)
AGCATTTACAGCTA

SEQ ID NO: 63 (V_L-CDR-3-ß3)
CAAAGCCAGGCTTATAGTGATAGTTATAGTTATGATAATAG

SEQ ID NO: 64 (V_H-CDR-1-ß3)
GACTTCAGTAGCGACTACTGGATGTCC

SEQ ID NO: 65 (V_H-CDR-2-ß3)
TACATTAATGTTGGTGATGGTAAA

SEQ ID NO: 66 (V_H-CDR-3-ß3)
GGCAAAGATTTAGGCTTG

SEQ ID NO: 67 (FR-1-V_L-ß3)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGTGCC

SEQ ID NO: 68 (FR-2-V_L-ß3)
ACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGGAGGCACAGTCACCATCAAGTGCCAGG
CCAGTCAG

SEQ ID NO: 69 (FR-3-V_L-ß3)
CTTATCCTGGTTTCAGCAGAAACCAGGGCAGCCTCCCAACCTCCTGATCTACGATGCATCC
AAACTGGCCTCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTC
TCACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTTCTACTGT

SEQ ID NO: 70 (ß3-immunogen)
CACGACCGAAAAGAATTCGCTAAATTTGAGGAAGAACGCGCCAGAGCAAAATGGGACACAGCCAACA
ACCCACTGTATAAAGAGGCCACGTCTACCTTCACCAATATCACGTACCGGGGCACTTAA

SEQ ID NO: 71 (FR-1-V_H-ß3)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGTTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGACACTCACCTGCAA
AGCCTCTGGATTC

SEQ ID NO: 72 (FR-2-V_H-ß3)
TGGGTCCGCCAGGGTCCAGGGAAGGGGCTGCAGTGGATCGCA

SEQ ID NO: 73 (FR-3-V_H-ß3)
ACTTACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGTCGACCACGG
TGACTCTGCAAATGACCAGTCTGGCAGCCGCGGACACGGCCACCTATTTCTGT

SEQ ID NO: 74 (FR-4-V_H-ß3)
TGGGGCCCAGGCACCCTGGTCACCGTCTCCTCA

SEQ ID NO: 75 (V_L-ß3: CDRs + FRs)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGTGCCA
GATTTGCCCAAATTGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGGAGGCAC
AGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTTACAGCTACTTATCCTGGTTTCAGCAG
AAACCAGGGCAGCCTCCCAACCTCCTGATCTACGATGCATCCAAACTGGCCTCTGGGGTCC
CATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCGACCTGGA
GTGTGCCGATGCTGCCACTTTCTACTGTCAAAGCCAGGCTTATAGTGATAGTTATAGTTAT
GATAATAG

SEQ ID NO: 76 (V_H-ß3: CDRs + FRs)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGTTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGACACTCACCTGCAA
AGCCTCTGGATTCGACTTCAGTAGCGACTACTGGATGTCCTGGGTCCGCCAGGGTCCAGGG
AAGGGGCTGCAGTGGATCGCATACATTAATGTTGGTGATGGTAAAACTTACTACGCGAGCT
GGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGTCGACCACGGTGACTCTGCAAATGAC
CAGTCTGGCAGCCGCGGACACGGCCACCTATTTCTGTGGCAAAGATTTAGGCTTGTGGGGC
CCAGGCACCCTGGTCACCGTCTCCTCA

SEQ ID NO: 77 (C_L-ß3)

TTTCGGCGGGGGGACCGAACTGGTGGTCGAAGGTGATCCAGTTGCACCTACTGTCCTCATC
TTCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATA
AATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCAT
CGAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTG
ACACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCA
CGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG

SEQ ID NO: 78 (C_H-ß3)

GGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCT
CCACGGTGACCCTGGGCTGCCTGGTCAAAGGGTACCTCCCGGAGCCAGTGACCGTGACCTG
GAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGC
CTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACG
TGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAA
GCCCACGTGCCCACCCCCTGAACTCCTGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGA
GCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGC
CCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCC
ATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCAC
TCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGT
CTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATG
ATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGG
ACAACTACAAGACCACGCCGGCCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAA
GCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCAC
GAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTA

SEQ ID NO: 79 (L-ß3: CDRs + FRs + C_L)

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTACTGCTCTGGCTCCCAGGTGCC[redacted]
[redacted]ACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGGAGGCAC
AGTCACCATCAAGTGCCAGGCCAGTCAGAGCATTTACAGCTACTTATCCTGGTTTCAGCAG
AAACCAGGGCAGCCTCCCAACCTCCTGATCTACGATGCATCCAAACTGGCCTCTGGGGTCC
CATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCGACCTGGA
GTGTGCCGATGCTGCCACTTTCTACTGT[redacted]
[redacted]TTCGGCGGGGGGACCGAACTGGTGGTCGAAGGTGATCCAGTTGCACCTACTG
TCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGT
GGCGAATAAATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACA
ACTGGCATCGAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCA
GCACTCTGACACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGAC
CCAGGGCACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG

SEQ ID NO: 80 (H-ß3: CDRs + FRs + C_H)

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGTTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGACACTCACCTGCAA
AGCCTCTGGATTC[redacted]TGGGTCCGCCAGGGTCCAGGG
AAGGGGCTGCAGTGGATCGCATACATTAATGTTGGTGATGGTAAAACTTACTACGCGAGCT
GGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGTCGACCACGGTGACTCTGCAAATGAC
CAGTCTGGCAGCCGCGGACACGGCCACCTATTTCTGT[redacted]TGGGGC
CCAGGCACCCTGGTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGG
CCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGGTA
CCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACC
TTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCT
CAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAA
GACCGTTGCGCCCTCGACATGCAGCAAGCCCACGTGCCCACCCCCTGAACTCCTGGGGGGA
CCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCG
AGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTA
CATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGC
ACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGT
TCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGC
CAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGC
AGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGG
AGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGGCCGTGCTGGACAG
CGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGC
GACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCA
TCTCCCGCTCTCCGGGTAAATGA

SEQ ID NO: 81 (CDR-1-V_L-αvß3)
TFAQVL

SEQ ID NO: 82 (CDR-2-V_L-αvß3)
ESVYADIA

SEQ ID NO: 83 (CDR-3-V_L-αvß3)
AGDYGAGTEPNL

SEQ ID NO: 84 (CDR-1-V_H-αvß3)
SLSSYGVS

SEQ ID NO: 85 (CDR-2-V_H-αvß3)
SISTTGI

SEQ ID NO: 86 (CDR-3-V_H-αvß3)
ARGFPGHLRKPSDI

SEQ ID NO: 87 (FR-1-V_L-αvß3)
MDTRAPTQLLGLLLLWLPGA

SEQ ID NO: 88 (FR-2-V_L-αvß3)
TQTPSSVSAAVGGTVSISCQSS

SEQ ID NO: 89 (FR-3-V_L-αvß3)
LSWFQQKPGQPPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISDVQCDAAATYYC

SEQ ID NO: 90 (DTM-αvß3)
GPNICTTRGVSSCQQCLAVSPMCAWCSDEALPLGSPRCDLKENLLKDNCAPESIEFPVSEA
RVLEDRPLSDKGSGDSSQVTQVSPQRIALRLRPDDSKNFSIQVRQVEDYPVDIYYLMDLSY
SMKDDLWSIQNLGTKLATQMRKLTSNLRIGFGAFVDKPVSPYMYISPPEALENPCYDMKTT
CLPMFGYKHVLTLTDQVTRFNEEVKKQSVSRNRDAPEGGFDAIMQATVCDEKIGWRNDASH
LLVFTTDAKTHIALDGRLAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEKLSQKNIN
LIFAVTENVVNLYQNYSELIPGTTVGVLSMDSSNVLQLIVDAYGKIRSKVELEVRDLPEEL
SLSFNATCLNNEVIPGLKSCMGLKIGDTVSFSIEAKVRGCPQEKEKSFTIKPVGFKDSLIV
QVTFDCDCACQAQAEPNSHRCNNGNGTFECGVCRCGPGWLGSQCECSEEDYRPSQQDECSP
REGQPVCSQRGECLCGQCVCHSSDFGKITGKYCECDDFSCVRYKGEMCSGHGQCSCGDCLC
DSDWTGYYCNCTTRTDTCMSSNGLLCSGRGKCECGSCVCIQPGSYGDTCEKCPTCPDACTF
KKECVECKKFDREPYMTENTCNRYCRDEIESVKELKDTGKDAVNCTYKNEDDCVVRFQYYE
DSSGKSILYVVEEPECPKGPD

SEQ ID NO: 91 (FR-1-V_H-αvß3)
METGLRWLLLVAVLKGVQCQSVKESEGGLFKPTDTLILTCTVSGF

SEQ ID NO: 92 (FR-2-V_H-αvß3)
WVRQAPGNGLEYIG

SEQ ID NO: 93 (FR-3-V_H-αvß3)
TYYASWAKSRSTITRNTNLYTVTLKMTGLTAADTATYFC

SEQ ID NO: 94 (FR-4-V_H-αvß3)
WGPGTLVTVSA

SEQ ID NO: 95 (V_L-αvß3: CDRs + FRs)
MDTRAPTQLLGLLLLWLPGATFAQVLTQTPSSVSAAVGGTVSISCQSSESVYADIALSWFQ
QKPGQPPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISDVQCDAAATYYCAGDYGAGTEP
NL

SEQ ID NO: 96 (V_H-αvß3: CDRs + FRs)
METGLRWLLLVAVLKGVQCQSVKESEGGLFKPTDTLILTCTVSGFSLSSYGVSWVRQAPGN
GLEYIGSISTTGITYYASWAKSRSTITRNTNLYTVTLKMTGLTAADTATYFCARGFPGHLR
KPSDIWGPGTLVTVSA

SEQ ID NO: 97 (C_L-αvß3)
FGGGTEVVVSGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTTGI
ENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC

SEQ ID NO: 98 (C_H-αvß3)
GQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSG
LYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPK
PKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLP
IAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCM
INGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMH
EALHNHYTQKSISRSPGK

SEQ ID NO: 99 (L-αvß3: CDRs + FRs + C_L)
MDTRAPTQLLGLLLLWLPGA[redacted]TQTPSSVSAAVGGTVSISCQSSESVYADIALSWFQ
QKPGQPPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISDVQCDAAATYYCAGDYGAGTEP
NLFGGGTEVVVSGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTT
GIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC

SEQ ID NO: 100 (H-αvß3: CDRs + FRs + C_H)
METGLRWLLLVAVLKGVQCQSVKESEGGLFKPTDTLILTCTVSGF[redacted]WVRQAPGN
GLEYIGSISTTGITYYASWAKSRSTITRNTNLYTVTLKMTGLTAADTATYFCAPGFPGHLR
KPSDIWGPGTLVTVSAGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGT
LTNGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCP
PPELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPL
REQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMG
PPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVP
TSEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK

SEQ ID NO: 101 (CDR-1-V_L-αvß3)
ACATTTGCCCAAGTGCTG

SEQ ID NO: 102 (CDR-2-V_L-αvß3)
AGTGTTTATGCTGACATCGC

SEQ ID NO: 103 (CDR-3-V_L-αvß3)
GCAGGCGATTATGGGGCTGGTACTGAGCCTAATCTT

SEQ ID NO: 104 (CDR-1-V_H-αvß3)
TCCCTCAGTAGCTATGGAGTGAGC

SEQ ID NO: 105 (CDR-2-V_H-αvß3)
TCCATTAGTACTACTGGTATC

SEQ ID NO: 106 (CDR-3-V_H-αvß3)
GAGGTTTTCCTGGTCATCTTCGTAAGCCGTCGGACA

SEQ ID NO: 107 (FR-1-V_L-αvß3)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC

SEQ ID NO: 108 (FR-2-V_L-αvß3)
ACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGAGGCACAGTCAGCATCAGTTGCCAGT
CCAGTGAG

SEQ ID NO: 109 (FR-3-V_L-αvß3)
CTTATCCTGGTTTCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGGTGCATCC
ACTCTGGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTC
TCACCATCAGCGACGTGCAGTGTGACGCTGCTGCCACTTACTATTGT

SEQ ID NO: 110 (DTM-αvß3 incl. signal peptide [lower case])

atgcgagcgcggccgcggccccggccgctctgggtgactgtgctggcgctgggggcgctgg
cgggcgttggcgtaggaGGGCCCAACATCTGTACCACGCGAGGTGTGAGCTCCTGCCAGCA
GTGCCTGGCTGTGAGCCCCATGTGTGCCTGGTGCTCTGATGAGGCCCTGCCTCTGGGCTCA
CCTCGCTGTGACCTGAAGGAGAATCTGCTGAAGGATAACTGTGCCCCAGAATCCATCGAGT
TCCCAGTGAGTGAGGCCCGAGTACTAGAGGACAGGCCCCTCAGCGACAAGGGCTCTGGAGA
CAGCTCCCAGGTCACTCAAGTCAGTCCCCAGAGGATTGCACTCCGGCTCCGGCCAGATGAT
TCGAAGAATTTCTCCATCCAAGTGCGGCAGGTGGAGGATTACCCTGTGGACATCTACTACT
TGATGGACCTGTCTTACTCCATGAAGGATGATCTGTGGAGCATCCAGAACCTGGGTACCAA
GCTGGCCACCCAGATGCGAAAGCTCACCAGTAACCTGCGGATTGGCTTCGGGGCATTTGTG
GACAAGCCTGTGTCACCATACATGTATATCTCCCCACCAGAGGCCCTCGAAAACCCCTGCT
ATGATATGAAGACCACCTGCTTGCCCATGTTTGGCTACAAACACGTGCTGACGCTAACTGA
CCAGGTGACCCGCTTCAATGAGGAAGTGAAGAAGCAGAGTGTGTCACGGAACCGAGATGCC
CCAGAGGGTGGCTTTGATGCCATCATGCAGGCTACAGTCTGTGATGAAAAGATTGGCTGGA
GGAATGATGCATCCCACTTGCTGGTGTTTACCACTGATGCCAAGACTCATATAGCATTGGA
CGGAAGGCTGGCAGGCATTGTCCAGCCTAATGACGGGCAGTGTCATGTTGGTAGTGACAAT
CATTACTCTGCCTCCACTACCATGGATTATCCCTCTTTGGGGCTGATGACTGAGAAGCTAT
CCCAGAAAAACATCAATTTGATCTTTGCAGTGACTGAAAATGTAGTCAATCTCTATCAGAA
CTATAGTGAGCTCATCCCAGGGACCACAGTTGGGGTTCTGTCCATGGATTCCAGCAATGTC
CTCCAGCTCATTGTTGATGCTTATGGGAAAATCCGTTCTAAAGTCGAGCTGGAAGTGCGTG
ACCTCCCTGAAGAGTTGTCTCTATCCTTCAATGCCACCTGCCTCAACAATGAGGTCATCCC
TGGCCTCAAGTCTTGTATGGGACTCAAGATTGGAGACACGGTGAGCTTCAGCATTGAGGCC
AAGGTGCGAGGCTGTCCCCAGGAGAAGGAGAAGTCCTTTACCATAAAGCCCGTGGGCTTCA
AGGACAGCCTGATCGTCCAGGTCACCTTTGATTGTGACTGTGCCTGCCAGGCCCAAGCTGA
ACCTAATAGCCATCGCTGCAACAATGGCAATGGGACCTTTGAGTGTGGGGTATGCCGTTGT
GGGCCTGGCTGGCTGGGATCCCAGTGTGAGTGCTCAGAGGAGGACTATCGCCCTTCCCAGC
AGGACGAGTGCAGCCCCCGAGAGGGTCAGCCCGTCTGCAGCCAGCGGGGCGAGTGCCTCTG
TGGTCAATGTGTCTGCCACAGCAGTGACTTTGGCAAGATCACGGGCAAGTACTGCGAGTGT
GACGACTTCTCCTGTGTCCGCTACAAGGGGGAGATGTGCTCAGGCCATGGCCAGTGCAGCT
GTGGGGACTGCCTGTGTGACTCCGACTGGACCGGCTACTACTGCAACTGTACCACGCGTAC
TGACACCTGCATGTCCAGCAATGGGCTGCTGTGCAGCGGCCGCGGCAAGTGTGAATGTGGC
AGCTGTGTCTGTATCCAGCCGGGCTCCTATGGGGACACCTGTGAGAAGTGCCCCACCTGCC
CAGATGCCTGCACCTTTAAGAAAGAATGTGTGGAGTGTAAGAAGTTTGACCGGGAGCCCTA
CATGACCGAAAATACCTGCAACCGTTACTGCCGTGACGAGATTGAGTCAGTGAAAGAGCTT
AAGGACACTGGCAAGGATGCAGTGAATTGTACCTATAAGAATGAGGATGACTGTGTCGTCA
GATTCCAGTACTATGAAGATTCTAGTGGAAAGTCCATCCTGTATGTGGTAGAAGAGCCAGA
GTGTCCCAAGGGCCCTGAC

SEQ ID NO: 111 (FR-1-V_H-αvß3)

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGGTGAAGGAGTCCGAGGGAGGTCTCTTCAAGCCAACGGATACCCTGATACTCACCTGCAC
AGTCTCTGGATTC

SEQ ID NO: 112 (FR-2-V_H-αvß3)

TGGGTCCGCCAGGCTCCAGGGAACGGGCTGGAATACATCGGA

SEQ ID NO: 113 (FR-3-V_H-αvß3)

ACATACTACGCGAGCTGGGCGAAAAGCCGATCCACCATCACCAGAAACACCAACCTGTACA
CGGTGACTCTGAAAATGACCGGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGA

SEQ ID NO: 114 (FR-4-V_H-αvß3)
TTTGGGGCCCCGGCACCCTGGTCACCGTCTCCGCA

SEQ ID NO: 115 (V_L-αvß3: CDRs + FRs)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCA
CATTTGCCCAAGTGCTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGAGGCACAGT
CAGCATCAGTTGCCAGTCCAGTGAGAGTGTTTATGCTGACATCGCCTTATCCTGGTTTCAG
CAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGG
TCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCGACGT
GCAGTGTGACGCTGCTGCCACTTACTATTGTGCAGGCGATTATGGGGCTGGTACTGAGCCT
AATCTT

SEQ ID NO: 116 (V_H-αvß3: CDRs + FRs)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGGTGAAGGAGTCCGAGGGAGGTCTCTTCAAGCCAACGGATACCCTGATACTCACCTGCAC
AGTCTCTGGATTCTCCCTCAGTAGCTATGGAGTGAGCTGGGTCCGCCAGGCTCCAGGGAAC
GGGCTGGAATACATCGGATCCATTAGTACTACTGGTATCACATACTACGCGAGCTGGGCGA
AAAGCCGATCCACCATCACCAGAAACACCAACCTGTACACGGTGACTCTGAAAATGACCGG
TCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGGTTTTCCTGGTCATCTTCGT
AAGCCGTCGGACATTTGGGGCCCCGGCACCCTGGTCACCGTCTCCGCA

SEQ ID NO: 117 (C_L-αvß3)
TTCGGCGGAGGGACCGAGGTGGTGGTCAGCGGTGATCCAGTTGCACCTACTGTCCTCATCT
TCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAA
ATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATC
GAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGA
CACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCAC
GACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG

SEQ ID NO: 118 (C_H-αvß3)
GGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCT
CCACGGTGACCCTGGGCTGCCTGGTCAAAGGGTACCTCCCGGAGCCAGTGACCGTGACCTG
GAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGC
CTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACG
TGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAA
GCCCACGTGCCCACCCCCTGAACTCCTGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGA
GCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGC
CCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCC
ATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCAC
TCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGT
CTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATG
ATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGG
ACAACTACAAGACCACGCCGGCCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAA
GCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCAC
GAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATGA

SEQ ID NO: 119 (L-αvß3: CDRs + FRs + C_L)

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC[redacted]
[redacted]ACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGAGGCACAGT
CAGCATCAGTTGCCAGTCCAGTGAGAGTGTTTATGCTGACATCGCCTTATCCTGGTTTCAG
CAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGG
TCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCGACGT
GCAGTGTGACGCTGCTGCCACTTACTATTGT[redacted]
[redacted]TTCGGCGGAGGGACCGAGGTGGTGGTCAGCGGTGATCCAGTTGCACCTACTGTCC
TCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGC
GAATAAATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACT
GGCATCGAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCA
CTCTGACACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCA
GGGCACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAG

SEQ ID NO: 120 (H-αvß3: CDRs + FRs + C_H)

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGGTGAAGGAGTCCGAGGGAGGTCTCTTCAAGCCAACGGATACCCTGATACTCACCTGCAC
AGTCTCTGGATTC[redacted]TGGGTCCGCCAGGCTCCAGGGAAC
GGGCTGGAATACATCGGATCCATTAGTACTACTGGTATCACATACTACGCGAGCTGGGCGA
AAAGCCGATCCACCATCACCAGAAACACCAACCTGTACACGGTGACTCTGAAAATGACCGG
TCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGA[redacted]
[redacted]TTTGGGGCCCCGGCACCCTGGTCACCGTCTCCGCAGGGCAACCTAAGG
CTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCT
GGGCTGCCTGGTCAAAGGGTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACC
CTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGA
GCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGC
CACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCACGTGCCCA
CCCCCTGAACTCCTGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCC
TCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCC
CGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTA
CGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGG
ACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCAT
CGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGC
CCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCT
ACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGAC
CACGCCGGCCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCC
ACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACA
ACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATGA

SEQ ID NO: 121 (CDR-1-V_L-αvß6)
RCAYDMTQTPASVEVV

SEQ ID NO: 122 (CDR-2-V_L-αvß6)
QSVGIN

SEQ ID NO: 123 (CDR-3-V_L-αvß6)
QTYSSGNVDNV

SEQ ID NO: 124 (CDR-1-V_H-αvß6)
IDLSSAAIN

SEQ ID NO: 125 (CDR-2-V_H-αvß6)
VIGGSTGPY

SEQ ID NO: 126 (CDR-3-V_H-αvß6)
GLFGINNDISRI

SEQ ID NO: 127 (FR-1-V_L-αvß6)
MDTRAPTQLLGLLLLWLPGA

SEQ ID NO: 128 (FR-2-V_L-αvß6)
VGGTVTIKCQAS

SEQ ID NO: 129 (FR-3-V_L-αvß6)
LAWYQKKSGQRPKLLIYAASTLASGVSSRFKGSGSGTQFTLTISDLECADAATYYCQ

SEQ ID NO: 130 (DTM-αvß6)
GRNDHVQGGCAVGGAETCEDCLLIGPQCAWCSQENFTHLSGVGERCDTPANLLAKGCQLTF
IENPVSQVEILTNKPLSIGRQKNSSDIVQISPQSLALKLRPGLEQTLQVQVRQTEDYPVDL
YYLMDLSASMDDDLNTIKELGSLLSKEMSKLTSNFRLGFGSFVEKPISPFMKTTPEEIANP
CSSIPYFCLPTFGFKHILPLTNDAERFNEIVKNQKISANIDTPEGGFDAIMQAAVCKEKIG
WRNDSLHLLVFVSDADSHFGMDSKLAGIVIPNDGLCHLDSKNEYSMSTILEYPTIGQLIDK
LVQNNVLLIFAVTQEQVHLYENYAKLIPGATVGVLQKDSGNILQLIISAYEELRSEVELEV
LGDTEGLNLSFTAICNTGIPVPHQKKCSHMKVGDTASFNVTVSLPNCERRSRHIILKPVGL
GDALEILVSPECSCDCQKEVEVNSSKCNNGNGSFQCGVCACHPGHMGHHCECGEDTLSTES
CKEAPGRPSCSGRGDCYCGQCVCHLSPYGNIYGPYCQCDNFSCVRHKGLLCGDNGDCDCGE
CVCRSGWTGEYCNCTTSTDPCVSEDGILCSGRGDCVCGKCICTNPGASGPTCERCPTCGDP
CNSKRSCIECYLSADGQAQEECVDKCKLAGATINEEEDFSKDSFVSCSLQGENECLITFLL
TTDNEGKTVIHSINEKDCPKPPN

SEQ ID NO: 131 (FR-1-V_H-αvß6)
METGLRWLLLVAVLKGVQCQSLEESGGRLVKPGTPLTLTCTVSG

SEQ ID NO: 132 (FR-2-V_H-αvß6)
WVRQAPGKGLEWIG

SEQ ID NO: 133 (FR-3-V_H-αvß6)
YASWVNGRFTISKTSTTVALKIAGPTTEDTATYFCAR

SEQ ID NO: 134 (FR-4-V_H-αvß6)
WGPGTLVTVSL

SEQ ID NO: 135 (V_L-αvß6: CDRs + FRs)
MDTRAPTQLLGLLLLWLPGARCAYDMTQTPASVEVVVGGTVTIKCQASQSVGINLAWYQKK
SGQRPKLLIYAASTLASGVSSRFKGSGSGTQFTLTISDLECADAATYYCQQTYSSGNVDNV

SEQ ID NO: 136 (V_H-αvß6: CDRs + FRs)
METGLRWLLLVAVLKGVQCQSLEESGGRLVKPGTPLTLTCTVSGIDLSSAAINWVRQAPGK
GLEWIGVIGGSTGPYYASWVNGRFTISKTSTTVALKIAGPTTEDTATYFCARGLFGINNDI
SRIWGPGTLVTVSL

SEQ ID NO: 137 (C_L-αvß6)
FGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTTGI
ENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTXGTTSVVQSFNRGDC

SEQ ID NO: 138 (C_H-αvß6)
GQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSG
LYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPK
PKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLP
IAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCM
INGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMH
EALHNHYTQKSISRSPGK

SEQ ID NO: 139 (L-αvß6: CDRs + FRs + C_L)
MDTRAPTQLLGLLLLWLPGA[redacted]VGGTVTIKCQASQSVGINLAWYQKK
SGQRPKLLIYAASTLASGVSSRFKGSGSGTQFTLTISDLECADAATYYCQQTYSSGNVDNV
FGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTTGI
ENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTXGTTSVVQSFNRGDC

SEQ ID NO: 140 (H-αvß6: CDRs + FRs + C_H)
METGLRWLLLVAVLKGVQCQSLEESGGRLVKPGTPLTLTCTVSG[redacted]WVRQAPGK
GLEWIGVIGGSTGPYYASWVNGRFTISKTSTTVALKIAGPTTEDTATYFCARGLFGINNDI
SRIWGPGTLVTVSLGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLT
NGVRTFPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPP
ELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLRE
QQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPP
REELSSRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTS
EWQRGDVFTCSVMHEALHNHYTQKSISRSPGK

SEQ ID NO: 141 (CDR-1-V_L-αvß6)
AGATGTGCCTATGATATGACCCAGACTCCAGCCTCTGTGGAGGTAGTT

SEQ ID NO: 142 (CDR-2-V_L-αvß6)
CAGAGCGTTGGTATTAAT

SEQ ID NO: 143 (CDR-3-V_L-αvß6)
CAGACTTATAGTAGTGGTAATGTTGATAATGTG

SEQ ID NO: 144 (CDR-1-V_H-αvß6)
TCGACCTCAGTAGCGCTGCAATAAAC

SEQ ID NO: 145 (CDR-2-V_H-αvß6)
GTCATTGGTGGTAGTACCGGTCCATAC

SEQ ID NO: 146 (CDR-3-V_H-αvß6)
GGCTTGTTTGGTATAAATAATGATATTAGTAGGATC

SEQ ID NO: 147 (FR-1-V_L-αvß6)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC

SEQ ID NO: 148 (FR-2-V_L-αvß6)
GTGGGAGGCACAGTCACCATCAAGTGCCAGGCCAGT

SEQ ID NO: 149 (FR-3-V_L-αvß6)
TTAGCCTGGTATCAAAAAAAATCAGGGCAGCGTCCCAAACTCCTGATCTATGCTGCATCCA
CTCTGGCATCTGGGGTCTCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCT
CACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTATTGTCAG

SEQ ID NO: 150 (DTM-αvß6 incl. signal peptide [lower case])
atggggattgaactgctttgcctgttctttctatttctaGGAAGGAATGATCACGTACAAG
GTGGCTGTGCCCTGGGAGGTGCAGAAACCTGTGAAGACTGCCTGCTTATTGGACCTCAGTG
TGCCTGGTGTGCTCAGGAGAATTTTACTCATCCATCTGGAGTTGGCGAAAGGTGTGATACC
CCAGCAAACCTTTTAGCTAAAGGATGTCAATTAAACTTCATCGAAAACCCTGTCTCCCAAG
TAGAAATACTTAAAAATAAGCCTCTCAGTGTAGGCAGACAGAAAAATAGTTCTGACATTGT
TCAGATTGCGCCTCAAAGCTTGATCCTTAAGTTGAGACCAGGTGGTGCGCAGACTCTGCAG
GTGCATGTCCGCCAGACTGAGGACTACCCGGTGGATTTGTATTACCTCATGGACCTCTCCG
CCTCCATGGATGACGACCTCAACACAATAAAGGAGCTGGGCTCCCGGCTTTCCAAAGAGAT
GTCTAAATTAACCAGCAACTTTAGACTGGGCTTCGGATCTTTTGTGGAAAAACCTGTATCC
CCTTTCGTGAAAACAACACCAGAAGAAATTGCCAACCCTTGCAGTAGTATTCCATACTTCT
GTTTACCTACATTTGGATTCAAGCACATTTTGCCATTGACAAATGATGCTGAAAGATTCAA
TGAAATTGTGAAGAATCAGAAAATTTCTGCTAATATTGACACACCCGAAGGTGGATTTGAT
GCAATTATGCAAGCTGCTGTGTGTAAGGAAAAAATTGGCTGGCGGAATGACTCCCTCCACC
TCCTGGTCTTTGTGAGTGATGCTGATTCTCATTTTGGAATGGACAGCAAACTAGCAGGCAT
CGTCATTCCTAATGACGGGCTCTGTCACTTGGACAGCAAGAATGAATACTCCATGTCAACT
GTCTTGGAATATCCAACAATTGGACAACTCATTGATAAACTGGTACAAAACAACGTGTTAT
TGATCTTCGCTGTAACCCAAGAACAAGTTCATTTATATGAGAATTACGCAAAACTTATTCC
TGGAGCTACAGTAGGTCTACTTCAGAAGGACTCCGGAAACATTCTCCAGCTGATCATCTCA
GCTTATGAAGAACTGCGGTCTGAGGTGGAACTGGAAGTATTAGGAGACACTGAAGGACTCA
ACTTGTCATTTACAGCCATCTGTAACAACGGTACCCTCTTCCAACACCAAAAGAAATGCTC
TCACATGAAAGTGGGAGACACAGCTTCCTTCAGCGTGACTGTGAATATCCCACACTGCGAG
AGAAGAAGCAGGCACATTATCATAAAGCCTGTGGGGCTGGGGGATGCCCTGGAATTACTTG
TCAGCCCAGAATGCAACTGCGACTGTCAGAAAGAAGTGGAAGTGAACAGCTCCAAATGTCA
CCACGGGAACGGCTCTTTCCAGTGTGGGGTGTGTGCCTGCCACCCTGGCCACATGGGGCCT
CGCTGTGAGTGTGGCGAGGACATGCTGAGCACAGATTCCTGCAAGGAGGCCCCAGATCATC
CCTCCTGCAGCGGAAGGGGTGACTGCTACTGTGGGCAGTGTATCTGCCACTTGTCTCCCTA
TGGAAACATTTATGGGCCTTATTGCCAGTGTGACAATTTCTCCTGCGTGAGACACAAAGGG
CTGCTCTGCGGAGGTAACGGCGACTGTGACTGTGGTGAATGTGTGTGCAGGAGCGGCTGGA
CTGGCGAGTACTGCAACTGCACCACCAGCACGGACTCCTGCGTCTCTGAAGATGGAGTGCT
CTGCAGCGGGCGCGGGGACTGTGTTTGTGGCAAGTGTGTTTGCACAAACCCTGGAGCCTCA
GGACCAACCTGTGAACGATGTCCTACCTGTGGTGACCCCTGTAACTCTAAACGGAGCTGCA
TTGAGTGCCACCTGTCAGCAGCTGGCCAAGCCCGAGAAGAATGTGTGGACAAGTGCAAACT
AGCTGGTGCGACCATCAGTGAAGAAGAAGATTTCTCAAAGGATGGTTCTGTTTCCTGCTCT
CTGCAAGGAGAAAATGAATGTCTTATTACATTCCTAATAACTACAGATAATGAGGGGAAAA
CCATCATTCACAGCATCAATGAAAAAGATTGTCCGAAGCCTCCAAAC

SEQ ID NO: 151 (FR-1-V_H-αvß6)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGCTGGAGGAGTCCGGGGGTCGCCTGGTCAAGCCTGGGACACCCCTGACACTCACCTGCAC
AGTCTCTGGAA

SEQ ID NO: 152 (FR-2-V_H-αvß6)
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGGATCGGG

SEQ ID NO: 153 (FR-3-V_H-αvß6)
TACGCGAGCTGGGTGAATGGCCGATTCACCATCTCCAAAACCTCGACCACGGTGGCTCTGA
AAATCGCCGGGCCGACAACCGAGGACACGGCCACCTATTTCTGTGCCAGA

SEQ ID NO: 154 (FR-4-V_H-αvß6)
TGGGGCCCAGGCACCCTGGTCACCGTCTCCTTA

SEQ ID NO: 155 (V_L-αvß6: CDRs + FRs)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCA
GATGTGCCTATGATATGACCCAGACTCCAGCCTCTGTGGAGGTAGTTGTGGGAGGCACAGT
CACCATCAAGTGCCAGGCCAGTCAGAGCGTTGGTATTAATTTAGCCTGGTATCAAAAAAAA
TCAGGGCAGCGTCCCAAACTCCTGATCTATGCTGCATCCACTCTGGCATCTGGGGTCTCAT
CGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATCAGCGACCTGGAGTG
TGCCGATGCTGCCACTTACTATTGTCAGCAGACTTATAGTAGTGGTAATGTTGATAATGTG

SEQ ID NO: 156 (V_H-αvß6: CDRs + FRs)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGCTGGAGGAGTCCGGGGGTCGCCTGGTCAAGCCTGGGACACCCCTGACACTCACCTGCAC
AGTCTCTGGAATCGACCTCAGTAGCGCTGCAATAAACTGGGTCCGCCAGGCTCCAGGGAAG
GGGCTGGAATGGATCGGGGTCATTGGTGGTAGTACCGGTCCATACTACGCGAGCTGGGTGA
ATGGCCGATTCACCATCTCCAAAACCTCGACCACGGTGGCTCTGAAAATCGCCGGGCCGAC
AACCGAGGACACGGCCACCTATTTCTGTGCCAGAGGCTTGTTTGGTATAAATAATGATATT
AGTAGGATCTGGGGCCCAGGCACCCTGGTCACCGTCTCCTTA

SEQ ID NO: 157 (C_L-αvß6)
TTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCT
TCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAA
ATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATC
GAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGA
CACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACNNAGGGCAC
GACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAGAGTGAGAGCGGCCGC

SEQ ID NO: 158 (C_H-αvß6)
GGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCT
CCACGGTGACCCTGGGCTGCCTGGTCAAAGGGTACCTCCCGGAGCCAGTGACCGTGACCTG
GAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGC
CTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACG
TGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAA
GCCCACGTGCCCACCCCCTGAACTCCTGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGA
GCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGC
CCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCC
ATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCAC
TCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGT
CTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATG
ATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGG
ACAACTACAAGACCACGCCGGCCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAA
GCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCAC
GAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATGAGCGC
TGTGCCGGCGAGCTGCGGCCGC

SEQ ID NO: 159 (L-αvß6: CDRs + FRs + C_L)

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC[redacted]GTGGGAGGCACAGT
CACCATCAAGTGCCAGGCCAGTCAGAGCGTTGGTATTAATTTAGCCTGGTATCAAAAAAAA
TCAGGGCAGCGTCCCAAACTCCTGATCTATGCTGCATCCACTCTGGCATCTGGGGTCTCAT
CGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATCAGCGACCTGGAGTG
TGCCGATGCTGCCACTTACTATTGTCAG[redacted]CATAATGTG
TTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCT
TCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAA
ATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATC
GAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGA
CACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACNNAGGGCAC
GACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAGAGTGAGAGCGGCCGC

SEQ ID NO: 160 (H-αvß6: CDRs + FRs + C_H)

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGCTGGAGGAGTCCGGGGGTCGCCTGGTCAAGCCTGGGACACCCCTGACACTCACCTGCAC
AGTCTCTGGAA[redacted]TGGGTCCGCCAGGCTCCAGGGAAG
GGGCTGGAATGGATCGGGGTCATTGGTGGTAGTACCGGTCCATACTACGCGAGCTGGGTGA
ATGGCCGATTCACCATCTCCAAAACCTCGACCACGGTGGCTCTGAAAATCGCCGGGCCGAC
AACCGAGGACACGGCCACCTATTTCTGTGCCAGA[redacted]
[redacted]TGGGGCCCAGGCACCCTGGTCACCGTCTCCTTAGGGCAACCTAAGGCTCCAT
CAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTG
CCTGGTCAAAGGGTACCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACC
AATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCG
TGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAA
CACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAAGCCCACGTGCCCACCCCCT
GAACTCCTGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGT
GCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAG
CAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACTGGC
TGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAA
AACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCC
CGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTT
CCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCC
GGCCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGT
GAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACT
ACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATGAGCGCTGTGCCGGCGAGCTGCGGC
CGC

SEQ ID NO: 161 (CDR-1-V_L-αvß8)
RCDVVMTQTPSSVSEP

SEQ ID NO: 162 (CDR-2-V_L-αvß8)
ENIYSS

SEQ ID NO: 163 (CDR-3-V_L-αvß8)
QCTGGIIIDGGA

SEQ ID NO: 164 (CDR-1-V_H-αvß8)
FSLNSGNMQ

SEQ ID NO: 165 (CDR-2-V_H-αvß8)
YIGSGGSTF

SEQ ID NO: 166 (CDR-3-V_H-αvß8)
GRYGGSRGV

SEQ ID NO: 167 (FR-1-V_L-αvß8)
MDTRAPTQLLGLLLLWLPGA

SEQ ID NO: 168 (FR-2-V_L-αvß8)
VGGTVTINCQAS

SEQ ID NO: 169 (FR-3-V_L-αvß8)
LAWYQQKPGQPPKLLIYAASNLASGVPSRFKGSGSGTEFTLTISDLACADAATYYC

SEQ ID NO: 170 (DTM-αvß8)
EDNRCASSNAASCARCLALGPECGWCVQEDFISGGSRSERCDIVSNLISKGCSVDSIEYPS
VHVIIPTENEINTQVTPGEVSIQLRPGAEANFMLKVHPLKKYPVDLYYLVDVSASMHNNIE
KLNSVGNDLSRKMAFFSRDFRLGFGSYVDKTVSPYISIHPERIHNQCSDYNLDCMPPHGYI
HVLSLTENITEFEKAVHRQKISGNIDTPEGGFDAMLQAAVCESHIGWRKEAKRLLLVMTDQ
TSHLALDSKLAGIVVPNDGNCHLKNNVYVKSTTMEHPSLGQLSEKLIDNNINVIFAVQGKQ
FHWYKDLLPLLPGTIAGEIESKAANLNNLVVEAYQKLISEVKVQVENQVQGIYFNITAICP
DGSRKPGMEGCRNVTSNDEVLFNVTVTMKKCDVTGGKNYAIIKPIGFNETAKIHIHRNCSC
QCEDNRGPKGKCVDETFLDSKCFQCDENKCHFDEDQFSSESCKSHKDQPVCSGRGVCVCGK
CSCHKIKLGKVYGKYCEKDDFSCPYHHGNLCAGHGECEAGRCQCFSGWEGDRCQCPSAAAQ
HCVNSKGQVCSGRGTCVCGRCECTDPRSIGRFCEHCPTCYTACKENWNCMQCLHPHNLSQA
ILDQCKTSCALMEQQHYVDQTSECFSSPSYLR

SEQ ID NO: 171 (FR-1-V_H-αvß8)
METGLRWLLLVAVLKGVQCQSVEESGGRLVTPGTPLTLTCAVSG

SEQ ID NO: 172 (FR-2-V_H-αvß8)
WVRQAPGKGLEYIG

SEQ ID NO: 173 (FR-3-V_H-αvß8)
YASWVNGRFTISKTSTTVDLKITSPTTEDTATYFC

SEQ ID NO: 174 (FR-4-V_H-αvß8)
WGPGTLVTVSL

SEQ ID NO: 175 (V_L-αvß8: CDRs + FRs)
MDTRAPTQLLGLLLLWLPGARCDVVMTQTPSSVSEPVGGTVTINCQASENIYSSLAWYQQK
PGQPPKLLIYAASNLASGVPSRFKGSGSGTEFTLTISDLACADAATYYCQCTGGIIIDGGA

SEQ ID NO: 176 (V_H-αvß8: CDRs + FRs)
METGLRWLLLVAVLKGVQCQSVEESGGRLVTPGTPLTLTCAVSGFSLNSGNMQWVRQAPGK
GLEYIGYIGSGGSTFYASWVNGRFTISKTSTTVDLKITSPTTEDTATYFCGRYGGSRGVWG
PGTLVTVSL

SEQ ID NO: 177 (C_L-αvß8)
FGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTTGI
ENSKTPHNSADCTYNLISTLTLTXTQYNSHKEYTCKVTQGTTSVVQXFNRGDCLE

SEQ ID NO: 178 (C_H-αvß8)
GQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSG
LYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPK
PKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLP
IAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCM
INGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMH
EALHNHYTQKSISRSPGK

SEQ ID NO: 179 (L-αvß8: CDRs + FRs + C_L)
MDTRAPTQLLGLLLLWLPGA[redacted]VGGTVTINCQASENIYSSLAWYQQK
PGQPPKLLIYAASNLASGVPSRFKGSGSGTEFTLTISDLACADAATYYCQCTGGIIIDGGA
FGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTTGI
ENSKTPHNSADCTYNLISTLTLTXTQYNSHKEYTCKVTQGTTSVVQXFNRGDCLE

SEQ ID NO: 180 (H-αvß8: CDRs + FRs + C_H)
METGLRWLLLVAVLKGVQCQSVEESGGRLVTPGTPLTLTCAVSG[redacted]WVRQAPGK
GLEYIGYIGSGGSTFYASWVNGRFTISKTSTTVDLKITSPTTEDTATYFCGRYGGSRGVWG
PGTLVTVSLGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRT
FPSVRQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGG
PSVFIFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNS
TIRVVSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELS
SRSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRG
DVFTCSVMHEALHNHYTQKSISRSPGK

SEQ ID NO: 181 (CDR-1-V_L-αvß8)
AGATGTGATGTTGTGATGACCCAGACTCCATCCTCCGTGTCTGAACCT

SEQ ID NO: 182 (CDR-2-V_L-αvß8)
GAGAACATTTACAGTTCT

SEQ ID NO: 183 (CDR-3-V_L-αvß8)
TGTACTGGTGGTATTATTATTGATGGGGGTGCT

SEQ ID NO: 184 (CDR-1-V_H-αvß8)
TTCTCCCTCAATAGTGGCAATATGCAA

SEQ ID NO: 185 (CDR-2-V_H-αvß8)
TACATTGGTAGTGGTGGTAGCACATTC

SEQ ID NO: 186 (CDR-3-V_H-αvß8)
GGCAGATATGGTGGTAGTAGGGGTGTA

SEQ ID NO: 187 (FR-1-V_L-αvß8)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC

SEQ ID NO: 188 (FR-2-V_L-αvß8)
GTGGGAGGCACAGTCACCATCAATTGCCAGGCCAGT

SEQ ID NO: 189 (FR-3-V_L-αvß8)
TTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATGCTGCATCCA
ATCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCT
CACCATCAGCGACCTGGCGTGTGCCGATGCTGCCACTTACTATTGTCAA

SEQ ID NO: 190 (DTM-αvß8 incl. signal peptide [lower case])
atgtgcggctcggccctggctttttttaccgctgcatttgtctgcctgcaaaacgaccggc
gaggtcccgcctcgttcctctgggcagcctgggtgttttcacttgttcttggactgggcca
aggtGAAGACAATAGATGTGCATCTTCAAATGCAGCATCCTGTGCCAGGTGCCTTGCGCTG
GGTCCAGAATGTGGATGGTGTGTTCAAGAGGATTTCATTTCAGGTGGATCAAGAAGTGAAC
GTTGTGATATTGTTTCCAATTTAATAAGCAAAGGCTGCTCAGTTGATTCAATAGAATACCC
ATCTGTGCATGTTATAATACCCACTGAAAATGAAATTAATACCCAGGTGACACCAGGAGAA
GTGTCTATCCAGCTGCGTCCAGGAGCCGAAGCTAATTTTATGCTGAAAGTTCATCCTCTGA
AGAAATATCCTGTGGATCTTTATTATCTTGTTGATGTCTCAGCATCAATGCACAATAATAT
AGAAAAATTAAATTCCGTTGGAAACGATTTATCTAGAAAAATGGCATTTTTCTCCCGTGAC
TTTCGTCTTGGATTTGGCTCATACGTTGATAAAACAGTTTCACCATACATTAGCATCCACC
CCGAAAGGATTCATAATCAATGCAGTGACTACAATTTAGACTGCATGCCTCCCCATGGATA
CATCCATGTGCTGTCTTTGACAGAGAACATCACTGAGTTTGAGAAAGCAGTTCATAGACAG
AAGATCTCTGGAAACATAGATACACCAGAAGGAGGTTTTGACGCCATGCTTCAGGCAGCTG
TCTGTGAAAGTCATATCGGATGGCGAAAAGAGGCTAAAAGATTGCTGCTGGTGATGACAGA
TCAGACGTCTCATCTCGCTCTTGATAGCAAATTGGCAGGCATAGTGGTGCCCAATGACGGA
AACTGTCATCTGAAAAACAACGTCTATGTCAAATCGACAACCATGGAACACCCCTCACTAG
GCCAACTTTCAGAGAAATTAATAGACAACAACATTAATGTCATCTTTGCAGTTCAAGGAAA
ACAATTTCATTGGTATAAGGATCTTCTACCCCTCTTGCCAGGCACCATTGCTGGTGAAATA
GAATCAAAGGCTGCAAACCTCAATAATTTGGTAGTGGAAGCCTATCAGAAGCTCATTTCAG
AAGTGAAAGTTCAGGTGGAAAACCAGGTACAAGGCATCTATTTTAACATTACCGCCATCTG
TCCAGATGGGTCCAGAAAGCCAGGCATGGAAGGATGCAGAAACGTGACGAGCAATGATGAA
GTTCTTTTCAATGTAACAGTTACAATGAAAAAATGTGATGTCACAGGAGGAAAAAACTATG
CAATAATCAAACCTATTGGTTTTAATGAAACCGCTAAAATTCATATACACAGAAACTGCAG
CTGTCAGTGTGAGGACAACAGAGGACCTAAAGGAAAGTGTGTAGATGAAACTTTTCTAGAT
TCCAAGTGTTTCCAGTGTGATGAGAATAAATGTCATTTTGATGAAGATCAGTTTTCTTCTG
AGAGTTGCAAGTCACACAAGGATCAGCCTGTTTGCAGTGGTCGAGGAGTTTGTGTTTGTGG
GAAATGTTCATGTCACAAAATTAAGCTTGGAAAAGTGTATGGAAAATACTGTGAAAAGGAT
GACTTTTCTTGTCCATATCACCATGGAAATCTGTGTGCTGGGCATGGAGAGTGTGAAGCAG
GCAGATGCCAATGCTTCAGTGGCTGGGAAGGTGATCGATGCCAGTGCCCTTCAGCAGCAGC
CCAGCACTGTGTCAATTCAAAGGGCCAAGTGTGCAGTGGAAGAGGCACGTGTGTGTGTGGA
AGGTGTGAGTGCACCGATCCCAGGAGCATCGGCCGCTTCTGTGAACACTGCCCCACCTGTT
ATACAGCCTGCAAGGAAAACTGGAATTGTATGCAATGCCTTCACCCTCACAATTTGTCTCA
GGCTATACTTGATCAGTGCAAAACCTCATGTGCTCTCATGGAACAACAGCATTATGTCGAC
CAAACTTCAGAATGTTTCTCCAGCCCAAGCTACTTGAGA

SEQ ID NO: 191 (FR-1-V_H-αvß8)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCGC
AGTCTCTGGA

SEQ ID NO: 192 (FR-2-V_H-αvß8)
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATACATCGGA

SEQ ID NO: 193 (FR-3-V_H-αvß8)
TACGCGAGCTGGGTGAATGGCCGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTGA
AGATCACCAGTCCGACAACCGAGGACACGGCCACCTATTTTTGT

SEQ ID NO: 194 (FR-4-V_H-αvß8)
TGGGGCCCAGGCACCCTG

SEQ ID NO: 195 (V_L-αvß8: CDRs + FRs)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCA
GATGTGATGTTGTGATGACCCAGACTCCATCCTCCGTGTCTGAACCTGTGGGAGGCACAGT
CACCATCAATTGCCAGGCCAGTGAGAACATTTACAGTTCTTTAGCCTGGTATCAGCAGAAA
CCAGGGCAGCCTCCCAAGCTCCTGATCTATGCTGCATCCAATCTGGCATCTGGGGTCCCAT
CGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCGACCTGGCGTG
TGCCGATGCTGCCACTTACTATTGTCAATGTACTGGTGGTATTATTATTGATGGGGGTGCT

SEQ ID NO: 196 (V_H-αvß8: CDRs + FRs)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCGC
AGTCTCTGGATTCTCCCTCAATAGTGGCAATATGCAATGGGTCCGCCAGGCTCCAGGGAAG
GGGCTGGAATACATCGGATACATTGGTAGTGGTGGTAGCACATTCTACGCGAGCTGGGTGA
ATGGCCGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTGAAGATCACCAGTCCGAC
AACCGAGGACACGGCCACCTATTTTTGTGGCAGATATGGTGGTAGTAGGGGTGTATGGGGC
CCAGGCACCCTG

SEQ ID NO: 197 (C_L-αvß8)
TTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCT
TCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAA
ATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATC
GAGAACAGTAAAACACCGCATAATTCTGCAGATTGTACCTACAACCTCATCAGCACTCTGA
CACTGACCANCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCAC
GACCTCAGTCGTCCAGANCTTCAATAGGGGTGACTGTTTAGAGTGAGAGCGGCCGC

SEQ ID NO: 198 (C_H-αvß8)
GTCACCGTCTCCTTAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCG
GGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGGTACCTCCCGGAGCC
AGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTC
CGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGC
CCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCC
CTCGACATGCAGCAAGCCCACGTGCCCACCCCCTGAACTCCTGGGGGGACCGTCTGTCTTC
ATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCG
TGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGA
GCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTG
GTCAGCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAG
TCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCC
CCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTC
AGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGA
ACGGGAAGGCAGAGGACAACTACAAGACCACGCCGGCCGTGCTGGACAGCGACGGCTCCTA
CTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACC
TGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTC
CGGGTAAATGAGCGCTGTGCCGGCGAGCTGCGGCCGC

SEQ ID NO: 199 (L-αvß8: CDRs + FRs + C_L)

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCC[redacted]
[redacted]GTGGGAGGCACAGT
CACCATCAATTGCCAGGCCAGTGAGAACATTTACAGTTCTTTAGCCTGGTATCAGCAGAAA
CCAGGGCAGCCTCCCAAGCTCCTGATCTATGCTGCATCCAATCTGGCATCTGGGGTCCCAT
CGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCGACCTGGCGTG
TGCCGATGCTGCCACTTACTATTGTCAA[redacted]TGCT
TTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCT
TCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAA
ATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATC
GAGAACAGTAAAACACCGCATAATTCTGCAGATTGTACCTACAACCTCATCAGCACTCTGA
CACTGACCANCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCAC
GACCTCAGTCGTCCAGANCTTCAATAGGGGTGACTGTTTAGAGTGAGAGCGGCCGC

SEQ ID NO: 200 (H-αvß8: CDRs + FRs + C_H)

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGT
CGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCGC
AGTCTCTGGA[redacted]TGGGTCCGCCAGGCTCCAGGGAAG
GGGCTGGAATACATCGGATACATTGGTAGTGGTGGTAGCACATTCTACGCGAGCTGGGTGA
ATGGCCGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTGAAGATCACCAGTCCGAC
AACCGAGGACACGGCCACCTATTTTTGT[redacted]TGGGGC
CCAGGCACCCTGGTCACCGTCTCCTTAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGG
CCCCCTGCTGCGGGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGGTA
CCTCCCGGAGCCAGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACC
TTCCCGTCCGTCCGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCT
CAAGCAGCCAGCCCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAA
GACCGTTGCGCCCTCGACATGCAGCAAGCCCACGTGCCCACCCCCTGAACTCCTGGGGGGA
CCGTCTGTCTTCATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCG
AGGTCACATGCGTGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTA
CATAAACAACGAGCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGC
ACGATCCGCGTGGTCAGCACCCTCCCCATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGT
TCAAGTGCAAAGTCCACAACAAGGCACTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGC
CAGAGGGCAGCCCCTGGAGCCGAAGGTCTACACCATGGGCCCTCCCCGGGAGGAGCTGAGC
AGCAGGTCGGTCAGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGG
AGTGGGAGAAGAACGGGAAGGCAGAGGACAACTACAAGACCACGCCGGCCGTGCTGGACAG
CGACGGCTCCTACTTCCTCTACAGCAAGCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGC
GACGTCTTCACCTGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCA
TCTCCCGCTCTCCGGGTAAATGAGCGCTGTGCCGGCGAGCTGCGGCCGC

SEQ ID NO: 201 (CDR-1-V_L-αv)
TFAQVLTQTPSSVSAA

SEQ ID NO: 202 (CDR-2-V_L-αv)
QSVASNNA

SEQ ID NO: 203 (CDR-3-V_L-αv)
LGGYDCRGTDCNV

SEQ ID NO: 204 (CDR-1-V_H-αv)
IDLTSNSLS

SEQ ID NO: 205 (CDR-2-V_H-αv)
AISSRATTY

SEQ ID NO: 206 (CDR-3-V_H-αv)
GKFNL

SEQ ID NO: 207 (FR-1-V_L-αv)
MDTRAPTQLLGLLLLWLPGA

SEQ ID NO: 208 (FR-2-V_L-αv)
VGGTVTINCQAS

SEQ ID NO: 209 (FR-3-V_L-αv)
LAWFQQKPGQPPKLLIYYASTLASGVPSRFKGSGSGTQFTLTISDLECADAATYYC

SEQ ID NO: 210 (DTM-αv)
FNLDVDSPAEYSGPEGSYFGFAVDFFVPSASSRMFLLVGAPKANTTQPGIVEGGQVLKCDW
SSTRRCQPIEFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQER
EPVGTCFLQDGTKTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADRVLLGGPGSFYWQGQL
ISDQVAEIVSKYDPNVYSIKYNNQLATRTAQAIFDDSYLGYSVAVGDFNGDGIDDFVSGVP
RAARTLGMVYIYDGKNMSSLYNFTGEQMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGS
DGKLQEVGQVSVSLQRASGDFQTTKLNGFEVFARFGSAIAPLGDLDQDGFNDIAIAAPYGG
EDKKGIVYIFNGRSTGLNAVPSQILEGQWAARSMPPSFGYSMKGATDIDKNGYPDLIVGAF
GVDRAILYRARPVITVNAGLEVYPSILNQDNKTCSLPGTALKVSCFNVRFCLKADGKGVLP
RKLNFQVELLLDKLKQKGAIRRALFLYSRSPSHSKNMTISRGGLMQCEELIAYLRDESEFR
DKLTPITIFMEYRLDYRTAADTTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSV
DSDQKKIYIGDDNPLTLIVKAQNQGEGAYEAELIVSIPLQADFIGVVRNNEALARLSCAFK
TENQTRQVVCDLGNPMKAGTQLLAGLRFSVHQQSEMDTSVKFDLQIQSSNLFDKVSPVVSH
KVDLAVLAAVEIRGVSSPDHIFLPIPNWEHKENPETEEDVGPVVQHIYELRNNGPSSFSKA
MLHLQWPYKYNNNTLLYILHYDIDGPMNCTSDMEINPLRIKISSLQTTEKNDTVAGQGERD
HLITKRDLALSEGDIHTLGCGVAQCLKIVCQVGRLDRGKSAILYVKSLLWTETFMNKENQN
HSYSLKSSASFNVIEFPYKNLPIEDITNSTLVTTNVTWGIQP

SEQ ID NO: 211 (FR-1-V_H-αv)
METGLRWLLLVAVLKGAQCQSVEESGGRLVTPGTSLTLTCTVSG

SEQ ID NO: 212 (FR-2-V_H-αv)
WVRQAPGKGLEWIG

SEQ ID NO: 213 (FR-3-V_H-αv)
FAAWAKGRFTISRTSTTVDLRITSLTASDTATYFC

SEQ ID NO: 214 (FR-4-V_H-αv)
WGQGTLVTVSS

SEQ ID NO: 215 (V_L-αv: CDRs + FRs)
MDTRAPTQLLGLLLLWLPGATFAQVLTQTPSSVSAAVGGTVTINCQASQSVASNNALAWFQ
QKPGQPPKLLIYYASTLASGVPSRFKGSGSGTQFTLTISDLECADAATYYCLGGYDCRGTD
CNV

SEQ ID NO: 216 (V_H-αv: CDRs + FRs)
METGLRWLLLVAVLKGAQCQSVEESGGRLVTPGTSLTLTCTVSGIDLTSNSLSWVRQAPGK
GLEWIGAISSRATTYFAAWAKGRFTISRTSTTVDLRITSLTASDTATYFCGKFNLWGQGTL
VTVSS

SEQ ID NO: 217 (C_L-αv)
FGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQTTGI
ENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC

SEQ ID NO: 218 (C_H-αv)
GQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSG
LYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVFIFPPK
PKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLP
IAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCM
INGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRGDVFTCSVMH
EALHNHYTQKSISRSPGK

SEQ ID NO: 219 (L-αv: CDRs + FRs + C_L)
MDTRAPTQLLGLLLLWLPGA[redacted]VGGTVTINCQASQSVASNNALAWFQ
QKPGQPPKLLIYYASTLASGVPSRFKGSGSGTQFTLTISDLECADAATYYCLGGYDCRGTD
CNVFGGGTEVVVKGDPVAPTVLIFPPAADQVATGTVTIVCVANKYFPDVTVTWEVDGTTQT
TGIENSKTPQNSADCTYNLSSTLTLTSTQYNSHKEYTCKVTQGTTSVVQSFNRGDC

SEQ ID NO: 220 (H-αv: CDRs + FRs + C_H)
METGLRWLLLVAVLKGAQCQSVEESGGRLVTPGTSLTLTCTVSG[redacted]WVRQAPGK
GLEWIGAISSRATTYFAAWAKGRFTISRTSTTVDLRITSLTASDTATYFCGKFNLWGQGTL
VTVSSGQPKAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSV
RQSSGLYSLSSVVSVTSSSQPVTCNVAHPATNTKVDKTVAPSTCSKPTCPPPELLGGPSVF
IFPPKPKDTLMISRTPEVTCVVVDVSQDDPEVQFTWYINNEQVRTARPPLREQQFNSTIRV
VSTLPIAHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSV
SLTCMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYSKLSVPTSEWQRGDVFT
CSVMHEALHNHYTQKSISRSPGK

SEQ ID NO: 221 (CDR-1-V_L-αv)
CATTTGCCCAAGTGCTGACCCAGACTCCATCCTCCGTGTCTGCAGC

SEQ ID NO: 222 (CDR-2-V_L-αv)
CAGAGTGTTGCTAGTAACAATGCC

SEQ ID NO: 223 (CDR-3-V_L-αv)
GGCGGTTATGATTGTAGGGGTACTGATTGTAATGTT

SEQ ID NO: 224 (CDR-1-V_H-αv)
ATCGACCTCACTAGCAATTCGCTGAGC

SEQ ID NO: 225 (CDR-2-V_H-αv)
GCCATTAGTAGTCGTGCTACCACATAT

SEQ ID NO: 226 (CDR-3-V_H-αv)
GGGAAATTTAATTTG

SEQ ID NO: 227 (FR-1-V_L-αv)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCA

SEQ ID NO: 228 (FR-2-V_L-αv)
TGTGGGGGGCACAGTCACCATCAATTGCCAGGCCAGT

SEQ ID NO: 229 (FR-3-V_L-αv)
TTAGCCTGGTTTCAGCAGAAACCAGGGCAGCCTCCCAAACTCCTGATCTATTATGCGTCCA
CTCTGGCATCTGGGGTCCCATCGCGATTCAAAGGCAGTGGATCTGGGACACAGTTCACTCT
CACCATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCTA

SEQ ID NO: 230 (DTM-αv incl. signal peptide [lower case])

atggcttttccgccgcggcgacggctgcgcctcggtccccgcggcctcccgcttcttctct
cgggactcctgctacctctgtgccgcgccTTCAACCTAGACGTGGACAGTCCTGCCGAGTA
CTCTGGCCCCGAGGGAAGTTACTTCGGCTTCGCCGTGGATTTCTTCGTGCCCAGCGCGTCT
TCCCGGATGTTTCTTCTCGTGGGAGCTCCCAAAGCAAACACCACCCAGCCTGGGATTGTGG
AAGGAGGGCAGGTCCTCAAATGTGACTGGTCTTCTACCCGCCGGTGCCAGCCAATTGAATT
TGATGCAACAGGCAATAGAGATTATGCCAAGGATGATCCATTGGAATTTAAGTCCCATCAG
TGGTTTGGAGCATCTGTGAGGTCGAAACAGGATAAAATTTTGGCCTGTGCCCCATTGTACC
ATTGGAGAACTGAGATGAAACAGGAGCGAGAGCCTGTTGGAACATGCTTTCTTCAAGATGG
AACAAAGACTGTTGAGTATGCTCCATGTAGATCACAAGATATTGATGCTGATGGACAGGGA
TTTTGTCAAGGAGGATTCAGCATTGATTTTACTAAAGCTGACAGAGTACTTCTTGGTGGTC
CTGGTAGCTTTTATTGGCAAGGTCAGCTTATTTCGGATCAAGTGGCAGAAATCGTATCTAA
ATACGACCCCAATGTTTACAGCATCAAGTATAATAACCAATTAGCAACTCGGACTGCACAA
GCTATTTTTGATGACAGCTATTTGGGTTATTCTGTGGCTGTCGGAGATTTCAATGGTGATG
GCATAGATGACTTTGTTTCAGGAGTTCCAAGAGCAGCAAGGACTTTGGGAATGGTTTATAT
TTATGATGGGAAGAACATGTCCTCCTTATACAATTTTACTGGCGAGCAGATGGCTGCATAT
TTCGGATTTTCTGTAGCTGCCACTGACATTAATGGAGATGATTATGCAGATGTGTTTATTG
GAGCACCTCTCTTCATGGATCGTGGCTCTGATGGCAAACTCCAAGAGGTGGGGCAGGTCTC
AGTGTCTCTACAGAGAGCTTCAGGAGACTTCCAGACGACAAAGCTGAATGGATTTGAGGTC
TTTGCACGGTTTGGCAGTGCCATAGCTCCTTTGGGAGATCTGGACCAGGATGGTTTCAATG
ATATTGCAATTGCTGCTCCATATGGGGGTGAAGATAAAAAAGGAATTGTTTATATCTTCAA
TGGAAGATCAACAGGCTTGAACGCAGTCCCATCTCAAATCCTTGAAGGGCAGTGGGCTGCT
CGAAGCATGCCACCAAGCTTTGGCTATTCAATGAAAGGAGCCACAGATATAGACAAAAATG
GATATCCAGACTTAATTGTAGGAGCTTTTGGTGTAGATCGAGCTATCTTATACAGGGCCAG
ACCAGTTATCACTGTAAATGCTGGTCTTGAAGTGTACCCTAGCATTTTAAATCAAGACAAT
AAAACCTGCTCACTGCCTGGAACAGCTCTCAAAGTTTCCTGTTTTAATGTTAGGTTCTGCT
TAAAGGCAGATGGCAAAGGAGTACTTCCCAGGAAACTTAATTTCCAGGTGGAACTTCTTTT
GGATAAACTCAAGCAAAAGGGAGCAATTCGACGAGCACTGTTTCTCTACAGCAGGTCCCCA
AGTCACTCCAAGAACATGACTATTTCAAGGGGGGGACTGATGCAGTGTGAGGAATTGATAG
CGTATCTGCGGGATGAATCTGAATTTAGAGACAAACTCACTCCAATTACTATTTTTATGGA
ATATCGGTTGGATTATAGAACAGCTGCTGATACAACAGGCTTGCAACCCATTCTTAACCAG
TTCACGCCTGCTAACATTAGTCGACAGGCTCACATTCTACTTGACTGTGGTGAAGACAATG
TCTGTAAACCCAAGCTGGAAGTTTCTGTAGATAGTGATCAAAAGAAGATCTATATTGGGGA
TGACAACCCTCTGACATTGATTGTTAAGGCTCAGAATCAAGGAGAAGGTGCCTACGAAGCT
GAGCTCATCGTTTCCATTCCACTGCAGGCTGATTTCATCGGGGTTGTCCGAAACAATGAAG
CCTTAGCAAGACTTTCCTGTGCATTTAAGACAGAAAACCAAACTCGCCAGGTGGTATGTGA
CCTTGGAAACCCAATGAAGGCTGGAACTCAACTCTTAGCTGGTCTTCGTTTCAGTGTGCAC
CAGCAGTCAGAGATGGATACTTCTGTGAAATTTGACTTACAAATCCAAAGCTCAAATCTAT
TTGACAAAGTAAGCCCAGTTGTATCTCACAAAGTTGATCTTGCTGTTTTAGCTGCAGTTGA
GATAAGAGGAGTCTCGAGTCCTGATCATATCTTTCTTCCGATTCCAAACTGGGAGCACAAG
GAGAACCCTGAGACTGAAGAAGATGTTGGGCCAGTTGTTCAGCACATCTATGAGCTGAGAA
ACAATGGTCCAAGTTCATTCAGCAAGGCAATGCTCCATCTTCAGTGGCCTTACAAATATAA
TAATAACACTCTGTTGTATATCCTTCATTATGATATTGATGGACCAATGAACTGCACTTCA
GATATGGAGATCAACCCTTTGAGAATTAAGATCTCATCTTTGCAAACAACTGAAAAGAATG
ACACGGTTGCCGGGCAAGGTGAGCGGGACCATCTCATCACTAAGCGGGATCTTGCCCTCAG
TGAAGGAGATATTCACACTTTGGGTTGTGGAGTTGCTCAGTGCTTGAAGATTGTCTGCCAA
GTTGGGAGATTAGACAGAGGAAAGAGTGCAATCTTGTACGTAAAGTCATTACTGTGGACTG
AGACTTTTATGAATAAAGAAAATCAGAATCATTCCTATTCTCTGAAGTCGTCTGCTTCATT
TAATGTCATAGAGTTTCCTTATAAGAATCTTCCAATTGAGGATATCACCAACTCCACATTG
GTTACCACTAATGTCACCTGGGGCATTCAGCCA

SEQ ID NO: 231 (FR-1-V_H-αv)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGCCCAGTGTCAGT
CGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACATCCCTGACACTCACCTGCAC
GGTCTCTGGA

SEQ ID NO: 232 (FR-2-V_H-αv)
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGGATCGGG

SEQ ID NO: 233 (FR-3-V_H-αv)
TTCGCGGCTTGGGCGAAGGGCCGATTCACCATCTCCAGAACCTCGACCACGGTGGATCTCA
GAATCACCAGTCTGACAGCTTCAGACACGGCCACCTATTTCTGT

SEQ ID NO: 234 (FR-4-V_H-αv)
TGGGGCCAAGGCACCCTGGTCACCGTCTCCTCA

SEQ ID NO: 235 (V_L-αv: CDRs + FRs)
ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCA
CATTTGCCCAAGTGCTGACCCAGACTCCATCCTCCGTGTCTGCAGCTGTGGGGGGCACAGT
CACCATCAATTGCCAGGCCAGTCAGAGTGTTGCTAGTAACAATGCCTTAGCCTGGTTTCAG
CAGAAACCAGGGCAGCCTCCCAAACTCCTGATCTATTATGCGTCCACTCTGGCATCTGGGG
TCCCATCGCGATTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATCAGCGACCT
GGAGTGTGCCGATGCTGCCACTTACTACTGTCTAGGCGGTTATGATTGTAGGGGTACTGAT
TGTAATGTT

SEQ ID NO: 236 (V_H-αv: CDRs + FRs)
ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGCCCAGTGTCAGT
CGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACATCCCTGACACTCACCTGCAC
GGTCTCTGGAATCGACCTCACTAGCAATTCGCTGAGCTGGGTCCGCCAGGCTCCAGGGAAG
GGGCTGGAATGGATCGGGGCCATTAGTAGTCGTGCTACCACATATTTCGCGGCTTGGGCGA
AGGGCCGATTCACCATCTCCAGAACCTCGACCACGGTGGATCTCAGAATCACCAGTCTGAC
AGCTTCAGACACGGCCACCTATTTCTGTGGGAAATTTAATTTGTGGGGCCAAGGCACCCTG
GTCACCGTCTCCTCA

SEQ ID NO: 237 (C_L-αv)
TTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGATCCAGTTGCACCTACTGTCCTCATCT
TCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGTGGCGAATAA
ATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACAACTGGCATC
GAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCAGCACTCTGA
CACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGACCCAGGGCAC
GACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAGAGTGAGAGCGGCCGC

SEQ ID NO: 238 (C_H-αv)

GGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCGGGGACACACCCAGCT
CCACGGTGACCCTGGGCTGCCTGGTCAAAGGGTACCTCCCGGAGCCAGTGACCGTGACCTG
GAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTCCGGCAGTCCTCAGGC
CTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGCCCGTCACCTGCAACG
TGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCCCTCGACATGCAGCAA
GCCCACGTGCCCACCCCCTGAACTCCTGGGGGGACCGTCTGTCTTCATCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCGTGGTGGTGGACGTGA
GCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGAGCAGGTGCGCACCGC
CCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTGGTCAGCACCCTCCCC
ATCGCGCACCAGGACTGGCTGAGGGGCAAGGAGTTCAAGTGCAAAGTCCACAACAAGGCAC
TCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAGAGGGCAGCCCCTGGAGCCGAAGGT
CTACACCATGGGCCCTCCCCGGGAGGAGCTGAGCAGCAGGTCGGTCAGCCTGACCTGCATG
ATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGAACGGGAAGGCAGAGG
ACAACTACAAGACCACGCCGGCCGTGCTGGACAGCGACGGCTCCTACTTCCTCTACAGCAA
GCTCTCAGTGCCCACGAGTGAGTGGCAGCGGGGCGACGTCTTCACCTGCTCCGTGATGCAC
GAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTCCGGGTAAATGAGCGC
TGTGCCGGCGAGCTGCGGCCGC

SEQ ID NO: 239 (L-αv: CDRs + FRs + C_L)

ATGGACACGAGGGCCCCCACTCAGCTGCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCCA
[redacted]TGTGGGGGGCACAGT
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CAGAAACCAGGGCAGCCTCCCAAACTCCTGATCTATTATGCGTCCACTCTGGCATCTGGGG
TCCCATCGCGATTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATCAGCGACCT
GGAGTGTGCCGATGCTGCCACTTACTACTGTCTA[redacted]
[redacted]TTCGGCGGAGGGACCGAGGTGGTGGTCAAAGGTGATCCAGTTGCACCTACTG
TCCTCATCTTCCCACCAGCTGCTGATCAGGTGGCAACTGGAACAGTCACCATCGTGTGTGT
GGCGAATAAATACTTTCCCGATGTCACCGTCACCTGGGAGGTGGATGGCACCACCCAAACA
ACTGGCATCGAGAACAGTAAAACACCGCAGAATTCTGCAGATTGTACCTACAACCTCAGCA
GCACTCTGACACTGACCAGCACACAGTACAACAGCCACAAAGAGTACACCTGCAAGGTGAC
CCAGGGCACGACCTCAGTCGTCCAGAGCTTCAATAGGGGTGACTGTTAGAGTGAGAGCGGC
CGC

SEQ ID NO: 240 (H-αv: CDRs + FRs + C_H)

ATGGAGACTGGGCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGCCCAGTGTCAGT
CGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACATCCCTGACACTCACCTGCAC
GGTCTCTGGA[redacted]TGGGTCCGCCAGGCTCCAGGGAAG
GGGCTGGAATGGATCGGGGCCATTAGTAGTCGTGCTACCACATATTTCGCGGCTTGGGCGA
AGGGCCGATTCACCATCTCCAGAACCTCGACCACGGTGGATCTCAGAATCACCAGTCTGAC
AGCTTCAGACACGGCCACCTATTTCTGT[redacted]TGGGGCCAAGGCACCCTG
GTCACCGTCTCCTCAGGGCAACCTAAGGCTCCATCAGTCTTCCCACTGGCCCCCTGCTGCG
GGGACACACCCAGCTCCACGGTGACCCTGGGCTGCCTGGTCAAAGGGTACCTCCCGGAGCC
AGTGACCGTGACCTGGAACTCGGGCACCCTCACCAATGGGGTACGCACCTTCCCGTCCGTC
CGGCAGTCCTCAGGCCTCTACTCGCTGAGCAGCGTGGTGAGCGTGACCTCAAGCAGCCAGC
CCGTCACCTGCAACGTGGCCCACCCAGCCACCAACACCAAAGTGGACAAGACCGTTGCGCC
CTCGACATGCAGCAAGCCCACGTGCCCACCCCCTGAACTCCTGGGGGGGACCGTCTGTCTTC
ATCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCACGCACCCCCGAGGTCACATGCG
TGGTGGTGGACGTGAGCCAGGATGACCCCGAGGTGCAGTTCACATGGTACATAAACAACGA
GCAGGTGCGCACCGCCCGGCCGCCGCTACGGGAGCAGCAGTTCAACAGCACGATCCGCGTG
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AGCCTGACCTGCATGATCAACGGCTTCTACCCTTCCGACATCTCGGTGGAGTGGGAGAAGA
ACGGGAAGGCAGAGGACAACTACAAGACCACGCCGGCCGTGCTGGACAGCGACGGCTCCTA
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TGCTCCGTGATGCACGAGGCCTTGCACAACCACTACACGCAGAAGTCCATCTCCCGCTCTC
CGGGTAAATGAGCGCTGTGCCGGCGAGCTGCGGCCGC