

>CD47-2G11_VH

SEQ ID NO.: 85

CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTTAGTAGCTATGGCATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCAACT
ATCAGTGGCAGTGGTAGTAGCACAACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTATTTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTTCTGTGCGAAAGGCCGA
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>CD47-6F4_VH

SEQ ID NO.: 86

CAGGTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
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ATTAGTGGTACTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGCATATTACTGTGCGAAAGATAAA
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>CD47-5H1_VH

SEQ ID NO.: 87

CAGGTGCAGCTGCAGGTGTGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTACCTTCAGTAGCTATAGCATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTCTCGCGCT
GTTAGTAATAGTGGTGTGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCC
AAGAACACGCTGTATTTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAACGAACT
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>CD47-5F6_VH

SEQ ID NO.: 88

CAGGTCAACTTAAGGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
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AAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGCGAGACGAGTC
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>CD47-1F3_VH

SEQ ID NO.: 89

CAGGTGCAGCTGCAGGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTTACACTCTCCTGTGCAGCCTCT
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GATTCAAAAAACACGCTGTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACCACA
GATAAGAGCTATGGTTACACATTTGACTACTGGGGCCAGGGCACCCCTSGTCACCGTCTCGGCC

>CD47-2A4_VH