SEQUENCES

>SC09-003 VH DNA (SEQ ID NO: 1)
GAGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTCAAGAAGGCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
TTCTGGAGGCACCTCCAACAACTTTGGTATCAGCTGGGTACGACAGGCCCCTGGCCAAGGCCTTGAGTGGA
TGGGCGGGATCAGCCCAATCTTTGGTTCGACAGTCTACGCACAGAAATTTCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCACACACTGCCTACATGGAGATGAACAGCCTGACATCTGAGGACACGGCCGTCTATTT
CTGTGCGAGGCACGGAAATTATTATTTCTACTCCGGTATGGACCTCTGGGGCCAAGGGACCACGGTCACC

>SC09-003 VH PROTEIN (SEQ ID NO: 2)
EVQLVESGAEVKKAGSSVKVSCKSSGGTSNNFGISWVRQAPGQGLEWMGGISPIFGSTVYAQKFQGRVTIS
ADIFSHTAYMEMNSLTSEDTAVYFCARHGNYYFYSGMDLWGQGTTVT

>SC09-003 VL DNA (SEQ ID NO: 3)
TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACGGCCACGATTTCCTGTGGGGG
AGACAACGTTGGAAGTAACAGTGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCCTGTGCTGGTCGTCT
ATGATGATCGCGACCGACCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACGGCCACC
CTGACCATCAGCAGGGTCGAAGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATAGTAGTAGTGA
TCATCGAGTCTTCGGAACTGGGACGAAGGTCACCGTCCTAG

>SC09-003 VL PROTEIN (SEQ ID NO: 4)
SYVLTQPPSVSVAPGQTATISCGGDNVGSNSVHWYQQKPGQAPVLVVYDDRDRPSGIPERFSGSNSGNTAT
LTISRVEAGDEADYYCQVWDSSSDHRVFGTGTKVTVL

>SC09-004 VH DNA (SEQ ID NO: 5)
CAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
TTCTGGCGGCACCTCCAATAACTATGCCATCAGCTGGGTGCGACAGGCCCCTGGACAAGGCCTTGACTGGA
TGGGCGGGGTCAGCCCTATCTTTGGTTCGACAGCCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCGAACACAGCCTACATGGAGCTGAACAGTCTGACATCTGAGGACACGGCCGTCTATTA
TTGTGCGAGACACGGGAATTATTATTACAACTCCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACC

>SC09-004 VH PROTEIN (SEQ ID NO: 6)
QVQLVQSGAEVKKPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGVSPIFGSTAYAQKFQGRVTIS
ADIFSNTAYMELNSLTSEDTAVYYCARHGNYYYNSGMDVWGQGTTVT

>SC09-004 VL DNA (SEQ ID NO: 7)
CAGTCTGTGCTGACGCAGCCGCCCGCAGTGTCTGGGACCCCCGGGCAGAGGTCACCATCTCGTGTTCTGG
AAGTGATTCCAACATCGGGAGAAGAAGTGTAAACTGGTACCAGCAGTTCCCAGGAACGGCCCCCAAACTCC
TCATCTATAGTAACGATCAGCGGCCCTCAGTGGTCCCTGACCGATTCTCTGGCTCCAAGTCCGGCACCTCA
GCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAAGATGAGGCCGAATATTACTGTGCAGCATGGGATGACAG
CCTGAAGGGGGCTGTGTTCGGAGGAGGCACCCAGCTGACCGTCCTCG

>SC09-004 VL PROTEIN (SEQ ID NO: 8)
QSVLTQPPAVSGTPGQRVTISCSGSDSNIGRRSVNWYQQFPGTAPKLLIYSNDQRPSVVPDRFSGSKSGTS
ASLAISGLQSEDEAEYYCAAWDDSLKGAVFGGGTQLTVL

>SC09-005 VH DNA (SEQ ID NO: 9)
CAGGTGCAGCTGGTGCAATCTGGGGCTGAGGTCAAGAGGCCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
TTCTGGAGGCACCTCCAATAACTATGCTATTAGTTGGGTGCGACAGGCCCCTGGACAAGGCCTTGACTGGA
TGGGCGGGATCAGCCCTATCTTTGGTTCGACAGTCTACGCACAGAAATTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCGAACACAGCCTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTATATTT
CTGTGCGAGGCACGGGAACTATTATTACTACTCCGGTATGGACCTCTGGGGCCAAGGGACCACGGTCACC

>SC09-005 VH PROTEIN (SEQ ID NO: 10)

QVQLVQSGAEVKRPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSTVYAQKFQGRVTIS
ADIFSNTAYMELNSLTSEDTAVYFCARHGNYYYYSGMDLWGQGTTVT

>SC09-005 VL DNA (SEQ ID NO: 11)
CAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGGTCTCCTGGACAGTCGATCACCATCTCCTGCACTGG
AACCAGCAGTGACGTCGGTGGTTATAACTATGTCTCCTGGTACCAACAACACCCAGGCAAAGCCCCCAAAC
TCCTGATTTTTGATGTCAGTGATCGGCCCTCAGGGGTTTCTGATCGCTTCTCTGGCTCCAAGTCTGCGGAC
ACGGCCTGCCTGACCATCTCTGGACTCCAGGCTCAGGACGAGGCTGATTATTACTGCTGCTCATATGCAGG
TAGTGCCAAGGGCGTCTTCGGAACTGGGACCAAGGTCACCGTCCTAG

>SC09-005 VL PROTEIN (SEQ ID NO: 12)
QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLLIFDVSDRPSGVSDRFSGSKSAD
TASLTISGLQAQDEADYYCCSYAGSAKGVFGTGTKVTVL

>SC09-006 VH DNA (SEQ ID NO: 13)
GAGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTCAAGAGGCCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
TTCTGGAGGCACCTCCAATAACTATGCTATTAGTTGGGTGCGACAGGCCCCTGGACAAGGCCTTGACTGGA
TGGGCGGGATCAGCCCTATCTTTGGTTCGACAGTCTACGCACAGAAATTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCGAACACAGCCTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTATATTT
CTGTGCGAGGCACGGGAACTATTATTACTACTCCGGTATGGACCTCTGGGGCCAAGGGACCACGGTCACC

>SC09-006 VH PROTEIN (SEQ ID NO: 14)
EVQLVESGAEVKRPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSTVYAQKFQGRVTIS
ADIFSNTAYMELNSLTSEDTAVYFCARHGNYYYYSGMDLWGQGTTVT

>SC09-006 VL DNA (SEQ ID NO: 15)
TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACGGCCAGGATTACCTGTGGGGG
AAACAACATTGGAAGTAAAACTGTGCATTGGTACCAGCAGAACTCAGGCCAGGCCCCTGTGCTGGTCGTCT
ATGGTGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGACCACGGCCACC
CTGACCATCAGCAGGGTCGAAGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATAGTAGTAGTGA
TCATCCCGGTGCTGTGTTCGGAGGAGGCACCCAGCTGACCGTCCTCG

>SC09-006 VL PROTEIN (SEQ ID NO: 16)
SYVLTQPPSVSVAPGQTARITCGGNNIGSKTVHWYQQNSGQAPVLVVYGDSDRPSGIPERFSGSNSGTTAT
LTISRVEAGDEADYYCQVWDSSSDHPGAVFGGGTQLTVL

>SC09-007 VH DNA (SEQ ID NO: 17)
CAGGTGCAGCTGGTGCAATCTGGAGCTGAGGTCAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGTC
TTCTGGAGGCACCTCCAATAACTATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGCCTTGACTGGA
TGGGAGGGATCAGCCCTATCTTTGGTTCAGCAGCCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTACC
GCGGACATATTTTCGAACACAGTGTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTGTATTA
CTGTGCGAGACACGGGAATTATTATTACTACTCCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-007 VH PROTEIN (SEQ ID NO: 18)
QVQLVQSGAEVKKPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSAAYAQKFQGRVTIT
ADIFSNTVYMELNSLTSEDTAVYYCARHGNYYYYSGMDVWGQGTTVTVSS

>SC09-007 VL DNA (SEQ ID NO: 19)
TCCTATGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGG
AAGCAGCTCCAACATCGGAAGTAATACTGTAAACTGGTACCAGCAGGTCCCCGGAACGGCCCCCAAACTCC
TCATCTATGGTGATGATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCA
GCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAACATGGGATGACAG
CCTGAATGGTCATGTGTTCGGAGGAGGCACCCAGCTGACCGTCCTCG

>SC09-007 VL PROTEIN (SEQ ID NO: 20)

SYVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQVPGTAPKLLIYGDDQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGHVFGGGTQLTVL

>SC09-008 VH DNA (SEQ ID NO: 21)
GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGTCCTCGGTGAGAGTCTCCTGTAAGTC
TTCTGGAGGCACCTCCAATAACTATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGCCTTGACTGGA
TGGGCGGGATCAGCCCTATCTTTGGTTCGACAGCCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCGAACACAGCCTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTATATTT
CTGTGCGAGGCACGGGAATTATTATTACTACTCCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-008 VH PROTEIN (SEQ ID NO: 22)
EVQLVQSGAEVKKPGSSVRVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSTAYAQKFQGRVTIS
ADIFSNTAYMELNSLTSEDTAVYFCARHGNYYYYSGMDVWGQGTTVTVSS

>SC09-008 VL DNA (SEQ ID NO: 23)
TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACGGCCAGGATTACCTGTGGGGG
AAACAACATTGGAAGTAAAACTGTGCATTGGTACCAGCAGAACTCAGGCCAGGCCCCTGTGCTGGTCGTCT
ATGGTGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGACCACGGCCACC
CTGACCATCAGCAGGGTCGAAGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATAGTAGTAGTGA
TCATCCCGGTGCTGTGTTCGGAGGAGGCACCCAGCTGACCGTCCTCG

>SC09-008 VL PROTEIN (SEQ ID NO: 24)
SYVLTQPPSVSVAPGQTARITCGGNNIGSKTVHWYQQNSGQAPVLVVYGDSDRPSGIPERFSGSNSGTTAT
LTISRVEAGDEADYYCQVWDSSSDHPGAVFGGGTQLTVL

>SC09-009 VH DNA (SEQ ID NO: 25)
CAGGTGCAGCTGGTGCAATCTGGGGCTGAGGTCAAGAAGCCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
TTCTGGAGGCACCTCCAATAACTATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGCCTTGACTGGA
TGGGCGGGATCAGCCCTATCTTTGGTTCGACAGCCTACGCACAGAAATTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCGAACACAGCCTACATGGAGCTGAACAGCCTGGCATCTGAGGACACGGCCGTATATTT
CTGTGCGAGGCACGGGAATTATTATTACTACTCCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-009 VH PROTEIN (SEQ ID NO: 26)
QVQLVQSGAEVKKPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSTAYAQKFQGRVTIS
ADIFSNTAYMELNSLASEDTAVYFCARHGNYYYYSGMDVWGQGTTVTVSS

>SC09-009 VL DNA (SEQ ID NO: 27)
GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCG
GGCGAGTCAGCATATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAGCCAGGGAAAGGCCCTCAGCTCCTGA
TCTATTCTGCATCCCGTTTGCAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTC
ACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCC
CCTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAAC

>SC09-009 VL PROTEIN (SEQ ID NO: 28)
DIQMTQSPSSVSASVGDRVTITCRASQHISSWLAWYQQKPGKGPQLLIYSASRLQSGVPSRFSGSGSGTDF
TLTISSLQPEDFATYYCQQANSFPLTFGPGTKVDIK

>SC09-010 VH DNA (SEQ ID NO: 29)
GAGGTGCAGCTGGTGGAGTCCGGGGCTGAGGTCAAGAAGCCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
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TGGGCGGGATCAGCCCTATCTTTGGTTCGACAGCCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCCAACACAGCCTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTATATTA
CTGTGCGAGGCACGGGAATTATTATTACTACTCCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-010 VH PROTEIN (SEQ ID NO: 30)
EVQLVESGAEVKKPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSTAYAQKFQGRVTIS
ADIFSNTAYMELNSLTSEDTAVYYCARHGNYYYYSGMDVWGQGTTVTVSS

>SC09-010 VL DNA (SEQ ID NO: 31)
TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACGGCCAGGATTACCTGTGGGGG
AAACAACATYGGAAGTAAAACTGTGCATTGGTACCAGCAGAACTCAGGCCAGGCCCCTGTGCTGGTCGTCT
TTGTTGATAGCGACCGTCCCTCAGGGATCCATGAGCGATTCTGTGGCTCCAACTCTGGGTCCACGGCCACC
CTGACCATCAGCAGCGTCGAAGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATAGTAATAGCGA
TCATCCCGGTGCTGTGTTCGGAGGAGGCACCCAGCTGACCGTCCTCG

>SC09-010 VL PROTEIN (SEQ ID NO: 32)
SYVLTQPPSVSVAPGQTARITCGGNNIGSKTVHWYQQNSGQAPVLVVFVDSDRPSGIHERFCGSNSGSTAT
LTISSVEAGDEADYYCQVWDSNSDHPGAVFGGGTQLTVL

>SC09-011 VH DNA (SEQ ID NO: 33)
GAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTCAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGTC
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TGGGAGGGATCAGCCCTATCTTTGGTTCAGCAGCCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTACC
GCGGACATATTTTCGAACACAGTGTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTGTATTA
CTGTGCGAGACACGGGAATTATTATTACTACTCCGGTACGGACGTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-011 VH PROTEIN (SEQ ID NO: 34)
EVQLVQSGAEVKKPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSAAYAQKFQGRVTIT
ADIFSNTVYMELNSLTSEDTAVYYCARHGNYYYYSGTDVWGQGTTVTVSS

>SC09-011 VL DNA (SEQ ID NO: 35)
TCCTATGTGCTGACTCAGCCACCCGCAGTGTCTGGGACTCCCGGGCAGAGGGTCACCATCTCGTGTTCTGG
AAGTGATTCCAACATCGGGAGAAGAAGTGTAAACTGGTACCAGCAGTTCCCAGGAACGGCCCCCAAACTCC
TCATCTATAGTAACGATCAGCGGCCCTCAGTGGTCCCTGACCGATTCTCTGGCTCCAAGTCCGGCACCTCA
GCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAAGATGAGGCCGAATATTACTGTGCAGCATGGGATGACAG
CCTGAAGGGGGCTGTGTTCGGAGGAGGCACCCAGCTGACCGTCCTCG

>SC09-011 VL PROTEIN (SEQ ID NO: 36)
SYVLTQPPAVSGTPGQRVTISCSGSDSNIGRRSVNWYQQFPGTAPKLLIYSNDQRPSVVPDRFSGSKSGTS
ASLAISGLQSEDEAEYYCAAWDDSLKGAVFGGGTQLTVL

>SC09-012 VH DNA (SEQ ID NO: 37)
GAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTCAAGAAGCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGTC
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TGGGAGGGATCAGCCCTATTTTTGGTTCAGCAGTCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTACC
GCGGACATATTTTCGAACACAGTGTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTGTATTA
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TCTCGAGC

>SC09-012 VH PROTEIN (SEQ ID NO: 38)
EVQLVQSGAEVKKPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSAVYAQKFQGRVTIT
ADIFSNTVYMELNSLTSEDTAVYYCARHGTYYYYSGMDVWGQGTTVTVSS

>SC09-012 VL DNA (SEQ ID NO: 39)
CAGTCTGTCGTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGG
GAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGCTTCCAGGGACAGCCCCCAAAC
TCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACC
TCAGCCTCCCTGGCCATCACTGGGCTCCAGGTTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACCA
GAACCTGAGTGAGGGGGTCTTCGGCGGAGGGACCAAGCTGACCGTCCTAG

>SC09-012 VL PROTEIN (SEQ ID NO: 40)
QSVVTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGT
SASLAITGLQVEDEADYYCQSYDQNLSEGVFGGGTKLTVL

>SC09-029 VH DNA (SEQ ID NO: 41)
GAGGTGCAGCTGGTGGAGTCCGGGGCTGAGGTCAAGAAGCCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
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TGGGCGGGATCAGCCCTATCTTTGGTTCGACAGCCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCGAACACAGCCTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTATATTA
CTGTGCGAGGCACGGGAATTATTATTACTACTCCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-029 VH PROTEIN (SEQ ID NO: 42)
EVQLVESGAEVKKPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSTAYAQKFQGRVTIS
ADIFSNTAYMELNSLTSEDTAVYYCARHGNYYYYSGMDVWGQGTTVTVSS

>SC09-029 VL DNA (SEQ ID NO: 43)
GAAATTGTGATGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCTGGGGAAAGAGGCACCCTCTCCTGCAG
GGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTCCTCA
TCTATGGTGCATCCACCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTC
ACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGGAGCTCACC
ATTCGCTTTCGGCCCTGGGACCAAGGTGGAGATCAAA

>SC09-029 VL PROTEIN (SEQ ID NO: 44)
EIVMTQSPGTLSLSPGERGTLSCRASQSVSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFTGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSPFAFGPGTKVEIK

>SC09-030 VH DNA (SEQ ID NO: 45)
CAGATGCAGCTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
TTCTGGAGGCACCTCCAATAACTATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGCCTTGACTGGA
TGGGCGGGATCAGCCCTATCTTTGGTTCGACAGCCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCGAACACAGCCTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTATATTT
CTGTGCGAGGCACGGGAATTATTATTACTACTCCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-030 VH PROTEIN (SEQ ID NO: 46)
QMQLVQSGAEVKKPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSTAYAQKFQGRVTIS
ADIFSNTAYMELNSLTSEDTAVYFCARHGNYYYYSGMDVWGQGTTVTVSS

>SC09-030 VL DNA (SEQ ID NO: 47)
TCCTATGTGCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACAGACGGCCACGATTACCTGTGGGGG
AAACAACATTGGAAGTAAAAGTGTGCACTGGTACCAGCAGAAGCCAGGCCAGGCCCCTGTGCTGGTCGTCT
ATGGTGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGACCACGGCCACC
CTGACCATCAGCAGGGTCGAAGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATAGTAGTAGTGA
TCATCCCGGTGCTGTGTTCGGAGGAGGCACCCAGCTGACCGTCCTCG

>SC09-030 VL PROTEIN (SEQ ID NO: 48)
SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYGDSDRPSGIPERFSGSNSGTTAT
LTISRVEAGDEADYYCQVWDSSSDHPGAVFGGGTQLTVL

>SC09-031 VH DNA (SEQ ID NO: 49)
CAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTCGAGAGGCCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
TTCTGGCGGCACCTCCAATAACTATGCCATCAGCTGGGTGCGACAGGCCCCTGGACAAGGCCTTGACTGGA
TGGGCGGGATCAGCCCTATCTTTGGTTCGACAGCCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCGAACACAGCCTACATGGAGCTGAACAGTCTGACATCTGAGGACACGGCCGTCTATTA

TTGTGCGAGACACGGGAATTATTATTACAACTCCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-031 VH PROTEIN (SEQ ID NO: 50)
QVQLVQSGAEVERPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSTAYAQKFQGRVTIS
ADIFNTAYMELNSLTSEDTAVYYCARHGNYYYNSGMDVWGQGTTVTVSS

>SC09-031 VL DNA (SEQ ID NO: 51)
CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGG
GAGCAGCTCCAACATCGGGGCAGGTTATGATGTACACTGGTACCAGCAGCTTCCAGAAACAGCCCCCAAAC
TCCTCATTTATGATAACAACAATCGTCCCTCAGGGGTTTCTGACCGATTCTCTGGCTCCAAGTCTGGCACT
TCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAG
CGGCCTGAGTGCTTGGCCTTATGTCTTCGGAGCTGGGACCAAGGTCACCGTCCTAG

>SC09-031 VL PROTEIN (SEQ ID NO: 52)
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPETAPKLLIYDNNNRPSGVSDRFSGSKSGT
SASLAITGLQAEDEADYYCQSYDSGLSASPYVFGAGTKVTVL

>SC09-112 VH DNA (SEQ ID NO: 53)
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
TTCTGGAGGCACCTCCAATAACTATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGCCTTGACTGGA
TGGGCGGGATCAGCCCTATCTTTGGTTCGACAGCCTACGCACAGAAGTTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCGAACACAGCCTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGTATATTA
CTGTGCGAGGCACGGGAATTATTATTACTACTCCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-112 VH PROTEIN (SEQ ID NO: 54)
QVQLVQSGAEVKKPGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLDWMGGISPIFGSTAYAQKFQGRVTIS
ADIFSNTAYMELNSLTSEDTAVYYCARHGNYYYYSGMDVWGQGTTVTVSS

>SC09-112 VL DNA (SEQ ID NO: 55)
CAGTCTGTGTTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGG
GAGCAGCGCCAACATCGGGGCAGGTTATGATGTCCACTGGTACCAGCAGTTTCCAGGAACAGCCCCCAAAC
TCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACC
TCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAG
CAGCCTGAGTGGTGCGTTATTCGGCGGAGGGACCAAGCTGACCGTCCTAG

>SC09-112 VL PROTEIN (SEQ ID NO: 56)
QSVLTQPPSVSGAPGQRVTISCTGSSANIGAGYDVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSGT
SASLAITGLQAEDEADYYCQSYDSSLSGALFGGGTKLTVL

>SC09-113 VH DNA (SEQ ID NO: 57)
CAGATGCAGCTGGTGCAGTCTGGGGCTGAGGTCAAGAAGGCTGGGTCCTCGGTGAAAGTCTCCTGCAAGTC
TTCTGGAGGCACCTCCAATAACTATGCTATCAGCTGGGTGCGACAGGCCCCTGGACAAGGCCTTGAGTGGA
TGGGCGGGATCAGTCCAATCTTTGGTTCGACAGTCTACGCACAGAAATTCCAGGGCAGAGTCACTATTTCC
GCGGACATATTTTCACACACTGCCTACATGGAGCTGAACAGCCTGACATCTGAGGACACGGCCGCATATTT
CTGTGCGAGGCACGGAAACTATTATTACTACTCCGGTATGGACCTCTGGGGCCAAGGGACCACGGTCACCG
TCTCGAGC

>SC09-113 VH PROTEIN (SEQ ID NO: 58)
QMQLVQSGAEVKKAGSSVKVSCKSSGGTSNNYAISWVRQAPGQGLEWMGGISPIFGSTVYAQKFQGRVTIS
ADIFSHTAYMELNSLTSEDTAAYFCARHGNYYYYSGMDLWGQGTTVTVSS

>SC09-113 VL DNA (SEQ ID NO: 59)
CAGTCTGTGCTGACTCAGCCACCCGCAGTGTCTGGGACCCCCGGGCAGAGGGTCACCATCTCGTGTTCTGG
AAGTGATTCCAACATCGGGAGAAGAAGTGTAAACTGGTACCAGCAGTTCCCAGGAACGGCCCCCAAACTCC
TCATCTATAGTAACGATCAGCGGCCCTCAGTGGTCCCTGACCGATTCTCTGGCTCCAAGTCCGGCACCTCA

GCCTCCCTGGCCATCAGTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGCCAG
CCTGAGTGGTCCTGTGTTCGGAGGAGGCACCCAGCTGACCGTCCTCG

>SC09-113 VL PROTEIN (SEQ ID NO: 60)
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Ferguson et al., (2003), Nature 422:428-443.

Fouchier AM et al. (2005), Characterization of a novel influenza A virus hemagglutinin subtype (H16) obtained from black-headed gulls. J Virol 79(5):2814-2822.

The World Health Organization Global Influenza Program Surveillance Network (2005), Evolution of H5N1 Avian Influenza Viruses in Asia. Emerg Infect Dis 11:1515-1521.

CLAIMS

1. An isolated binding molecule, capable of specifically binding to an epitope in the stem region of the hemagglutinin protein (HA) of influenza A virus subtypes of phylogenetic group 1 and influenza A virus subtypes of phylogenetic group 2 subtypes, and capable of neutralizing influenza A virus subtypes of phylogenetic group 1 and phylogenetic group 2, characterized in that the binding molecule is also capable of specifically binding to the hemagglutinin protein (HA) of influenza B virus subtypes.

2. A binding molecule according to claim 1, wherein the binding molecule is capable of neutralizing influenza B virus subtypes.

3. A binding molecule according to claim 1 or 2, wherein the binding molecule is capable of neutralizing at least one or more group 1 influenza A virus subtypes, selected from the group consisting of influenza A viruses comprising HA of the H1, H2, H5, H6, H8, H9 and H11 subtype, and at least one or more group 2 influenza A virus subtypes, selected from the group consisting of influenza A viruses comprising HA of the H3, H4, H7, and H10 subtype, and at least one or more influenza B virus subtypes.

4. A binding molecule according to any of the preceding claims, wherein the binding molecule has no hemagglutination inhibiting activity.

5. A binding molecule according to any of the preceding claims, wherein the binding molecules comprise a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 133 or SEQ ID NO: 139, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 134, SEQ ID NO: 140 or SEQ ID NO: 151, and a heavy chain CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 135, SEQ ID NO: 141, SEQ ID NO: 145, SEQ ID NO: 152, SEQ ID NO: 161, and SEQ ID NO: 162.

6. A binding molecule according to any of the preceding claims, wherein the binding molecule is selected from the group consisting of:

a) a binding molecule comprising a heavy chain CDR1 region of SEQ ID NO:133, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:135,

b) a binding molecule comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:140, and a heavy chain CDR3 region of SEQ ID NO:141,

c) a binding molecule comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:145,

d) a binding molecule comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:151, and a heavy chain CDR3 region of SEQ ID NO:152,

e) a binding molecule comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:152,

f) a binding molecule comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:151, and a heavy chain CDR3 region of SEQ ID NO:161,

g) a binding molecule comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:151, and a heavy chain CDR3 region of SEQ ID NO:162, and

h) a binding molecule comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:141.

7. A binding molecule according to any of the preceding claims, wherein the binding molecule comprises a heavy chain CDR1 region comprising the amino acid sequence of SEQ ID NO:139, a heavy chain CDR2 region comprising an amino acid sequence of

SEQ ID NO:134, and a heavy chain CDR3 region comprising the amino acid sequence of SEQ ID NO:145 or SEQ ID NO: 152.

8. A binding molecule according to any one of the preceding claims, wherein said binding molecule is a human monoclonal antibody, or an antigen-binding fragment thereof.

9. A nucleic acid molecule encoding a binding molecule according to any one of claims 1-8.

10. A binding molecule according to any one of claims 1-8, and/or a nucleic acid molecule according to claim 9, for use as a medicament and preferably for the diagnostic, therapeutic and/or prophylactic treatment of influenza infection.

11. A pharmaceutical composition comprising a binding molecule according to any one of claims 1–8, and/or a nucleic acid molecule according to claim 9, and a pharmaceutically acceptable excipient.

0190 WO 00 ORD 9 September 2013

AMENDED CLAIMS

1. An isolated antibody or antigen-binding fragment thereof, capable of specifically binding to an epitope in the stem region of the hemagglutinin protein (HA) of influenza A virus subtypes of phylogenetic group 1 and influenza A virus subtypes of phylogenetic group 2 subtypes, and capable of neutralizing at least one or more group 1 influenza A virus subtypes, selected from the group consisting of influenza A viruses comprising HA of the H1, H2, H5, H6, H8, H9 and H11 subtype, and at least one or more group 2 influenza A virus subtypes, selected from the group consisting of influenza A viruses comprising HA of the H3, H4, H7, and H10 subtype, characterized in that the antibody or antigen-binding fragment thereof is also capable of specifically binding to the hemagglutinin protein (HA) of influenza B virus subtypes.

2. An antibody or antigen-binding fragment thereof according to claim 1, wherein the antibody or antigen-binding fragment thereof has no hemagglutination inhibiting activity.

3. An antibody or antigen-binding fragment thereof according to any of the preceding claims, wherein the antibody or antigen-binding fragment thereof is selected from the group consisting of:

an antibody or antigen-binding fragment thereof comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:145, and a light chain CDR1 region of SEQ ID NO: 146, a light chain CDR2 region of SEQ ID NO: 174, and a light chain CDR3 region of SEQ ID NO: 147,

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a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:145, and a light chain CDR1 region of SEQ ID NO: 148, a light chain CDR2 region of SEQ ID NO: 149, and a light chain CDR3 region of SEQ ID NO: 150,

a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:145, and a light chain CDR1 region of SEQ ID NO: 142, a light chain CDR2 region of SEQ ID NO: 143, and a light chain CDR3 region of SEQ ID NO: 173;

an antibody or antigen-binding fragment thereof comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:152, and a light chain CDR1 region of SEQ ID NO: 148, a light chain CDR2 region of SEQ ID NO: 149, and a light chain CDR3 region of SEQ ID NO: 150,

a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:152, and a light chain CDR1 region of SEQ ID NO: 156, a light chain CDR2 region of SEQ ID NO: 157, and a light chain CDR3 region of SEQ ID NO: 158,

a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:152, and a light chain CDR1 region of SEQ ID NO: 171, a light chain CDR2 region of SEQ ID NO: 164, and a light chain CDR3 region of SEQ ID NO: 172, and

a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:152, and a light chain CDR1 region of SEQ ID

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NO: 142, a light chain CDR2 region of SEQ ID NO: 143, and a light chain CDR3 region of SEQ ID NO: 144.

4. A nucleic acid molecule encoding an antibody or antigen-binding fragment thereof according to any one of claims 1-3.

5. An antibody or antigen-binding fragment thereof according to any one of claims 1-3, and/or a nucleic acid molecule according to claim 4, for use as a medicament

6. An antibody or antigen-binding fragment thereof according to claim 5 for use in the prophylactic and/or thereapeutic treatment of influenze infection.

7. A pharmaceutical composition comprising an antibody or antigen-binding fragment thereof according to any one of claims 1-3, and/or a nucleic acid molecule according to claim 4, and a pharmaceutically acceptable excipient.

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De Kruif J et al. (1995), Rapid selection of cell subpopulation-specific human monoclonal antibodies from a synthetic phage antibody library. Proc Natl Acad Sci USA 92:3938.

Ferguson et al., (2003), Nature 422:428-443.

Fouchier AM et al. (2005), Characterization of a novel influenza A virus hemagglutinin subtype (H16) obtained from black-headed gulls. J Virol 79(5):2814-2822.

The World Health Organization Global Influenza Program Surveillance Network (2005), Evolution of H5N1 Avian Influenza Viruses in Asia. Emerg Infect Dis 11:1515-1521.

CLAIMS

1. An isolated antibody or antigen-binding fragment thereof, capable of specifically binding to an epitope in the stem region of the hemagglutinin protein (HA) of influenza A virus subtypes of phylogenetic group 1 and influenza A virus subtypes of phylogenetic group 2 subtypes, and capable of neutralizing at least one or more group 1 influenza A virus subtypes, selected from the group consisting of influenza A viruses comprising HA of the H1, H2, H5, H6, H8, H9 and H11 subtype, and at least one or more group 2 influenza A virus subtypes, selected from the group consisting of influenza A viruses comprising HA of the H3, H4, H7, and H10 subtype, characterized in that the antibody or antigen-binding fragment thereof is also capable of specifically binding to the hemagglutinin protein (HA) of influenza B virus subtypes.

2. An antibody or antigen-binding fragment thereof according to claim 1, wherein the antibody or antigen-binding fragment thereof has no hemagglutination inhibiting activity.

3. An antibody or antigen-binding fragment thereof according to any of the preceding claims, wherein the antibody or antigen-binding fragment thereof is selected from the group consisting of:

an antibody or antigen-binding fragment thereof comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:145, and a light chain CDR1 region of SEQ ID NO: 146, a light chain CDR2 region of SEQ ID NO: 174, and a light chain CDR3 region of SEQ ID NO: 147,

a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:145, and a light chain CDR1 region of SEQ ID NO: 148, a light chain CDR2 region of SEQ ID NO: 149, and a light chain CDR3 region of SEQ ID NO: 150,

a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:145, and a light chain CDR1 region of SEQ ID NO: 142, a light chain CDR2 region of SEQ ID NO: 143, and a light chain CDR3 region of SEQ ID NO: 173;

an antibody or antigen-binding fragment thereof comprising a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:152, and a light chain CDR1 region of SEQ ID NO: 148, a light chain CDR2 region of SEQ ID NO: 149, and a light chain CDR3 region of SEQ ID NO: 150,

a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:152, and a light chain CDR1 region of SEQ ID NO: 156, a light chain CDR2 region of SEQ ID NO: 157, and a light chain CDR3 region of SEQ ID NO: 158,

a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:152, and a light chain CDR1 region of SEQ ID NO: 171, a light chain CDR2 region of SEQ ID NO: 164, and a light chain CDR3 region of SEQ ID NO: 172, and

a heavy chain CDR1 region of SEQ ID NO:139, a heavy chain CDR2 region of SEQ ID NO:134, and a heavy chain CDR3 region of SEQ ID NO:152, and a light chain CDR1 region of SEQ ID

NO: 142, a light chain CDR2 region of SEQ ID NO: 143, and a light chain CDR3 region of SEQ ID NO: 144.

4. A nucleic acid molecule encoding an antibody or antigen-binding fragment thereof according to any one of claims 1-3.

5. An antibody or antigen-binding fragment thereof according to any one of claims 1-3, and/or a nucleic acid molecule according to claim 4, for use as a medicament

6. An antibody or antigen-binding fragment thereof according to claim 5 for use in the prophylactic and/or thereapeutic treatment of influenze infection.

7. A pharmaceutical composition comprising an antibody or antigen-binding fragment thereof according to any one of claims 1-3, and/or a nucleic acid molecule according to claim 4, and a pharmaceutically acceptable excipient.

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Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

Leu Ile Phe Asp Val Ser Asp Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Ala Asp Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Gln Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser
85 90 95

Ala Lys Gly Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 13
<211> 354
<212> DNA
<213> Artificial

<220>
<223> SC09-006 VH DNA

<400> 13
gaggtgcagc tggtggagtc tggggctgag gtcaagaggc ctgggtcctc ggtgaaagtc 60

tcctgcaagt cttctggagg cacctccaat aactatgcta ttagttgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggcggg atcagcccta tctttggttc gacagtctac 180

gcacagaaat tccagggcag agtcactatt tccgcggaca tattttcgaa cacagcctac 240

atggagctga acagcctgac atctgaggac acggccgtat atttctgtgc gaggcacggg 300

aactattatt actactccgg tatggacctc tggggccaag ggaccacggt cacc 354

<210> 14
<211> 118
<212> PRT
<213> Artificial

<220>
<223> SC09-006 VH PROTEIN

<400> 14

Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Val Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Leu Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr
115

<210> 15
<211> 331
<212> DNA
<213> Artificial

<220>
<223> SC09-006 VL DNA

<400> 15
tcctatgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa actgtgcatt ggtaccagca gaactcaggc 120

caggcccctg tgctggtcgt ctatggtgat agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaccacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatagtagta gtgatcatcc cggtgctgtg 300

ttcggaggag gcacccagct gaccgtcctc g 331

<210> 16
<211> 110
<212> PRT
<213> Artificial

<220>
<223> SC09-006 VL PROTEIN

<400> 16

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Thr Val
20 25 30

His Trp Tyr Gln Gln Asn Ser Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Gly Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Thr Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Pro Gly Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 17
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-007 VH DNA

<400> 17
caggtgcagc tggtgcaatc tggagctgag gtcaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagt cttctggagg cacctccaat aactatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggaggg atcagcccta tctttggttc agcagcctac 180

gcacagaagt tccagggcag agtcactatt accgcggaca tattttcgaa cacagtgtac 240

atggagctga acagcctgac atctgaggac acggccgtgt attactgtgc gagacacggg 300

aattattatt actactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 18

<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-007 VH PROTEIN

<400> 18

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Ala Ala Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Ile Phe Ser Asn Thr Val Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 19
<211> 331
<212> DNA
<213> Artificial

<220>
<223> SC09-007 VL DNA

<400> 19
tcctatgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc 60

tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccagcaggtc 120

cccggaacgg cccccaaact cctcatctat ggtgatgatc agcggccctc aggggtccct 180

gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaggatg aggctgatta ttactgtgca acatgggatg acagcctgaa tggtcatgtg 300

ttcggaggag gcacccagct gaccgtcctc g 331

<210> 20
<211> 110
<212> PRT
<213> Artificial

<220>
<223> SC09-007 VL PROTEIN

<400> 20

Ser Tyr Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Thr Val Asn Trp Tyr Gln Gln Val Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Gly Asp Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu
85 90 95

Asn Gly His Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 21
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-008 VH DNA

<400> 21
gaggtccagc tggtgcagtc tggggctgag gtcaagaagc ctgggtcctc ggtgagagtc 60

tcctgtaagt cttctggagg cacctccaat aactatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggcggg atcagcccta tctttggttc gacagcctac 180

gcacagaagt tccagggcag agtcactatt tccgcggaca tattttcgaa cacagcctac 240

atggagctga acagcctgac atctgaggac acggccgtat atttctgtgc gaggcacggg 300

aattattatt actactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 22
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-008 VH PROTEIN

<400> 22

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

1 5 10 15

Ser Val Arg Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Ala Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 23
<211> 331
<212> DNA
<213> Artificial

<220>
<223> SC09-008 VL DNA

<400> 23
tcctatgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccaggatt 60

acctgtgggg gaaacaacat tggaagtaaa actgtgcatt ggtaccagca gaactcaggc 120

caggcccctg tgctggtcgt ctatggtgat agcgaccggc cctcagggat ccctgagcga 180

ttctctggct ccaactctgg gaccacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatagtagta gtgatcatcc cggtgctgtg 300

ttcggaggag gcacccagct gaccgtcctc g 331

<210> 24
<211> 110
<212> PRT
<213> Artificial

<220>
<223> SC09-008 VL PROTEIN

<400> 24

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Thr Val

20 25 30

His Trp Tyr Gln Gln Asn Ser Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Gly Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Thr Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Pro Gly Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 25
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-009 VH DNA

<400> 25
caggtgcagc tggtgcaatc tggggctgag gtcaagaagc ctgggtcctc ggtgaaagtc 60

tcctgcaagt cttctggagg cacctccaat aactatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggcggg atcagcccta tctttggttc gacagcctac 180

gcacagaaat tccagggcag agtcactatt tccgcggaca tattttcgaa cacagcctac 240

atggagctga acagcctggc atctgaggac acggccgtat atttctgtgc gaggcacggg 300

aattattatt actactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 26
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-009 VH PROTEIN

<400> 26

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Ala Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Ala Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 27
<211> 322
<212> DNA
<213> Artificial

<220>
<223> SC09-009 VL DNA

<400> 27
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gcatattagc agttggttag cctggtatca gcagaagcca 120

gggaaaggcc ctcagctcct gatctattct gcatcccgtt tgcaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag gctaacagtt tccccctcac tttcggccct 300

gggaccaaag tggatatcaa ac 322

<210> 28
<211> 107
<212> PRT
<213> Artificial

<220>
<223> SC09-009 VL PROTEIN

<400> 28

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln His Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Gly Pro Gln Leu Leu Ile
35 40 45

Tyr Ser Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 29
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-010 VH DNA

<400> 29
gaggtgcagc tggtggagtc cggggctgag gtcaagaagc ctgggtcctc ggtgaaagtc 60

tcctgcaagt cttctggagg cacctccaat aattatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggcggg atcagcccta tctttggttc gacagcctac 180

gcacagaagt tccagggcag agtcactatt tccgcggaca tattttccaa cacagcctac 240

atggagctga acagcctgac atctgaggac acggccgtat attactgtgc gaggcacggg 300

aattattatt actactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 30
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-010 VH PROTEIN

<400> 30

Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Ala Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 31
<211> 331
<212> DNA
<213> Artificial

<220>
<223> SC09-010 VL DNA

<400> 31
tcctatgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccaggatt 60

acctgtgggg gaaacaacat yggaagtaaa actgtgcatt ggtaccagca gaactcaggc 120

caggcccctg tgctggtcgt ctttgttgat agcgaccgtc cctcagggat ccatgagcga 180

ttctgtggct ccaactctgg gtccacggcc accctgacca tcagcagcgt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatagtaata gcgatcatcc cggtgctgtg 300

ttcggaggag gcacccagct gaccgtcctc g 331

<210> 32
<211> 110
<212> PRT
<213> Artificial

<220>
<223> SC09-010 VL PROTEIN

<400> 32

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Thr Val
20 25 30

His Trp Tyr Gln Gln Asn Ser Gly Gln Ala Pro Val Leu Val Val Phe
35 40 45

Val Asp Ser Asp Arg Pro Ser Gly Ile His Glu Arg Phe Cys Gly Ser
50 55 60

Asn Ser Gly Ser Thr Ala Thr Leu Thr Ile Ser Ser Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Asn Ser Asp His
85 90 95

Pro Gly Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu

100 105 110

<210> 33
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-011 VH DNA

<400> 33
gaggtccagc tggtacagtc tggggctgag gtcaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagt cttctggagg cacctccaat aactatgcta tcagctgggt gcggcaggcc 120

cctggacaag gccttgactg gatgggaggg atcagcccta tctttggttc agcagcctac 180

gcacagaagt tccagggcag agtcactatt accgcggaca tattttcgaa cacagtgtac 240

atggagctga acagcctgac atctgaggac acggccgtgt attactgtgc gagacacggg 300

aattattatt actactccgg tacggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 34
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-011 VH PROTEIN

<400> 34

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Ala Ala Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Ile Phe Ser Asn Thr Val Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Thr Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 35
<211> 331
<212> DNA
<213> Artificial

<220>
<223> SC09-011 VL DNA

<400> 35
tcctatgtgc tgactcagcc acccgcagtg tctgggaccc ccgggcagag ggtcaccatc 60

tcgtgttctg gaagtgattc caacatcggg agaagaagtg taaactggta ccagcagttc 120

ccaggaacgg cccccaaact cctcatctat agtaacgatc agcggccctc agtggtccct 180

gaccgattct ctggctccaa gtccggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaagatg aggccgaata ttactgtgca gcatgggatg acagcctgaa gggggctgtg 300

ttcggaggag gcacccagct gaccgtcctc g 331

<210> 36
<211> 110
<212> PRT
<213> Artificial

<220>
<223> SC09-011 VL PROTEIN

<400> 36

Ser Tyr Val Leu Thr Gln Pro Pro Ala Val Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Asp Ser Asn Ile Gly Arg Arg
20 25 30

Ser Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asp Gln Arg Pro Ser Val Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Lys Gly Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 37
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-012 VH DNA

<400> 37
gaggtccagc tggtacagtc tggggctgag gtcaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagt cttctggagg cacctccaat aattatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggaggg atcagcccta tttttggttc agcagtctac 180

gcacagaagt tccagggcag agtcactatt accgcggaca tattttcgaa cacagtgtac 240

atggagctga acagcctgac atctgaggac acggccgtgt attactgtgc gagacacggg 300

acttattatt actactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 38
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-012 VH PROTEIN

<400> 38

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Ala Val Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Ile Phe Ser Asn Thr Val Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Thr Tyr Tyr Tyr Tyr Ser Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 39
<211> 334
<212> DNA
<213> Artificial

<220>
<223> SC09-012 VL DNA

<400> 39

cagtctgtcg tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccaggga cagccccaa actcctcatc tatggtaaca acaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggttgagg atgaggctga ttattactgc cagtcctatg accagaacct gagtgagggg 300

gtcttcggcg gagggaccaa gctgaccgtc ctag 334

<210> 40
<211> 111
<212> PRT
<213> Artificial

<220>
<223> SC09-012 VL PROTEIN

<400> 40

Gln Ser Val Val Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Val Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gln Asn
85 90 95

Leu Ser Glu Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 41
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-029 VH DNA

<400> 41
gaggtgcagc tggtggagtc cggggctgag gtcaagaagc ctgggtcctc ggtgaaagtc 60

tcctgcaagt cttctggagg cacctccaat aactatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggcggg atcagcccta tctttggttc gacagcctac 180

gcacagaagt tccagggcag agtcactatt tccgcggaca tattttcgaa cacagcctac 240

atggagctga acagcctgac atctgaggac acggccgtat attactgtgc gaggcacggg 300

aattattatt actactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 42
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-029 VH PROTEIN

<400> 42

Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Ala Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 43
<211> 321
<212> DNA
<213> Artificial

<220>
<223> SC09-029 VL DNA

<400> 43
gaaattgtga tgacgcagtc tccaggcacc ctgtctttgt ctcctgggga aagaggcacc 60

ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg catcccagac 180

aggttcactg gcagtgggtc tgggacagac ttcactctca ccatcagcag actggagcct 240

gaagattttg cagtgtatta ctgtcagcag tatgggagct caccattcgc tttcggccct 300

gggaccaagg tggagatcaa a 321

<210> 44
<211> 107
<212> PRT
<213> Artificial

<220>
<223> SC09-029 VL PROTEIN

<400> 44

Glu Ile Val Met Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Gly Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Phe
85 90 95

Ala Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
100 105

<210> 45
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-030 VH DNA

<400> 45
cagatgcagc tggtgcagtc tggggctgag gtcaagaagc ctgggtcctc ggtgaaagtc 60

tcctgcaagt cttctggagg cacctccaat aactatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggcggg atcagcccta tctttggttc gacagcctac 180

gcacagaagt tccagggcag agtcactatt tccgcggaca tattttcgaa cacagcctac 240

atggagctga acagcctgac atctgaggac acggccgtat atttctgtgc gaggcacggg 300

aattattatt actactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 46
<211> 121
<212> PRT

<213> Artificial

<220>
<223> SC09-030 VH PROTEIN

<400> 46

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Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
        35                  40                  45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Ala Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser Asn Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Val Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<210> 47
<211> 331
<212> DNA
<213> Artificial

<220>
<223> SC09-030 VL DNA

<400> 47

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tcctatgtgc tgactcagcc accctcggtg tcagtggccc caggacagac ggccaggatt       60

acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc      120

caggcccctg tgctggtcgt ctatggtgat agcgaccggc cctcagggat ccctgagcga      180

ttctctggct ccaactctgg gaccacggcc accctgacca tcagcagggt cgaagccggg      240

gatgaggccg actattactg tcaggtgtgg gatagtagta gtgatcatcc cggtgctgtg      300

ttcggaggag gcacccagct gaccgtcctc g                                     331
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<210> 48
<211> 110
<212> PRT
<213> Artificial

<220>
<223> SC09-030 VL PROTEIN

<400> 48

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Gly Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Thr Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Pro Gly Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 49
<211> 362
<212> DNA
<213> Artificial

<220>
<223> SC09-031 VH DNA

<400> 49
caggtccagc tggtacagtc tggggctgag gtcgagaggc ctgggtcctc ggtgaaagtc 60

tcctgcaagt cttctggcgg cacctccaat aactatgcca tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggcggg atcagcccta tctttggttc gacagcctac 180

gcacagaagt tccagggcag agtcactatt tccgcggaca tattttcgaa cacagcctac 240

atggagctga acagtctgac atctgaggac acggccgtct attattgtgc gagacacggg 300

aattattatt acaactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

ag 362

<210> 50
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-031 VH PROTEIN

<400> 50

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Glu Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Ala Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Asn Ser Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 51
<211> 340
<212> DNA
<213> Artificial

<220>
<223> SC09-031 VL DNA

<400> 51
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tcctgcactg ggagcagctc caacatcggg gcaggttatg atgtacactg gtaccagcag 120

cttccagaaa cagccccaa actcctcatt tatgataaca acaatcgtcc ctcaggggtt 180

tctgaccgat tctctggctc caagtctggc acttcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcggcct gagtgcttcg 300

ccttatgtct tcggagctgg gaccaaggtc accgtcctag 340

<210> 52
<211> 113
<212> PRT
<213> Artificial

<220>
<223> SC09-031 VL PROTEIN

<400> 52

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Glu Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Asp Asn Asn Asn Arg Pro Ser Gly Val Ser Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly
85 90 95

Leu Ser Ala Ser Pro Tyr Val Phe Gly Ala Gly Thr Lys Val Thr Val
100 105 110

Leu

<210> 53
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-112 VH DNA

<400> 53
caggtgcagc tggtgcagtc tggggctgag gtcaagaagc ctgggtcctc ggtgaaagtc 60

tcctgcaagt cttctggagg cacctccaat aactatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggcggg atcagcccta tctttggttc gacagcctac 180

gcacagaagt tccagggcag agtcactatt tccgcggaca tattttcgaa cacagcctac 240

atggagctga acagcctgac atctgaggac acggccgtat attactgtgc gaggcacggg 300

aattattatt actactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 54
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-112 VH PROTEIN

<400> 54

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met

35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Ala Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 55
<211> 334
<212> DNA
<213> Artificial

<220>
<223> SC09-112 VL DNA

<400> 55
cagtctgtgt tgacgcagcc gccctcagtg tctggggccc cagggcagag ggtcaccatc 60

tcctgcactg ggagcagcgc caacatcggg gcaggttatg atgtccactg gtaccagcag 120

tttccaggaa cagcccccaa actcctcatc tatggtaaca acaatcggcc ctcaggggtc 180

cctgaccgat tctctggctc caagtctggc acctcagcct ccctggccat cactgggctc 240

caggctgagg atgaggctga ttattactgc cagtcctatg acagcagcct gagtggtgcg 300

ttattcggcg gagggaccaa gctgaccgtc ctag 334

<210> 56
<211> 111
<212> PRT
<213> Artificial

<220>
<223> SC09-112 VL PROTEIN

<400> 56

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ala Asn Ile Gly Ala Gly
20 25 30

Tyr Asp Val His Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu
35 40 45

Leu Ile Tyr Gly Asn Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe

50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

Leu Ser Gly Ala Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 57
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-113 VH DNA

<400> 57
cagatgcagc tggtgcagtc tggggctgag gtcaagaagg ctgggtcctc ggtgaaagtc 60

tcctgcaagt cttctggagg cacctccaat aactatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgagtg gatgggcggg atcagtccaa tctttggttc gacagtctac 180

gcacagaaat tccagggcag agtcactatt tccgcggaca tattttcaca cactgcctac 240

atggagctga acagcctgac atctgaggac acggccgcat atttctgtgc gaggcacgga 300

aactattatt actactccgg tatggacctc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 58
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-113 VH PROTEIN

<400> 58

Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Ala Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Val Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser His Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Ala Tyr Phe Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Leu Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 59
<211> 331
<212> DNA
<213> Artificial

<220>
<223> SC09-113 VL DNA

<400> 59
cagtctgtgc tgactcagcc acccgcagtg tctgggaccc ccgggcagag ggtcaccatc 60

tcgtgttctg gaagtgattc caacatcggg agaagaagtg taaactggta ccagcagttc 120

ccaggaacgg cccccaaact cctcatctat agtaacgatc agcggccctc agtggtccct 180

gaccgattct ctggctccaa gtccggcacc tcagcctccc tggccatcag tgggctccag 240

gctgaggatg aggctgatta ttactgtgca gcatgggatg ccagcctgag tggtcctgtg 300

ttcggaggag gcacccagct gaccgtcctc g 331

<210> 60
<211> 110
<212> PRT
<213> Artificial

<220>
<223> SC09-113 VL PROTEIN

<400> 60

Gln Ser Val Leu Thr Gln Pro Pro Ala Val Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Asp Ser Asn Ile Gly Arg Arg
20 25 30

Ser Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asp Gln Arg Pro Ser Val Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Ala Ser Leu
85 90 95

Ser Gly Pro Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 61
<211> 363
<212> DNA
<213> Artificial

<220>
<223> SC09-114 VH DNA

<400> 61
caggtgcagc tggtgcaatc tggggctgag gtcaagaagc ctgggtcctc ggtgaaagtc 60

tcctgcaagt cttctggagg cacctccaat aactatgcta tcagctgggt gcgacaggcc 120

cctggacaag gccttgactg gatgggcggg atcagcccta tctttggttc gacagcctac 180

gcacagaaat tccagggcag agtcactatt tccgcggaca tattttcgaa cacagcctac 240

atggagctga acagcctgac atctgaggac acggccgtat atttctgtgc gaggcacggg 300

aattattatt actactccgg tatggacgtc tggggccaag ggaccacggt caccgtctcg 360

agc 363

<210> 62
<211> 121
<212> PRT
<213> Artificial

<220>
<223> SC09-114 VH PROTEIN

<400> 62

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Gly Thr Ser Asn Asn Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
35 40 45

Gly Gly Ile Ser Pro Ile Phe Gly Ser Thr Ala Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ala Asp Ile Phe Ser Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Gly Asn Tyr Tyr Tyr Tyr Ser Gly Met Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 63
<211> 331
<212> DNA
<213> Artificial

<220>
<223> SC09-114 VL DNA

<400> 63
tcctatgtgc tgactcagcc acccgcagtg tctgggaccc ccgggcagag ggtcaccatc 60

tcgtgttctg gaagtgattc caacatcggg agaagaagtg taaactggta ccagcagttc 120

ccaggaacgg cccccaaact cctcatctat agtaacgatc agcggccctc agtggtccct 180

gaccgattct ctggctccaa gtccggcacc tcagcctccc tggccatcag tgggctccag 240

tctgaagatg aggccgaata ttactgtgca gcatgggatg acagcctgaa gggggctgtg 300

ttcggaggag gcacccagct gaccgtcctc g 331

<210> 64
<211> 110
<212> PRT
<213> Artificial

<220>
<223> SC09-114 VL PROTEIN

<400> 64

Ser Tyr Val Leu Thr Gln Pro Pro Ala Val Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Asp Ser Asn Ile Gly Arg Arg
20 25 30

Ser Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Ser Asn Asp Gln Arg Pro Ser Val Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Lys Gly Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 65
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OK1 (HuVK1B)

<400> 65
gacatccagw tgacccagtc tcc 23

<210> 66
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OK2 (HuVK2)

<400> 66
gatgttgtga tgactcagtc tcc 23

<210> 67
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OK3 (HuVK2B2)

<400> 67
gatattgtga tgacccagac tcc 23

<210> 68
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OK4 (HuVK3B)

<400> 68
gaaattgtgw tgacrcagtc tcc 23

<210> 69
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OK5 (HuVK5)

<400> 69
gaaacgacac tcacgcagtc tcc 23

<210> 70
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OK6 (HuVK6)

<400> 70
gaaattgtgc tgactcagtc tcc 23

<210> 71

<211> 24
<212> DNA
<213> Artificial

<220>
<223> OCK (HuCK)

<400> 71
acactctccc ctgttgaagc tctt 24

<210> 72
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OL1 (HuVL1A)

<400> 72
cagtctgtgc tgactcagcc acc 23

<210> 73
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OL1 (HuVL1B)

<400> 73
cagtctgtgy tgacgcagcc gcc 23

<210> 74
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OL1 (HuVL1C)

<400> 74
cagtctgtcg tgacgcagcc gcc 23

<210> 75
<211> 20
<212> DNA
<213> Artificial

<220>
<223> OL2 (HuVL2B)

<400> 75
cagtctgccc tgactcagcc 20

<210> 76
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OL3 (HuVL3A)

<400> 76

tcctatgwgc tgactcagcc acc 23

<210> 77
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OL4 (HuVL3B)

<400> 77
tcttctgagc tgactcagga ccc 23

<210> 78
<211> 20
<212> DNA
<213> Artificial

<220>
<223> OL5 (HuVL4B)

<400> 78
cagcytgtgc tgactcaatc 20

<210> 79
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OL6 (HuVL5)

<400> 79
caggctgtgc tgactcagcc gtc 23

<210> 80
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OL7 (HuVL6)

<400> 80
aattttatgc tgactcagcc cca 23

<210> 81
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OL8 (HuVL7/8)

<400> 81
cagrctgtgg tgacycagga gcc 23

<210> 82
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OL9 (HuVL9)

<400> 82
cwgcctgtgc tgactcagcc mcc 23

<210> 83
<211> 18
<212> DNA
<213> Artificial

<220>
<223> OL9 (HuVL10

<400> 83
caggcagggc tgactcag 18

<210> 84
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OCL (HuCL2)

<400> 84
tgaacattct gtaggggcca ctg 23

<210> 85
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OCL (HuCL7)

<400> 85
agagcattct gcaggggcca ctg 23

<210> 86
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OH1(HuVH1B7A)

<400> 86
cagrtgcagc tggtgcartc tgg 23

<210> 87
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OH1 (HuVH1C)

<400> 87
saggtccagc tggtrcagtc tgg 23

<210> 88

<211> 23
<212> DNA
<213> Artificial

<220>
<223> OH2 (HuVH2B)

<400> 88
cagrtcacct tgaaggagtc tgg 23

<210> 89
<211> 18
<212> DNA
<213> Artificial

<220>
<223> OH3 (HuVH3A)

<400> 89
gaggtgcagc tggtggag 18

<210> 90
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OH4 (HuVH3C)

<400> 90
gaggtgcagc tggtggagwc ygg 23

<210> 91
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OH5 (HuVH4B)

<400> 91
caggtgcagc tacagcagtg ggg 23

<210> 92
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OH6 (HuVH4C)

<400> 92
cagstgcagc tgcaggagtc sgg 23

<210> 93
<211> 23
<212> DNA
<213> Artificial

<220>
<223> OH7 (HuVH6A)

<400> 93

caggtacagc tgcagcagtc agg 23

<210> 94
<211> 24
<212> DNA
<213> Artificial

<220>
<223> OCM (HuCIgM)

<400> 94
tggaagaggc acgttctttt cttt 24

<210> 95
<211> 41
<212> DNA
<213> Artificial

<220>
<223> OK1S (HuVK1B-SAL)

<400> 95
tgagcacaca ggtcgacgga catccagwtg acccagtctc c 41

<210> 96
<211> 41
<212> DNA
<213> Artificial

<220>
<223> OK2S (HuVK2-SAL)

<400> 96
tgagcacaca ggtcgacgga tgttgtgatg actcagtctc c 41

<210> 97
<211> 41
<212> DNA
<213> Artificial

<220>
<223> OK3S (HuVK2B2-SAL)

<400> 97
tgagcacaca ggtcgacgga tattgtgatg acccagactc c 41

<210> 98
<211> 41
<212> DNA
<213> Artificial

<220>
<223> OK4S (HuVK3B-SAL)

<400> 98
tgagcacaca ggtcgacgga aattgtgwtg acrcagtctc c 41

<210> 99
<211> 41
<212> DNA
<213> Artificial

<220>
<223> OK5S (HuVK5-SAL)

<400> 99
tgagcacaca ggtcgacgga aacgacactc acgcagtctc c 41

<210> 100
<211> 41
<212> DNA
<213> Artificial

<220>
<223> OK6S (HuVK6-SAL)

<400> 100
tgagcacaca ggtcgacgga aattgtgctg actcagtctc c 41

<210> 101
<211> 48
<212> DNA
<213> Artificial

<220>
<223> OJK1 (HuJK1-NOT)

<400> 101
gagtcattct cgacttgcgg ccgcacgttt gatttccacc ttggtccc 48

<210> 102
<211> 48
<212> DNA
<213> Artificial

<220>
<223> OJK2 (HuJK2-NOT)

<400> 102
gagtcattct cgacttgcgg ccgcacgttt gatctccagc ttggtccc 48

<210> 103
<211> 48
<212> DNA
<213> Artificial

<220>
<223> OJK3 (HuJK3-NOT)

<400> 103
gagtcattct cgacttgcgg ccgcacgttt gatatccact ttggtccc 48

<210> 104
<211> 48
<212> DNA
<213> Artificial

<220>
<223> OJK4 (HuJK4-NOT)

<400> 104
gagtcattct cgacttgcgg ccgcacgttt gatctccacc ttggtccc 48

<210> 105

<211> 48
<212> DNA
<213> Artificial

<220>
<223> OJK5 (HuJK5-NOT)

<400> 105
gagtcattct cgacttgcgg ccgcacgttt aatctccagt cgtgtccc 48

<210> 106
<211> 41
<212> DNA
<213> Artificial

<220>
<223> OL1S (HuVL1A-SAL)

<400> 106
tgagcacaca ggtcgacgca gtctgtgctg actcagccac c 41

<210> 107
<211> 41
<212> DNA
<213> Artificial

<220>
<223> OL1S (HuVL1B-SAL)

<400> 107
tgagcacaca ggtcgacgca gtctgtgytg acgcagccgc c 41

<210> 108
<211> 41
<212> DNA
<213> Artificial

<220>
<223> OL1S (HuVL1C-SAL)

<400> 108
tgagcacaca ggtcgacgca gtctgtcgtg acgcagccgc c 41

<210> 109
<211> 38
<212> DNA
<213> Artificial

<220>
<223> OL2S (HuVL2B-SAL)

<400> 109
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