SEQUENCE LISTING

SEQ ID NO:1 TAU P10636-8

MAEPRQEFEV MEDHAGTYGL GDRKDQGGYT MHQDQEGDTD AGLKESPLQT TEDGSEEPG
SETSDAKSTP TAEDVTAPLV DEGAPGKQAA AQPHTEIPEG TTAEEAGIGD PSLEDEAAG
HVTQARMVSK SKDGTGSDDK KAKGADGKTK IATPRGAAPP GQKGQANATR PAKTPPAPK
TPPSSGEPPK SGDRSGYSSP GSPGTPGSRS RTPSLPTPPT REPKKVAVVR PPKSPSSAK
SRLQTAPVPM PDLKNVKSKI GSTENLKHQP GGGKVQIINK KLDLSNVQSK GSKDNIKHV
PGGGSVQIVY KPVDLSKVTS KCGSLGNIHH KPGGGQVEVK SEKLDFKDRV SKIGSLDNI
THVPGGGNKK IETHKLTFRE NAKAKTDHGA EIVYKSPVVS GDTSPRHLSN SSTGSIDMV
DSPQLATLAD EVSASLAKQG L

SEQ ID NO:2 TAU P10636-7

MAEPRQEFEV MEDHAGTYGL GDRKDQGGYT MHQDQEGDTD AGLKESPLQT TEDGSEEPG
SETSDAKSTP TAEAEEAGIG DTPSLEDEAA GHVTQARMVS KSKDGTGSDD KAKGADGKT
KIATPRGAAP PGQKGQANAT RIPAKTPPAP KTPPSSGEPP KSGDRSGYSS GSPGTPGSR
SRTPSLPTPP TREPKKVAVV RTPPKSPSSA KSRLQTAPVP MPDLKNVKSK GSTENLKHQ
PGGGKVQIIN KKLDLSNVQS KCGSKDNIKH VPGGGSVQIV YKPVDLSKVT KCGSLGNIH
HKPGGGQVEV KSEKLDFKDR VQSKIGSLDN ITHVPGGGNK KIETHKLTFR NAKAKTDHG
AEIVYKSPVV SGDTSPRHLS NVSSTGSIDM VDSPQLATLA DEVSASLAKQ GL

SEQ ID NO:3 TAU P10636-6

MAEPRQEFEV MEDHAGTYGL GDRKDQGGYT MHQDQEGDTD AGLKAEEAGI DTPSLEDEA
AGHVTQARMV SKSKDGTGSD DKKAKGADGK TKIATPRGAA PPGQKGQANA RIPAKTPPA
PKTPPSSGEP PKSGDRSGYS SPGSPGTPGS RSRTPSLPTP PTREPKKVAV RTPPKSPSS
AKSRLQTAPV PMPDLKNVKS KIGSTENLKH QPGGGKVQII NKKLDLSNVQ KCGSKDNIK
HVPGGGSVQI VYKPVDLSKV TSKCGSLGNI HHKPGGGQVE VKSEKLDFKD VQSKIGSLD
NITHVPGGGN KKIETHKLTF RENAKAKTDH GAEIVYKSPV VSGDTSPRHL NVSSTGSID
MVDSPQLATL ADEVSASLAK QGL

SEQ ID NO:4 TAU P10636-5

MAEPRQEFEV MEDHAGTYGL GDRKDQGGYT MHQDQEGDTD AGLKESPLQT TEDGSEEPG
SETSDAKSTP TAEDVTAPLV DEGAPGKQAA AQPHTEIPEG TTAEEAGIGD PSLEDEAAG
HVTQARMVSK SKDGTGSDDK KAKGADGKTK IATPRGAAPP GQKGQANATR PAKTPPAPK
TPPSSGEPPK SGDRSGYSSP GSPGTPGSRS RTPSLPTPPT REPKKVAVVR PPKSPSSAK
SRLQTAPVPM PDLKNVKSKI GSTENLKHQP GGGKVQIVYK PVDLSKVTSK GSLGNIHHK
PGGGQVEVKS EKLDFKDRVQ SKIGSLDNIT HVPGGGNKKI ETHKLTFREN KAKTDHGAE
IVYKSPVVSG DTSPRHLSNV SSTGSIDMVD SPQLATLADE VSASLAKQGL

SEQ ID NO:5 TAU P10636-4

MAEPRQEFEV MEDHAGTYGL GDRKDQGGYT MHQDQEGDTD AGLKESPLQT TEDGSEEPG
SETSDAKSTP TAEAEEAGIG DTPSLEDEAA GHVTQARMVS KSKDGTGSDD KAKGADGKT
KIATPRGAAP PGQKGQANAT RIPAKTPPAP KTPPSSGEPP KSGDRSGYSS GSPGTPGSR
SRTPSLPTPP TREPKKVAVV RTPPKSPSSA KSRLQTAPVP MPDLKNVKSK GSTENLKHQ
PGGGKVQIVY KPVDLSKVTS KCGSLGNIHH KPGGGQVEVK SEKLDFKDRV SKIGSLDNI
THVPGGGNKK IETHKLTFRE NAKAKTDHGA EIVYKSPVVS GDTSPRHLSN SSTGSIDMV
DSPQLATLAD EVSASLAKQG L

SEQ ID NO:6 TAU P10636-2

MAEPRQEFEV MEDHAGTYGL GDRKDQGGYT MHQDQEGDTD AGLKAEEAGI GDTPSLEDE
AAGHVTQARM VSKSKDGTGS DDKKAKGADG KTKIATPRGA APPGQKGQAN ATRIPAKTP
PAPKTPPSSG EPPKSGDRSG YSSPGSPGTP GSRSRTPSLP TPPTREPKKV AVVRTPPKS
PSSAKSRLQT APVPMPDLKN VKSKIGSTEN LKHQPGGGKV QIVYKPVDLS KVTSKCGSL
GNIHHKPGGG QVEVKSEKLD FKDRVQSKIG SLDNITHVPG GGNKKIETHK LTFRENAKA
KTDHGAEIVY KSPVVSGDTS PRHLSNVSST GSIDMVDSPQ LATLADEVSA SLAKQGL

SEQ ID NO:7

CTA ATA CGA CTC ACT ATA GGG C

SEQ ID NO:8

CTC AAT TTT CTT GTC CAC CTT GGT GC

SEQ ID NO: 9

CTC AAG TTT TTT GTC CAC CGT GGT GC

SEQ ID NO:10 - 16B5-HC

MDWVWNLLFLMAAAQSIQAQIQLVQSGPELKKPGETVKISCKASGYPFTYHGMDWVKQAPWGGL
EWMGWINTYSGVPTYADDFKGRFAFSLETSVGTAYLQINNLKNEDTATYFCARRRDFTMDFWGQ
GTSVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAV
LQSDLYTLSSSVTVPSSTWPSETVTCNVAHPAS

SEQ ID NO:11 - 16B5 CDR-H1 (Kabat numbering)

YHGMD

SEQ ID NO:12 - 16B5 CDR-H2

WINTYSGVPTYADDFKG

SEQ ID NO:13 - 16B5 CDR-H3

RRDFTMDF

SEQ ID NO: 14 - Hu VH Acceptor FR (Acc#BAC02002.1)

QVQLVQSGSELKRPGASVKVSCKASGYSFTSYAVNWVRQAPGQGLEWVGWINTNTGNPTYAQGF
TGRFVFSLDTSVSTAYLQISSLKAADTAVYYCARARGQNGMDVWGQGTTVTVSS

SEQ ID NO: 15 – 16B5 Heavy Chain Humanized Design v1 (R13K, V48M, Y91F)

QVQLVQSGSELKKPGASVKVSCKASGYTFTYHGMDWVRQAPGQGLEWMGWINTYSGVPTYADDF
KGRFVFSLDTSVSTAYLQISSLKAEDTAVYFCARRRDFTMDFWGQGTTVTVSS

SEQ ID NO: 16 - 16B5-LC

MDSQAQVLILLLLWVSGTCGNIVLSQSPSSLAVSPGEKVTMSCKSSQSLLNSRTRKNYLAWFQQ
KPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCKQSYTLRTFGGGTN
LEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD
SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPI

SEQ ID NO: 17 - 16B5-LC CDR-L1

KSSQSLLNSRTRKNYLA

SEQ ID NO: 18 - 16B5-LC CDR-L2
WASTRES

SEQ ID NO: 19 - 16B5-LC CDR-L3
KQSYTLRT

SEQ ID NO: 20 - Hu VL Acceptor Fr (Acc#ACJ71718.1)
DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPQTFGGGTKVEIKR

SEQ ID NO: 21 - 16B5 Light Chain Humanized Design v1 (D1N, M4L, Y36F)
NIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWFQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYTLRTFGGGTKVEIKR

SEQ ID NO: 22 - 16B5 Light Chain Humanized Design v2 (D1N, M4L, Y36F, P43S)
NIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWFQQKPGQSPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYTLRTFGGGTKVEIKR

SEQ ID NO: 23 - 16B5 Light Chain Humanized Design v3 (M4L, Y36F, P43S)
DIVLTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWFQQKPGQSPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYTLRTFGGGTKVEIKR

SEQ ID NO:24 - 16B5 CDR-H1 (Combined Kabat AND Chothia numbering)
GYPFTYHGMD

SEQ ID NO:25 – Nucleic acid encoding 16B5 Heavy Chain Humanized Design v1
CAGgTCCAGTTGGTGCAGTCTGGATCTGAGCTGAAGAAGCCTGGAGCCTCCGTCAAGgtgTCCT
GCAAGGCTTCTGGGTATCCCTTCACATACCATGGAATGGACTGGGTGcgtCAGGCTCCTggtca
GGGTttaGAGTGGATGGGCTGGATAAACACCTACTCTGGAGTGCCAACATATGCTGATGACTTC
AAGGGACGATTTGtgTTCTCTTTGGAcACCTCTGTCtctACTGCCTATTTGCAGATCtcttctC
TCAAAgccGAGGACacgGCCgtgTATTTTTGTGCAAGACGGCGTGATTTTACAATGGACTTCTG
GGGTCAAGGAACCACCGTGACCGTCTCCTCA

SEQ ID NO:26 – Nucleic acid encoding 16B5 Light Chain Humanized Design v1
AACATCGTGCTGACCCAGAGCCCCGATAGCCTGGCCGTGAGCCTGGGCGAGAGAGCCACCATCA
ACTGCAAGAGCAGCCAGAGCCTGCTGAACAGCAGGACCAGGAAGAACTACCTGGCCTGGTTCCA
GCAGAAGCCCGGCCAGCCCCCCAAGCTGCTGATCTACTGGGCCAGCACCAGGGAGAGCGGCGTG
CCCGATAGGTTCAGCGGCAGCGGCAGCGGCACCGATTTCACCCTGACCATCAGCAGCCTGCAGG
CCGAGGATGTGGCCGTGTACTACTGCAAGCAGAGCTACACCCTGAGAACCTTCGGCGGCGGCAC
CAAGGTGGAAATTAAACGT

SEQ ID NO:27 – Nucleic acid encoding 16B5 Light Chain Humanized Design v2
AACATCGTGCTGACCCAGAGCCCCGATAGCCTGGCCGTGAGCCTGGGCGAGAGAGCCACCATCA
ACTGCAAGAGCAGCCAGAGCCTGCTGAACAGCAGGACCAGGAAGAACTACCTGGCCTGGTTCCA
GCAGAAGCCCGGCCAGAGCCCCAAGCTGCTGATCTACTGGGCCAGCACCAGGGAGAGCGGCGTG
CCCGATAGGTTCAGCGGCAGCGGCAGCGGCACCGATTTCACCCTGACCATCAGCAGCCTGCAGG
CCGAGGATGTGGCCGTGTACTACTGCAAGCAGAGCTACACCCTGAGAACCTTCGGCGGCGGCAC
CAAGGTGGAAATTAAACGT

SEQ ID NO:28 – Nucleic acid encoding 16B5 Light Chain Humanized Design v3

GACATCGTGCTGACCCAGAGCCCCGATAGCCTGGCCGTGAGCCTGGGCGAGAGAGCCACCATCA
ACTGCAAGAGCAGCCAGAGCCTGCTGAACAGCAGGACCAGGAAGAACTACCTGGCCTGGTTCCA
GCAGAAGCCCGGCCAGAGCCCCAAGCTGCTGATCTACTGGGCCAGCACCAGGGAGAGCGGCGTG
CCCGATAGGTTCAGCGGCAGCGGCAGCGGCACCGATTTCACCCTGACCATCAGCAGCCTGCAGG
CCGAGGATGTGGCCGTGTACTACTGCAAGCAGAGCTACACCCTGAGAACCTTCGGCGGCGGCAC
CAAGGTGGAAATTAAACGT

SEQ ID NO: 29 – Human IgG1 constant region (C-terminal lysine can be omitted)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY
PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
QKSLSLSPGK

SEQ ID NO: 30 – Human IgG1 constant region cDNA

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCA
CAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTC
AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCC
CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA
ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCA
CACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA
AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA
GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAA
GACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG
CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC
CCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC
CCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC
CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAG
GTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACG
CAGAAGAGCCTCTCCCTGTCTCCGGGTAAA

SEQ ID NO: 31 – Human IgG1 constant region cDNA with 5' intron

GGTGAGTGGATCCGCGGCCGCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAA
AGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTC
CAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCA
AGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG
TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTACT
TAAACACCATCCTGTTTGCTTCTTTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTT
CCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCT
TGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAG
AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTG
GGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCC
CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG

TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGT
GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCA
GCCCCGAGAACCACAGGTGTACACGCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC
AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATG
GGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT
CTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAATGA

SEQ ID NO: 32 – Human kappa constant region
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST
YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 33 – Human kappa constant region cDNA
ACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTG
CCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGA
TAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACC
TACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCT
GCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO: 34 – Human kappa constant region cDNA with 5’ intron
CGTGAGTGGATCCGCGGCCGCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAA
AGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTC
CAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCA
AGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG
TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTACT
TAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCC
CGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTA
TCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAG
AGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCA
AAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC
CGTCACAAAGAGCTTCAACAGGGGAGAGTGT