

>CD47-1F8_VH

SEQ ID NO.: 80

AAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
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ATTAAAGGAAAACCTGATGGTGAGACAACAGACTACGCTGCACCCGTGAAAGGCAGATTACAGCATCTCAAGAGAT
GATTCAAAAAACACCCCTGTATCTGCAAATGAACAGCTTGAAAACCGAGGACACAGCCGTGTATTACTGCGCTGGC
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>CD47-2A11_VH

SEQ ID NO.: 81

CAGGTACAGCTGCAGCAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
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ATTACTTCTACTGGTGGTCCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCCACCTCCAGAGACAATTCC
AGGAACACGTTGTATCTGCAAATGAACAGCCTGAGAGCCGAAGACACGGCCGTATATTACTGTGCGAGAGAGTCA
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>CD47-2C2_VH

SEQ ID NO.: 82

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTTAGACTCTCCTGTGCAGCCTCT
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ATTTATAGCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGGGGCTAGG
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>CD47-2D7_VH

SEQ ID NO.: 83

CAGGTCAACTTAAGGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
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CAGAACTCACTATATCTGCAAATGAACAGCCTGAGGGCCGAGGACACGGCTGTTTATTACTGTGTGAGAGATGTA
CATAACAGGGATGCCTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCGGCC

>CD47-2G4_VH

SEQ ID NO.: 84

CAGGTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
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ATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCAGAGACAATTCC
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TACTATGATAGTAGTAGCCATACCCCGCTGACTACTGGGGCCAGGGCACCCCTGGTCACCGTCTCGGCC