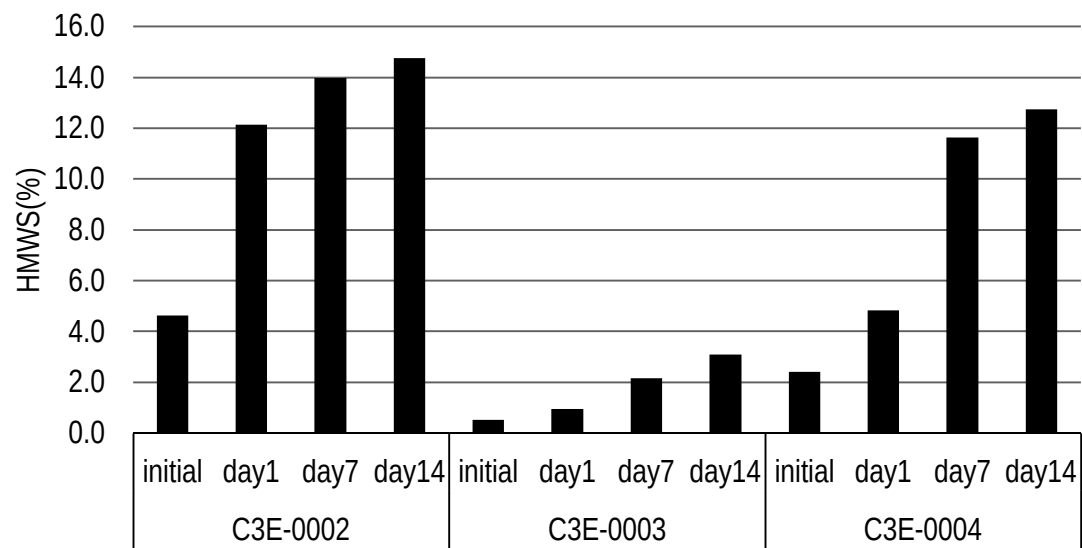
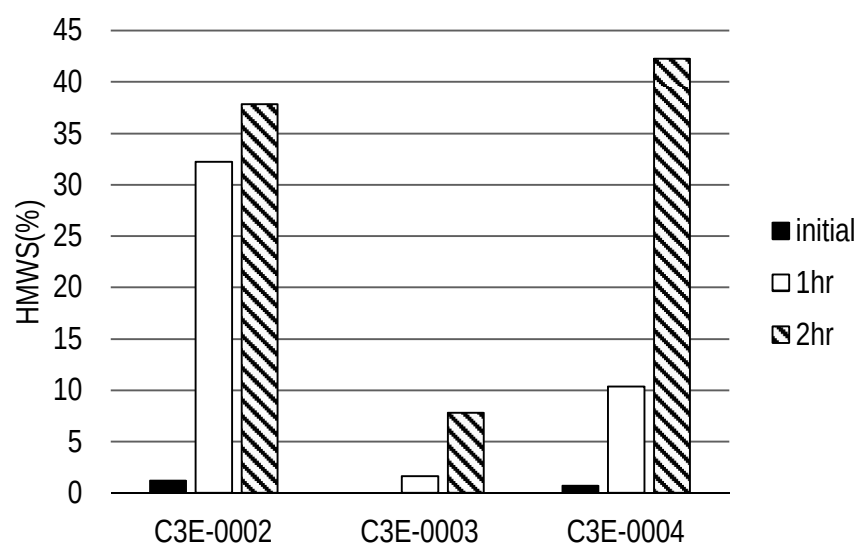


[Fig. 1]

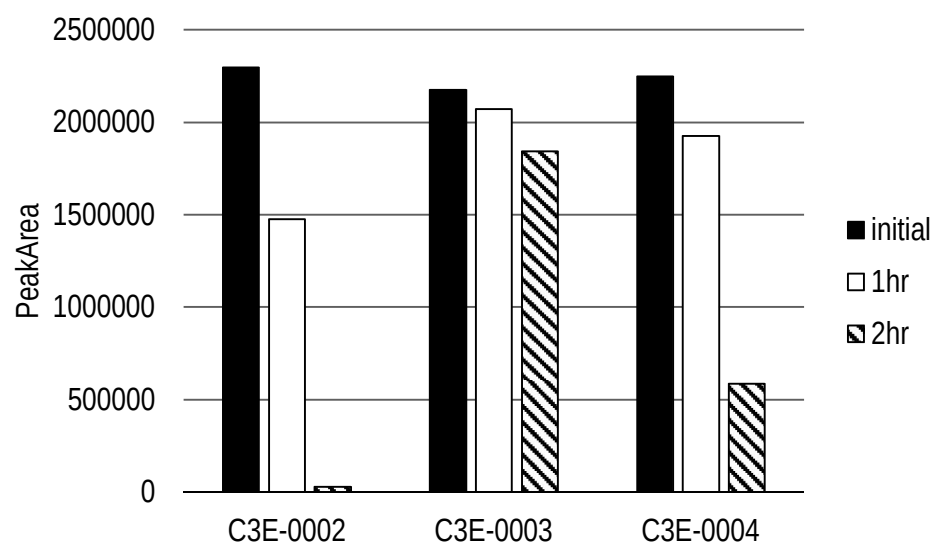


[Fig. 2]

A

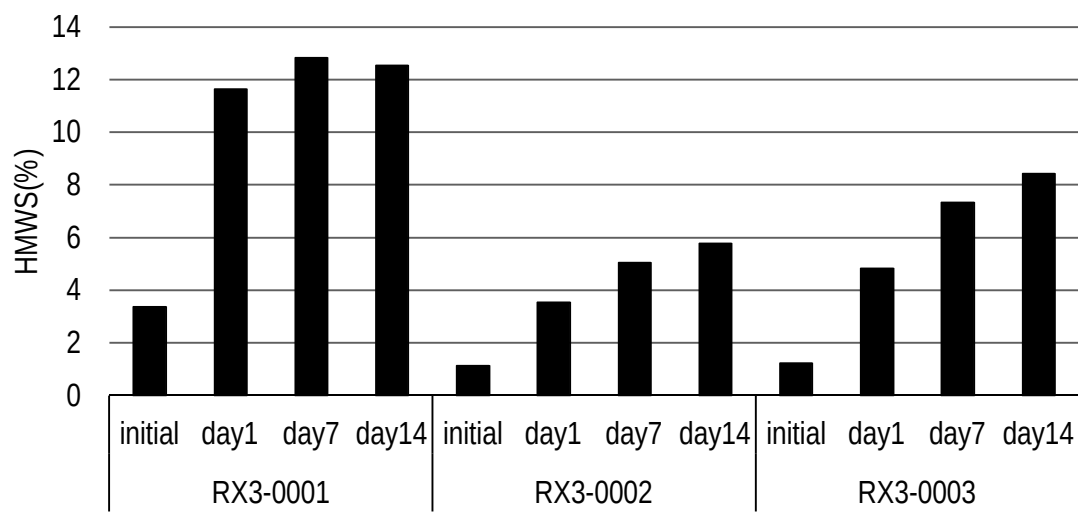


B

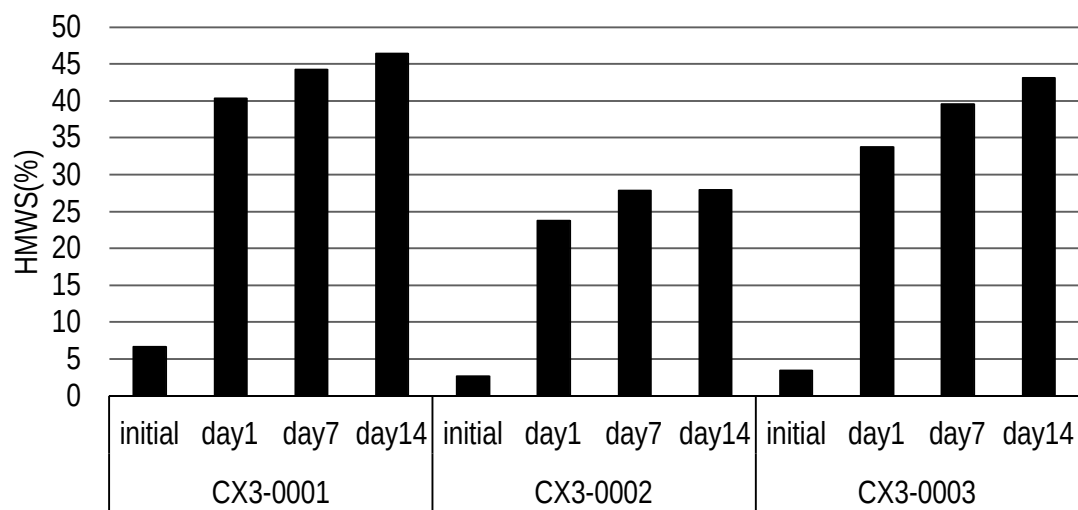


[Fig. 3]

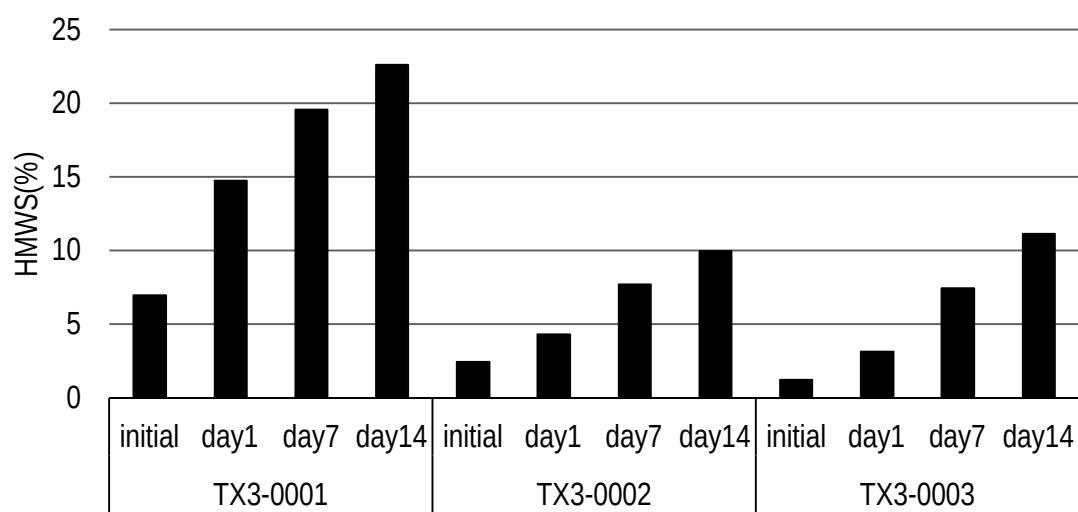
A



B

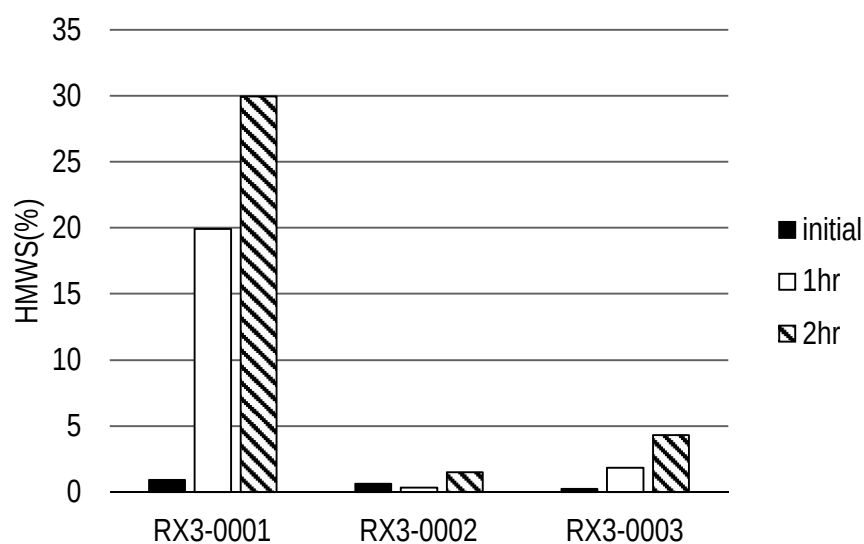


C

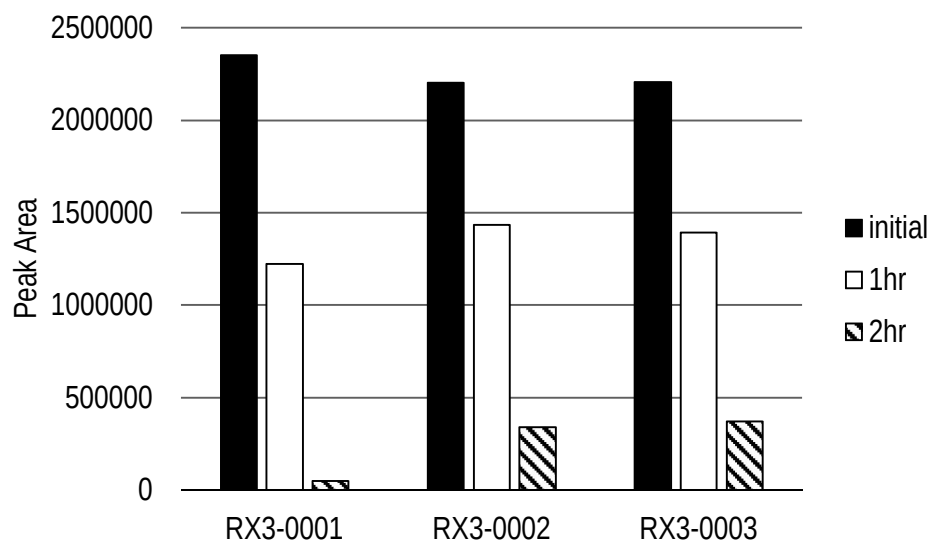


[Fig. 4-1]

A

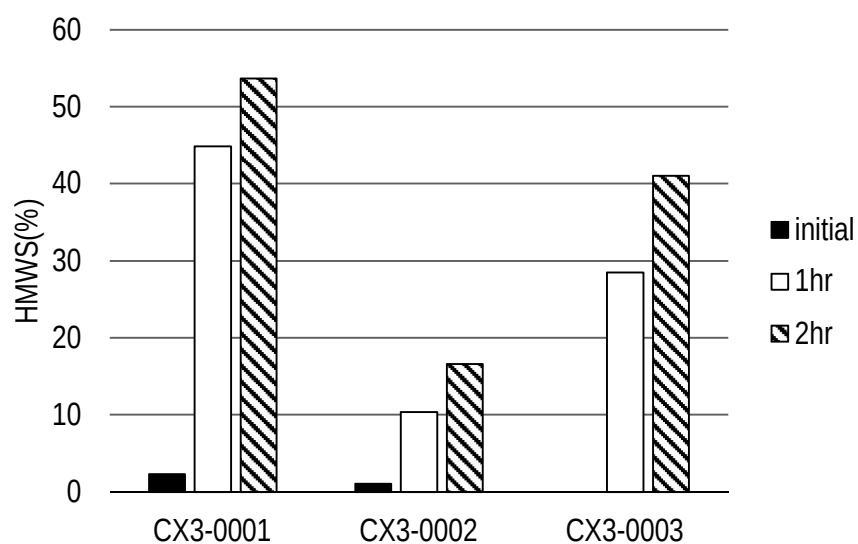


B

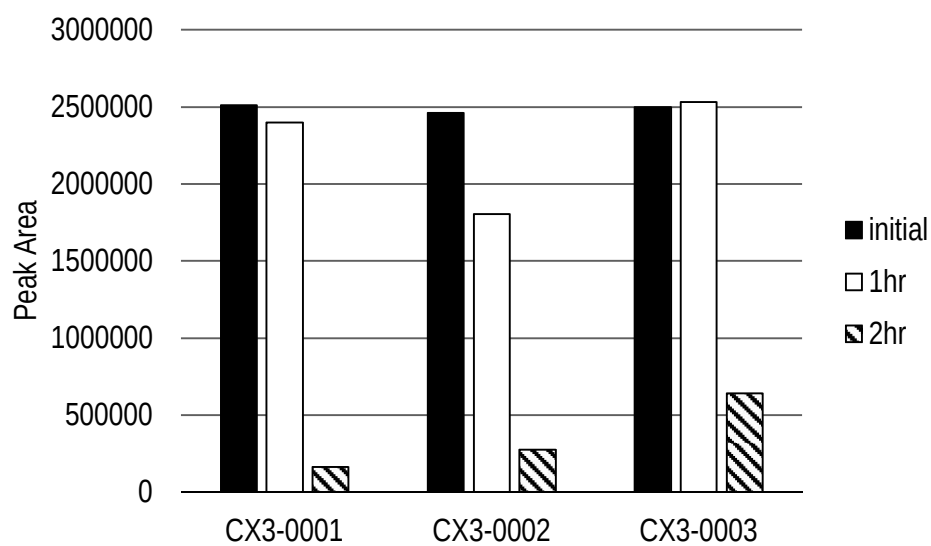


[Fig. 4-2]

A

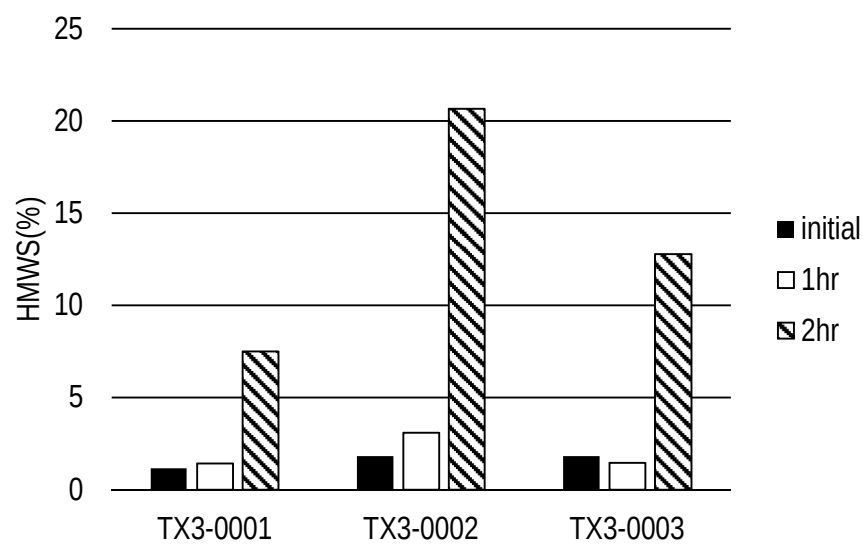


B

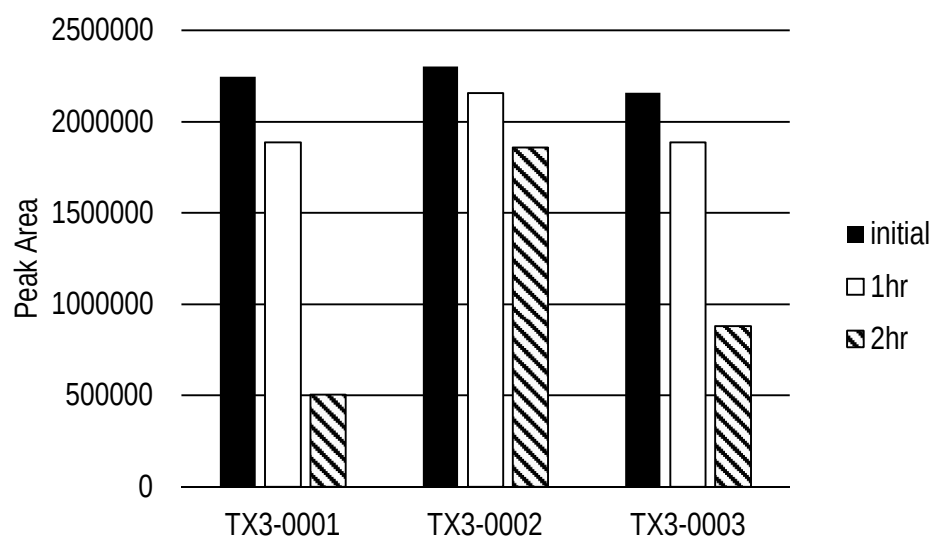


[Fig. 4-3]

A



B



[Fig. 5]

C3E-7085-Fab

**EVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGG
RIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVAYWGQGT
LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVDKRV
(SEQ ID NO: 1)**

[Fig. 6]

C3E-7085-LC

**NFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTAPKLLIYRDDKRP
SGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGGGTKLTVLGQPKA
APSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ
SNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
(SEQ ID NO: 2)**

[Fig. 7]

C3E - 7096

**EVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGG
RIIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVAYWGCGT
LVTVSSGGGGSGGGGSGGGGSNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVN
WYQQLPGTCPKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQS
YSSGFIFGGGTKLTVL**

(SEQ ID NO: 3)

[Fig. 8]

HC_h

**ATGAAGCACCTCTGGTTCTTTCTCCTGTTGGTGGCTGCACCAAGATGGGTCCTGAG
CGACAAGACGCACACTTGCCCTCCGTGTCCAGCTCCCGAAGCTGCAGGAGGTCCCA
GCGTTTTCTGTTTCTCCAAAGCCCAAAGACACCCTGATGATCTCCAGGACTCCC
GAGGTGACCTGTGTAGTTGTGACGTTAGCCATGAGGATCCCGAGGTCAAGTTTAA
CTGGTATGTGCGACGGAGTTGAAGTCCACAATGCCAAGACCAAACCACGAGAAGAGC
AGTACAATAGCACATATCGCGTAGTGTCTGTACTGACCGTGTTGCATCAGGATTGG
CTTAATGGGAAGGAGTACAAGTGCAAAGTGAGCAACAAAGCCCTTCCGGCGCCCAT
AGAGAAAACCATCAGCAAGGCAAAGGGGCAACCTCGGGAACCTCAGGTCTGCACAC
TGCCACCTTCTCGTGATGAGCTGACTAAGAACCAGGTGTCACTGTCCTGTGCCGTG
AAAGGCTTTTACCCCTCCGACATTGCCGTGGAATGGGAGTCAAATGGTCAGCCTGA
GAACAACTACAAGACTACACCGCCAGTGCTCGATTGAGATGGCTCTTTCTTCCTGG
TTTCCAAGCTGACAGTGGACAAATCCAGATGGCAACAGGGCAATGTGTTTCAGCTGC
AGTGTGATGCATGAAGCCCTTCACAACCACTATACGCAGAAAAGTCTGAGTCTCTC
TCCTGGAAAA**

**(SEQ ID NO: 4) Signal sequence(1-57), Hinge(58-87),
CH2(88-417), CH3(418-738)**

[Fig. 9]

C3E-7085-HC-k

ATGAAGCATCTCTGGTTTTTCTTGCTGCTCGTCGCTGCACCTCGATGGGTGCTGTC
AGGCGAAGTCCAGCTGGTTGAATCTGGCGGTGGCCTGGTGCAACCTGGAGGGTCTT
TGAGACTGAGTTGTGCCGCATCAGGAGTCACCTTCAACTACTATGGCATGTCATGG
ATACGCCAAGCTCCCGGGAAAGGGCTCGAATGGGTTCGCATCAATCACTCGGTCTGG
GGGGAGAATCTACTATCCAGACTCAGTCAAGGGCCGCTTTACCATCAGCCGTGAGA
ATACCCAGAAAACGCTGTACCTACAGATGAACTCCCTTCGGGCAGAGGACACTGCC
GTGTACTACTGTACACTGGATGGGCGAGATGGGTGGGTTCCTATTGGGGCCAAGG
TACTCTTGTGACTGTGTCTTCGGGAGGCGGCGGTTCGGTGGTGGTGGTTCCGGAG
GAGGAGGAAGCAACTTCATGCTGACACAGCCGTCTTCGTATCTGGCGTACCAGGT
CAACGCGTGACCATTTCTTGACCCGGCAATACAGGGAACATTGGCAGCAACTATGT
GAACTGGTATCAGCAGCTTCCCGGAACTGCTCCTAAACTCCTGATATACAGGGATG
ATAAGCGGCCTTCTGGGGTCCCTGATCGGTTTAGTGGCTCCAAAAGCGGAACCTCG
GCGAGCCTGGCAATCACAGGCTTTCAGGCTGAGGATGAGGCCGACTATTATTGCCA
GAGTTATAGTAGCGGATTCATCTTTGGCGGGGGCACGAAGTTAACCGTGCTTGGTG
GAGAGCCCAAAAGCGCCGACAAGACCCACACCTGTCCACCTTGTCCCGCTCCAGAA
GCCGCTGGGGGGCCTTCCGTCTTTCTTTCCCCGAAACCCAAAGACACACTGAT
GATCTCCAGAACACCCGAAGTAACCTGCGTTGTGGTTGACGTATCCCACGAAGATC
CCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTTGAGGTGCACAATGCCAAAACA
AAGCCTAGGGAGGAACAGTACAATTCGACATATAGGGTAGTGTGAGTCTGACAGT
GTTACACCAGGACTGGTTGAACGGGAAAGAGTACAAGTGCAAGGTGAGCAACAAAG
CGCTTCAGCGCCAATTGAGAAGACGATTTCAAAGCCAAAGGACAGCCGAGGGAA
CCGCAGGTCTACACCTTACCCCCATGCAGAGACGAGTTGACCAAGAATCAGGTGAG
TCTATGGTGCCTCGTGAAGGGCTTCTATCCCAGCGATATTGCCGTGAGTGGGAAT
CTAATGGCCAACCAGAGAACAACTACAAGACTACGCCACCCGTTCTGGACAGTGAT
GGGAGCTTCTTCCTATACTCCAAGCTCACTGTGGACAAGTCACGTTGGCAACAGGG
AAATGTTTTTCAGTTGTAGCGTGATGCATGAGGCCTTGCATAATCACTACACTCAGA
AAAGCCTGTCCCTGTCACCTGGAAAG

(SEQ ID NO: 5) Signal sequence(1-57), C3E-7085(61-780),
linker(781-786), Hinge(787-831), CH2(832-1161),
CH3(1162-1482)

[Fig. 10]

C3E-7085-Fab-HC-k

ATGAAACATCTCTGGTTCTTTCTGCTGCTGGTAGCCGCCCTAGATGGGTCCTCAG
TGAGGTTTCAGCTTGTAGAGTCCGGCGGCGGCTTGGTGCAGCCCGGAGGTTCCCTCC
GGCTTTCTTGCGCTGCTTCAGGAGTTACGTTCAATTACTATGGGATGTCCTGGATA
AGGCAGGCTCCCGGTAAGGGGTTGGAATGGGTGGCCAGTATTACCCGCAGTGGAGG
AAGAATCTACTATCCGGATTCTGTGAAAGGACGGTTCACTATCAGCAGAGAAAATA
CACAGAAAACCCTTTATCTCCAGATGAACTCCCTTCGTGCCGAGGATACCGCTGTG
TACTACTGCACACTGGATGGCCGAGATGGGTGGGTAGCCTACTGGGGTCAAGGAAC
GCTTGTGACAGTTTCCTCAGCCAGCACTAAGGGACCAAGCGTCTTTCGGTTGGCAC
CCAGCAGCAAAAGTACTAGCGGCGGCACAGCTGCACTGGGCTGCCTGGTGAAGGAC
TATTTCCCTGAACCCGTACCCGTGTCTGGAAGTCCGGTGCCTTGACTTCCGGTGT
TCACACATTCCCCGCAGTGCTCCAGAGTTCCGGGCTCTACTCACTGTCATCTGTGG
TCACCGTGCCTAGCTCAAGTCTGGGGACCCAACTTACATCTGCAATGTGAACCAT
AAGCCTAGTAACACCAAAGTCGACAAACGCGTCGAGCCCAAGTCATGCGACAAGAC
CCACACATGTCCACCTTGTCCCGCACCTGAGGCGGCTGGTGGCCCATCCGTGTTTC
TGTTTCCACCAAAGCCTAAAGACACCCTGATGATTAGTCGAACACCAGAGGTGACT
TGC GTTGTGTCGATGTGTACACGAAGATCCGGAGGTAAGTTCAACTGGTACGT
CGATGGGGTGGAGGTTTATAACGCCAAGACTAAGCCAAGAGAAGAGCAGTACAAC
CTACGTATAGGGTGGTAAGCGTACTGACAGTGTTGCACCAGGATTGGCTCAATGGC
AAGGAATACAAGTGTAAGGTGTCTAATAAGGCGCTGCCTGCGCCAATTGAGAAAAC
GATCTCTAAGGCCAAAGGGCAACCAAGGGAGCCCCAAGTCTATACCCTGCCTCCGT
GTCGGGACGAACTGACTAAGAACCAAGTGAGCCTCTGGTGCCTGGTCAAAGGCTTT
TATCCCAGCGACATAGCAGTGGAATGGGAGAGCAATGGGCAGCCAGAGAACAATA
CAAGACCACACCTCCCGTTCTGGACTCTGACGGATCATTCTTTCTGTATTCCAAAC
TGACAGTTGACAAGTCTCGCTGGCAGCAGGGAAATGTGTTTCAGCTGTAGCGTGATG
CATGAAGCCCTGCACAATCACTATACCCAGAAAAGCCTGAGCCTGTCTCCCGGCAA
A

(SEQ ID NO: 6) Signal sequence(1-57), C3E-7085-VH(58-411), CH1(412-705), Hinge(706-750), CH2(751-1080), CH3(1081-1401)

[Fig. 11]

C3E-7085-LC

**ATGGTTCTGCAGACTCAGGTGTTCAATTTCCCTTCTGCTGTGGATTAGTGGGGCATA
TGGGAATTTTCATGCTGACTCAGCCAAGCTCCGTAAGCGGAGTACCCGGCCAAAGAG
TCACAATCAGTTGCACTGGTAACACCGGTAATATCGGCTCTAACTACGTGAATTGG
TACCAGCAGTTGCCAGGAACAGCACCCAACTCCTGATCTACCGCGATGACAAGCG
ACCATCTGGCGTGCCTGATCGGTTTAGCGGGAGCAAAAGTGGCACAAGTGCCTCAT
TGGCCATAACGGGGTTCCAGGCGGAGGATGAAGCAGACTACTATTGCCAGTCCTAC
TCCTCTGGCTTCATCTTTGGCGGAGGGACCAAGCTCACCGTGCTTGGACAACCCAA
AGCAGCTCCATCAGTGACCCTGTTTCCTCCTTCTTCTGAGGAGCTGCAGGCCAATA
AGGCCACACTGGTGTGTCTCATTAGCGACTTTTATCCGGGTGCGGTCACTGTGGCC
TGGAAGCCGACTCAAGTCCGGTTAAGGCTGGAGTTGAGACAACCACACCCTCTAA
GCAGAGCAACAACAAGTATGCTGCCTCAAGCTACCTCTCACTGACCCCTGAGCAGT
GGAAATCCCATAGGAGCTATTCCTGCCAAGTCACCCACGAAGGCTCCACCGTCGAA
AAGACTGTGGCTCCCACGGAATGTAGC**

(SEQ ID NO: 7) Signal sequence(1-60), C3E-7085_VL(61-381), CL(382-699)

[Fig. 12]

C3E - 7096 - HC - k

ATGAAGCACCTGTGGTTTTTCTGTTACTCGTTGCTGCTCCCAGATGGGTCTTGAG
CGGAGAAGTACAGCTTGTAGAGTCAGGAGGAGGACTGGTACAACCAGGTGGCTCGT
TACGGCTCAGTTGCGCAGCCTCCGGTGTGACTTTCAACTACTACGGCATGAGCTGG
ATACGGCAAGCGCCTGGAAAGGGGCTCGAATGGGTAGCCTCCATAACACGGAGTGG
GGGTCGCATTTACTACCCCGATTCTGTCAAAGGCCGCTTCACAATCAGCAGAGAAA
ACACGCAGAAAACATTGTACCTCCAGATGAATAGCCTTAGGGCCGAAGATACGGCA
GTCTACTATTGCACCCTGGATGGCAGGGACGGTTGGGTTGCCTATTGGGGTTGTGG
CACCTTAGTGACCGTATCCTCTGGAGGAGGCGGCAGTGGAGGAGGGGGATCAGGGG
GTGGAGGGAGTAACTTCATGCTTACACAGCCAAGTTCTGTTTCAGGTGTTCTGGG
CAGAGGGTTACCATCTCTTGACACAGGGAATACAGGCAACATTGGCAGCAACTATGT
GAATTGGTATCAGCAGCTACCAGGCACGTGTCCGAAACTGTTGATCTATCGGGATG
ACAAAAGACCGTCCGGAGTGCCTGATCGCTTTTCCGGCTCTAAATCCGGGACTTCA
GCGAGTTTGGCCATTACTGGGTTTCAGGCAGAAGATGAGGCCGACTACTACTGCCA
GAGCTACTCTAGCGGGTTCATCTTTGGCGGTGGGACCAAGCTGACTGTGCTGGGCG
GCGAACCCAAATCCGCCGACAAAACCCACACTTGTCCGCCATGTCCTGCTCCAGAG
GCAGCTGGTGGCCCCTCTGTCTTTCTGTTTCCCCCTAAGCCCAAGGACACACTGAT
GATTTCCGCTACTCCAGAGGTGACGTGTGTGGTGGTGGATGTGTCTCATGAAGATC
CCGAGGTGAAGTTCAATTGGTATGTGGACGGAGTGGAAGTCCACAACGCTAAGACA
AAGCCTAGGGAAGAGCAGTATAACTCCACCTACAGAGTCGTTAGCGTGCTGACCGT
GCTCCATCAAGACTGGCTCAATGGCAAGGAGTACAAGTGCAAAGTCTCCAATAAGG
CCCTTCCTGCTCCCATCGAGAAAACCATCTCAAAGGCGAAAGGACAACCCCGAGAA
CCTCAGGTCTATACCCTACCACCCTGTCGTGACGAGCTGACTAAAAATCAGGTGTC
ACTGTGGTGCCTAGTCAAAGGGTTCTATCCCTCTGACATTGCCGTGGAGTGGGAGA
GCAATGGCCAGCCAGAGAACAACTACAAGACCACACCTCCAGTCCTGGACTCGGAT
GGCTCCTTCTTCCTGTACAGCAAGCTCACCGTTGACAAGTCACGATGGCAGCAAGG
GAATGTGTTCTCATGCAGCGTGATGCATGAGGCACTTCACAACCACTATACTCAGA
AGTCCCTGAGCTTGAGTCCGGGGAAA

(SEQ ID NO: 8) Signal sequence(1-57), C3E-7096(61-780),
linker(781-786), Hinge(787-831), CH2(832-1161),
CH3(1162-1482)

[Fig. 13]

HC_h

MKHLWFFLLLVAAPRWVLSDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVCTLPSSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

(SEQ ID NO: 9) Signal sequence(1-19), Hinge(20-29), CH2(30-139), CH3(140-246)

[Fig. 14]

C3E-7085-HC-k

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSW
IRQAPGKGLEWVASITRSGGRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTA
VYYCTLDGRDGWVAYWGQGLTVTVSSGGGGSGGGGSGGGGSNFMLTQPSSVSGVPG
QRTVISCTGNTGNIGSNYVNWYQQLPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTS
ASLAITGFQAEDEADYYCQSYSSGFIFGGGTKLTVLGGEPKSADKTHTCPPCPAPE
AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS
GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK**

**(SEQ ID NO: 10) Signal sequence(1-19), C3E-7085(21-260),
linker(261-262), Hinge(263-277), CH2(278-387), CH3(388-
494)**

[Fig. 15]

C3E-7085-Fab-HC-k

**MKHLWFFLLLVAAPRWVLSEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWI
RQAPGKGLEWVASITRSGGRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAV
YYCTLDGRDGWVAYWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH
KPSNTKVDKRVKPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGF
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVM
HEALHNHYTQKSLSLSPGK**

(SEQ ID NO: 11) Signal sequence(1-19), C3E-7085-VH(20-137), CH1(138-235)Hinge(236-250), CH2(251-360), CH3(361-467)

[Fig. 16]

C3E-7085-LC

**MVLQTQVFISLLLWISGAYGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNW
YQQLPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSY
SSGFIFGGGKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVA
WKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS**

**(SEQ ID NO: 12) Signal sequence(1-20), C3E-7085_VL(21-
127),CL(128-233)**

[Fig. 17]

C3E-7096-HC-k

**MKHLWFFLLLVAAPRWVLSGEVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSW
IRQAPGKGLEWVASITRSGGRIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTA
VYYCTLDGRDGWVAYWGCGLTVTVSSGGGGSGGGGSGGGGSNFMLTQPSSVSGVPG
QRTVISCTGNTGNIGSNYVNWYQQLPGTCPKLLIYRDDKRPSGVPDRFSGSKSGTS
ASLAITGFQAEDEADYYCQSYSSGFIFGGGTKLTVLGGEPKSADKTHTCPPCPAPE
AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS
GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK**

**(SEQ ID NO: 13) Signal sequence(1-19), C3E-7096(21-260),
linker(261-262), Hinge(263-277), CH2(278-387), CH3(388-
494)**

[Fig. 18]

TX3-0001-HC_k

**ATGAAGCACCTGTGGTTCTTTCTGCTGCTTGTGGCCGCACCACGGTGGGTGCTGTC
AGGTCAGGTGCAGTTAGTGCAGTCAGGCGCAGAAGTAAAGAAACCAGGAGCTTCAG
TGAAGGTCAGTTGCAAGGCTTCTGGGTATACGTTCACTACCGCAGGGATGCAGTGG
GTGCGCCAAGCTCCAGGGCAGGGACTGGAGTGGATGGGGTGGATTAATACCCATAG
CGGGGTCCCAAAGTACGCGGAAGATTTCAAAGGCAGAGTCACCATTTCTGCCGATA
CGAGCACATCGACAGCATACCTCCAGCTTAGTTCCCTTGAAGAGTGAGGACACAGCT
GTATACTACTGCGCCAGATCCGGTTTTGGTAGCAGTTACTGGTACTTCGACGTGTG
GGGCCAAGGCACACTCGTGACTGTATCCTCAGGAGGGGGAGGTTCCGGTGGCGGCG
GCTCTGGAGGAGGCGGAAGCGACATTAGATGACCCAGTCTCCAGTAGCCTTAGC
GCCAGTGTGGCGATAGAGTGACAATCACCTGTAAAGCCTCTCAGGACGTGTGCAC
AGCAGTGGCATGGTATCAGCAGAAACCCGGAAAGGCTCCCAAGCTACTGATATATT
CCGCGTCGTATCGGTACACAGGGGTACCATCTCGCTTCTCGGGTTCGGGCAGCGGC
ACCGACTTTACCCTCACAATTAGCTCTTTACAGCCCGAAGACTTCGCAGTGTATTA
TTGCCAGCAACACTATATCACCCCGCTGACTTTTGGGCAGGGTACGAAGCTTGAGA
TCAAACGGACTGGCGGGGGTGGGTCTGAGGTCCAGCTGGTTGAATCCGGCGGGGGA
TTAGTGCAGCCAGGCGGTTCACTGAGGTTGAGCTGTGCAGCCTCTGGAGTCACGTT
TAACTACTATGGCATGTCTTGATTAGACAAGCCCCAGGCAAAGGCCTGGAGTGGG
TAGCCTCTATCACCCGAAGCGGTGGACGCATCTATTACCAGATAGCGTGAAGGGC
CGGTTACAATCAGTAGAGAGAACACCCAGAAGACACTGTACCTACAAATGAACAG
CCTAAGAGCCGAGGATACCGCGGTGTACTACTGTACACTCGATGGAAGGGATGGGT
GGGTGGCTTACTGGGGGCAGGGGACTCTCGTCACCGTTAGTAGTGGCGGTGGCGGT
AGCGGAGGAGGAGGTAGCGGCGGAGGTGGGTCAAATTTTCATGCTCACACAGCCAG
CTCAGTCTCCGGGGTACCTGGCCAGCGTGTGACTATCTCCTGCACTGGCAATACCG
GAAACATAGGAAGCAATTACGTAAACTGGTATCAACAGCTTCCGGGCACTGCCCCT
AAACTCCTGATTTACCGCGATGATAAAAGGCCTTCCGGCGTCCCAGACAGGTTTAG
TGGCTCGAAATCCGGGACAAGCGCCAGTTTGGCAATTACCGGATTTCAAGCCGAAG
ATGAAGCTGACTACTACTGCCAGTCCTATTCATCAGGGTTCATATTTGGCGGTGGA
ACTAAACTGACCGTCTTTGGAGGGGAACCCAAGAGCGCCGACAAAACACACTTG
TCCTCCGTGTCCCGCGCCCGAAGCTGCTGGGGGGCCAGTGTGTTCTATTTCCCC
CCAAGCCAAAGGACACGTTGATGATCTCTCGTACCCCTGAGGTCACGTGCGTTGTG
GTTGACGTCTCCACGAAGATCCCGAGGTGAAATTCAACTGGTATGTGGACGGCGT
TGAGGTGCACAATGCCAAAATAAGCCGAGGGAAGAGCAGTACAACCTCTACCTATC
GGGTGGTGTCTGTTTTGACAGTTCTCCATCAGGACTGGCTGAATGGAAAAGAGTAC
AAGTGCAAGGTGAGTAACAAAGCTCTGCCAGCCCCTATCGAGAAAACCATCTCCAA
GGCCAAAGGCCAACCACGAGAGCCTCAAGTTTACACCCTCCCTCCTTGTGAGACG
AGCTGACCAAGAACCAAGTCTCCTTATGGTGTCTCGTGAAGGGATTTTATCCCTCA
GACATTGCCGTGGAGTGGGAATCTAATGGCCAGCCTGAGAACAATTATAAGACAAC
TCCTCCTGTCCTTGATTCCGATGGCTCCTTTTTCTGTACTCTAAGTTGACTGTGCG
ACAAGTCACGCTGGCAGCAGGGGAATGTTTTCTTTGCAGCGTTATGCATGAAGCT
CTGCATAACCACTATACTCAGAAAAGCCTGTCACTGTACCGGGGAAG
(SEQ ID NO: 14) Signal sequence(1-57), HT1-11 scFv(61-
795), linker(796-810), C3E-7085(811-1530), linker(1531-
1536), Hinge(1537-1581), CH2(1582-1911), CH3(1912-2232)**

[Fig. 19]

TX3-0003-HC_k

ATGAAGCATCTCTGGTTTTTCCTGCTCCTGGTGGCGGCTCCAAGATGGGTGTTGAG
CGGTCAGGTGCAACTGGTGCAAGTCAGGAGCGGAGGTCAAGAAACCCGGCGGAGTG
TCAAAGTGAGTTGCAAAGCTTCCGGATATACTTTCACTACCGCTGGAATGCAATGG
GTGAGACAAGCACCAGGGCAAGGCTTGGAATGGATGGGCTGGATCAACACACACTC
TGGGGTTCCCAAGTATGCCGAAGACTTTAAGGGTAGGGTCACCATATCAGCCGATA
CATCAACCTCGACCGCATACCTCCAGCTGTCTCCCTTAAGAGCGAGGATACTGCT
GTTTACTATTGCGCTAGGTCAGGATTGGGCTCTTCTTACTGGTACTTTGATGTGTG
GGGGCAGGGCACACTTGTGACGGTTTTCTCTGGCGGCGGCGGGTTCAGGAGGTGGTG
GCTCTGGAGGGGGTGGTTCAGACATCCAGATGACCCAGAGTCCTTCCTCCTTGAGT
GCCAGTGTAGGCGACAGAGTCACTATTACCTGCAAGGCCTCTCAGGACGTGTGCAC
AGCGGTTGCATGGTATCAGCAGAAACCTGGGAAGGCTCCAAAGCTCCTGATCTACT
CAGCCAGCTATCGGTACACTGGGGTCCCTTCTCGCTTTAGCGGCTCTGGTAGCGGG
ACCGACTTCACGCTTACCATCAGTTCCTGCAACCGGAGGACTTTGCAGTGTACTA
CTGTCAGCAGCATTACATCACCCCACTGACATTTGGGCAGGGGACAAAGCTTGAGA
TTAAACGGACAGGCGGCGGAGGAAGCGAGGTGCAGTTAGTGGAGAGCGGAGGGGGT
TTAGTCCAACCGGGCGGGAGCCTCCGTCTGAGCTGTGCTGCTTCCGGCGTTACCTT
CAACTATTATGGAATGAGCTGGATCAGGCAAGCCCCTGGCAAAGGTCTTGAATGGG
TTGCATCTATCACTCGATCAGGGGGTTCGCATTTATTACCCGGATAGCGTTAAAGGC
AGGTTCACAATCTCTCGGGAGAACACTCAGAAAACCCCTCTATCTACAGATGAACTC
TTTACGGGCGCAAGATACAGCCGTCTATTATTGCACTCTAGATGGTCGAGATGGCT
GGGTCGCCTATTGGGGGTGTGGAACCTTGGTCACTGTTAGCAGTGGAGGAGGAGGA
TCAGGAGGGGGCGGGTCCGGCGGTGGGGGTAGCAATTTTCATGCTGACACAACCTTC
TTCAGTATCTGGCGTGCCAGGACAGCGGTCAACCATCTCTTGTACCGGCAATACAG
GTAACATTGGCTCCAATTACGTGAATTGGTACCAGCAGCTTCCTGGCACCTGCCCT
AAGCTGCTGATTTACCGGGACGATAAGAGGCCCTCGGGGGTGCCCGACCGTTTCTC
GGGAAGCAAGTCCGGGACATCCGCCTCACTTGCCATTACGGGGTTTCAGGCCGAGG
ATGAAGCTGATTACTACTGCCAGTCTTACTCCAGTGGCTTCATTTTTGGCGGAGGC
ACCAAGCTGACAGTGCTAGGCGGAGAACCCAAAAGTGCAGACAAGACGCATACTTG
CCCCCGTGTCTGCTCCAGAAGCAGCAGGAGGACCCTCTGTTTTCTCTTTCCAC
CTAAACCAAGGACACTCTGATGATAAGCAGAACACCTGAAGTGACGTGTGTTGTG
GTAGATGTCTCCCATGAAGATCCCGAAGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCACAATGCCAAAACGAAGCCAGAGAGGAGCAGTATAACTCCACATACA
GAGTTGTGAGCGTACTGACTGTATTGCACCAAGACTGGCTGAATGGTAAGGAGTAC
AAGTGCAAGGTGTCAAACAAAGCTCTGCCTGCACCCATAGAGAAAACCATCAGTAA
GGCAAAGGGCAGCCACGCGAGCCACAGGTGTATACTCTGCCACCATGCCGAGACG
AGCTCACTAAGAATCAGGTGAGCTTGTGGTGTCTCGTAAAGGGCTTTTACCCCTCG
GACATTGCCGTAGAGTGGGAATCCAATGGGCAACCCGAGAACAATTACAAAACCAC
ACCGCCAGTGTTAGACAGCGATGGAAGCTTCTTTCTCTATAGCAAGCTGACCGTCG
ACAAAAGTCGCTGGCAGCAGGGGAACGTCTTCAGTTGTTCCGTGATGCACGAAGCC
CTACACAACCACTATAACCCAGAAATCCCTGTCACTGAGTCCTGGCAA
(SEQ ID NO: 15) Signal sequence(1-57), HT1-11 scFv(61-
795), linker(796-810), C3E-7096(811-1530), linker(1531-
1536), Hinge(1537-1581), CH2(1582-1911), CH3(1912-2232)

[Fig. 20]

CX3-0001-HC_k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGACAGGTTTCAGCTGGTTTCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCTG
TGAAGGTGTCCTGCAAGGCCTCTGGCTACGCCTTCAGCAACTACCTGATCGAGTGG
GTCCGACAGGCCCTGGACAAGGACTTGAATGGATGGGCGTGATCAACCCTGGCAG
CGGCGTGACCAACTACAACGAGAAGTTCAAGGGCAGAGTGACCATCACCGCCGACA
CCAGCACAAGCACCGCCTACATGGAAGTGAAGCAGCCTGAGAAGCGAGGACACCGCC
GTGTACTATTGTGCCAGAGCCGAGGCTTGGTTTGCCTATTGGGGACAGGGCACCCCT
GGTCACCGTTAGCTCTGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGCGGTGGCG
GGAGTGATATTGTGATGACACAGAGCCCCGACAGCCTGGCCGTGTCTCTTGAGAA
AGAGCCACCATCAACTGCAAGAGCAGCCAGAGCCTGCTGTACTCCAGCAACCAGAA
GAACTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGCCTCCTAAGCTGCTGATCT
ACTGGGCCAGCACCCAGAGAAAGCGGCGTGCCCGATAGATTTTCTGGCTCTGGCAGC
GGCACCGACTTCACCCCTGACAATTTCTAGCCTGCAAGCCGAGGACGTGGCCGTGTA
CTACTGCCAGAGATATTACGGCTACCCCTGGACCTTTGGCCAGGGCACCAAGGTGG
AAATCAAGGGAGGCGGAGGATCTGAAGTGCAGCTGGTGGAAATCCGGGGGGGGCCTG
GTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCTCTGGGGTGACATTTAA
CTACTATGGCATGTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGTGGGTGG
CCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAGGGCAGG
TTCACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAATAGCCT
GAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATGGGTGGG
TCGCCTATTGGGGGCAGGGAACCCCTGGTGACAGTCAGCTCCGGAGGAGGAGGATCT
GGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCCGTCCTC
TGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAAATACGGGA
ATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCTCCCAAG
TTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATTTAGTGG
CAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGGCCGAAGATG
AGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGCGGAACT
AAGCTGACAGTGTTGGGCGGAGAACCCAAGAGCGCAGACAAGACCCACACCTGTCC
TCCATGTCTCTGCTCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCTGTTCCCTCCAA
AGCCTAAGGACACCCTGATGATCAGCCGGACACCTGAAGTGACCTGCGTGGTGGTG
GATGTGTCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGA
AGTGCAACACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAG
TGGTGTCTGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAG
TGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACCATCAGCAAGGC
CAAGGGCCAGCCTAGGGAACCCAGGTTTACACCCTGCCTCCATGCAGGGATGAGC
TGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCTACCCCTCCGAT
ATCGCCGTGGAATGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACAACCCC
TCCTGTGCTGGACTCCGACGGCTCATTCTTCCCTGTACAGCAAGCTGACCGTGGACA
AGAGCAGATGGCAGCAGGGCAACGTGTTTCAGCTGCAGCGTGATGCACGAGGCCCTG
CACAACCACTACACACAGAAGTCCCTGTCTCTGAGCCCCGGCAA

(SEQ ID NO: 16) Signal sequence(1-57)、hM23-H1L1 scFv(61-792), linker(793-807), C3E-7085(808-1527), linker(1528-1533), Hinge(1534-1578), CH2(1579-1908), CH3(1909-2229)

[Fig. 21]

CX3-0003-HC_k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGACAGGTTTCAGCTGGTTTCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCTG
TGAAGGTGTCCTGCAAGGCCTCTGGCTACGCCTTCAGCAACTACCTGATCGAGTGG
GTCCGACAGGCCCTGGACAAGGACTTGAATGGATGGGCGTGATCAACCCTGGCAG
CGGCGTGACCAACTACAACGAGAAGTTCAAGGGCAGAGTGACCATCACCGCCGACA
CCAGCACAAAGCACCGCCTACATGGAAGTGAAGCAGCCTGAGAAGCGAGGACACCGCC
GTGTACTATTGTGCCAGAGCCGAGGCTTGGTTTGCCTATTGGGGACAGGGCACCCCT
GGTCACCGTTAGCTCTGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGCGGTGGCG
GGAGTGATATTGTGATGACACAGAGCCCCGACAGCCTGGCCGTGTCTCTTGGAGAA
AGAGCCACCATCAACTGCAAGAGCAGCCAGAGCCTGCTGTACTCCAGCAACCAGAA
GAACTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGCCTCCTAAGCTGCTGATCT
ACTGGGCCAGCACCCAGAGAAAAGCGGCGTGCCCGATAGATTTTCTGGCTCTGGCAGC
GGCACCGACTTCACCCCTGACAATTTCTAGCCTGCAAGCCGAGGACGTGGCCGTGTA
CTACTGCCAGAGATATTACGGCTACCCCTGGACCTTTGGCCAGGGCACCAAGGTGG
AAATCAAGGGAGGCGGAGGATCTGAAGTGCAGCTGGTGGAAATCCGGGGGGGGCCTG
GTGCAGCCTGGGGGGAGCCTGAGACTGAGTTGTGCCGCTCTGGGGTGACATTTAA
CTACTATGGCATGTCTTGGATCCGCCAGGCACCTGGAAAGGGCCTGGAGTGGGTGG
CCAGCATCACTAGGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAGGGCAGG
TTCACAATTTCCCGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAATAGCCT
GAGAGCCGAAGATACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATGGGTGGG
TCGCCTATTGGGGGTGTGGAACCTGGTGACAGTCAGCTCCGGAGGAGGAGGATCT
GGCGGAGGAGGCAGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCCGTCCTC
TGTTTCTGGCGTACCTGGCCAACGGGTGACCATTAGCTGTACGGGTAAATACGGGA
ATATCGGGTCTAACTACGTGAACTGGTATCAGCAGCTTCCAGGGACATGTCCCAAG
TTGCTGATCTATCGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATTTAGTGG
CAGCAAAAGCGGTACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGGCCGAAGATG
AGGCAGACTACTATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGCGGAACT
AAGCTGACAGTGTTGGGCGGAGAACCCAAGAGCGCAGACAAGACCCACACCTGTCC
TCCATGTCTGCTCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCTGTTCCCTCCAA
AGCCTAAGGACACCCTGATGATCAGCCGGACACCTGAAGTGACCTGCGTGGTGGTG
GATGTGTCCACGAGGATCCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGA
AGTGCAACAACGCCAAGACCAAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAG
TGGTGTCTGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAG
TGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTATCGAGAAAACCATCAGCAAGGC
CAAGGGCCAGCCTAGGGAACCCAGGTTTACACCCTGCCTCCATGCAGGGATGAGC
TGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCTACCCCTCCGAT
ATCGCCGTGGAATGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACAACCCC
TCCTGTGCTGGACTCCGACGGCTCATTCTTCCCTGTACAGCAAGCTGACCGTGGACA
AGAGCAGATGGCAGCAGGGCAACGTGTTTCAGCTGCAGCGTGATGCACGAGGCCCTG
CACAACCACTACACACAGAAGTCCCTGTCTCTGAGCCCCGGCAA
(SEQ ID NO: 17) Signal sequence(1-57)、hM23-H1L1 scFv(61-
792), linker(793-807), C3E-7096(808-1527), linker(1528-
1533), Hinge(1534-1578), CH2(1579-1908), CH3(1909-2229)

[Fig. 22]

RX3-0001-HC_k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGACAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCG
TGAAGGTGTCCTGCAAGGCCAGCGGCTACACCTTTACCGGCTACTACATGCACTGG
GTGCGCCAGGCTCCAGGCCAGGGACTGGAATGGATGGGCCGGATCAACCCCAATAG
CGGCGGCACCAACTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACA
CCAGCATCAGCACCGCCTACATGGAAGTGAAGCGGCCTGAGAAGCGACGACACCGCC
GTGTACTACTGTGCCTCTGGCTCTGTGCGGCACCCTTGGGGACAGGGAACACTCGT
GACCGTGTCCAGCGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGGA
GTCAGCCTGTGCTGACACAGCCTCCAAGCGCCTCTGGCACACCTGGCCAGAGAGTG
ACAATCAGCTGCAGCGGCAGCAGAAGCAACATCGGCGGCAACATCGTGTCTGGTA
TCAGCAGTTCCCCGGCACCGCCCCCTAGACTGCTGACCTACGCCGACAACCAGAGGC
CTAGCGGCGTGCCCGATAGATTCAGCGGCTCTAAGAGCGGCACCAGCGCCAGCCTG
GCCATCTCTGGCCTGCAGTCTGAGGACGAGGCCGACTACTATTGCGCCGCCTGGGA
CGACAGCCTGAACGGCGTGGTGTGTTGGCGGAGGCACCAAGCTGACAGTGCTGggag
gcgaggatctGAAGTGCAGCTGGTGGAAATCCGGGGGGGGCCTGGTGCAGCCTGGG
GGGAGCCTGAGACTGAGTTGTGCCGCTCTGGGGTGACATTTAACTACTATGGCAT
GTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGTGGGTGGCCAGCATCACTA
GGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAGGGCAGGTTCACAATTTCC
CGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAATAGCCTGAGAGCCGAAGA
TACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATGGGTGGGTGCGCTATTGGG
GGCAGGGAACCCTGGTGCAGTCAGCTCCGGAGGAGGAGGATCTGGCGGAGGAGGC
AGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCCGTCTCTGTTTCTGGCGT
ACCTGGCCAACGGGTGACCATTAGCTGTACGGTAATACCGGGAATATCGGGTCTA
ACTACGTGAACTGGTATCAGCAGCTTCCAGGGACAGCTCCCAAGTTGCTGATCTAT
CGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATTTAGTGGCAGCAAAAGCGG
TACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCGAAGATGAGGCAGACTACT
ATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGCGGAACTAAGCTGACAGTG
TTGGGCGGAGAACCCAAGAGCGcaGACAAGACCCACACCTGTCCTCCATGTCCTGC
TCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCTGTTCCCTCAAAGCCTAAGGACA
CCCTGATGATCAGCCGGACACCTGAAGTGACCTGCGTGGTGGTGGATGTGTCCAC
GAGGATCCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGTGACAACGC
CAAGACCAAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAGTGGTGTCTGTGC
TGACAGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCC
AACAAGGCCCTGCCTGCTCCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCC
TAGGGAACCCAGGTTTACACCCTGCCTCCATGCAGGGATGAGCTGACCAAGAACC
AGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCTACCCCTCCGATATCGCCGTGGAA
TGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACAACCCCTCCTGTGCTGGA
CTCCGACGGCTCATTCTTCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGC
AGCAGGGCAACGTGTTTCAGCTGCAGCGTGATGCACGAGGCCCTGCACAACCACTAC
ACACAGAAGTCCCTGTCTCTGAGCCCCGGCAAA

(SEQ ID NO: 18) Signal sequence(1-57)、C3022 scFv(61-780),
linker(781-795), C3E-7085(796-1515), linker(1516-1521),
Hinge(1522-1566), CH2(1567-1896), CH3(1897-2217)

[Fig. 23]

RX3-0003-HC_k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGACAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCG
TGAAGGTGTCCTGCAAGGCCAGCGGCTACACCTTTACCGGCTACTACATGCACTGG
GTGCGCCAGGCTCCAGGCCAGGGACTGGAATGGATGGGCCGGATCAACCCCAATAG
CGGCGGCACCAACTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACA
CCAGCATCAGCACCGCCTACATGGAAGTGAAGCGGCCTGAGAAGCGACGACACCGCC
GTGTACTACTGTGCCTCTGGCTCTGTGCGGCACCCTTGGGGACAGGGAACACTCGT
GACCGTGTCCAGCGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGGA
GTCAGCCTGTGCTGACACAGCCTCCAAGCGCCTCTGGCACACCTGGCCAGAGAGTG
ACAATCAGCTGCAGCGGCAGCAGAAGCAACATCGGCGGCAACATCGTGTCTGGTA
TCAGCAGTTCCCCGGCACCGCCCCCTAGACTGCTGACCTACGCCGACAACCAGAGGC
CTAGCGGCGTGCCCGATAGATTCAGCGGCTCTAAGAGCGGCACCAGCGCCAGCCTG
GCCATCTCTGGCCTGCAGTCTGAGGACGAGGCCGACTACTATTGCGCCGCCTGGGA
CGACAGCCTGAACGGCGTGGTGTGTTGGCGGAGGCACCAAGCTGACAGTGCTGGGAG
GCGGAGGATCTGAAGTGCAGCTGGTGAATCCGGGGGGGGCCTGGTGCAGCCTGGG
GGGAGCCTGAGACTGAGTTGTGCCGCTCTGGGGTGACATTTAACTACTATGGCAT
GTCTTGATCCGCCAGGCACCTGGAAAGGGCCTGGAGTGGGTGGCCAGCATCACTA
GGTCCGGCGGGCGAATCTACTATCCCGACAGCGTCAAGGGCAGGTTCACAATTTCC
CGCGAGAACACACAGAAAACCTCTGTACCTGCAGATGAATAGCCTGAGAGCCGAAGA
TACAGCTGTGTACTATTGCACTCTGGACGGCAGGGATGGGTGGGTGCGCTATTGGG
GGTGTGGAACCCTGGTGCAGTCAGCTCCGGAGGAGGAGGATCTGGCGGAGGAGGC
AGTGGGGGAGGCGGGTCAAACCTTTATGCTCACTCAGCCGTCTCTGTTTCTGGCGT
ACCTGGCCAACGGGTGACCATTAGCTGTACGGTAATACCGGGAATATCGGGTCTA
ACTACGTGAACTGGTATCAGCAGCTTCCAGGGACATGTCCCAAGTTGCTGATCTAT
CGCGACGACAAAAGACCCTCAGGGGTCCCTGACCGATTTAGTGGCAGCAAAAGCGG
TACTTCCGCTTCCCTGGCGATAACCGGCTTTCAGGCCGAAGATGAGGCAGACTACT
ATTGCCAGTCATATTCCAGCGGCTTCATCTTCGGAGGCGGAACTAAGCTGACAGTG
TTGGGCGGAGAACCCAAGAGCGCAGACAAGACCCACACCTGTCCTCCATGTCCTGC
TCCAGAAGCTGCAGGCGGCCCTTCCGTGTTTCTGTTCCCTCAAAGCCTAAGGACA
CCCTGATGATCAGCCGGACACCTGAAGTGACCTGCGTGGTGGTGGATGTGTCCAC
GAGGATCCCGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGTGACAACGC
CAAGACCAAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAGTGGTGTCTGTGC
TGACAGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCC
AACAAGGCCCTGCCTGCTCCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCC
TAGGGAACCCAGGTTTACACCCTGCCTCCATGCAGGGATGAGCTGACCAAGAACC
AGGTGTCCCTGTGGTGCCTGGTTAAGGGCTTCTACCCCTCCGATATCGCCGTGGAA
TGGGAGAGCAATGGCCAGCCAGAGAACAACCTACAAGACAACCCCTCCTGTGCTGGA
CTCCGACGGCTCATTCTTCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGC
AGCAGGGCAACGTGTTTCAGCTGCAGCGTGATGCACGAGGCCCTGCACAACCACTAC
ACACAGAAGTCCCTGTCTCTGAGCCCCGGCAAA

(SEQ ID NO: 19) Signal sequence(1-57), C3022 scFv(61-780), linker(781-795), C3E-7096(796-1515), linker(1516-1521), Hinge(1522-1566), CH2(1567-1896), CH3(1897-2217)

[Fig. 24]

TX3-0001-HC_k

**MKHLWFFLLLVAAPRWVLSGQVQLVQSGAEVKKPGASVKVSCKASGYTFTTAGMQW
VRQAPGGGLEWMGWINTHSGVPKYAEDFKGRVTISADTSTSTAYLQLSSLKSEDTA
VYYCARSGFGSSYWYFDVWGQGLTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLS
ASVGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPSRFSGSGSG
TDFTLTISSLQPEDFAVYYCQQHYITPLTFGQGTKLEIKRTGGGGSEVQLVESGGG
LVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSKG
RFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWGQGLTVTVSSGGGG
SGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTAP
KLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDADYYCQSYSSGFIFGGG
TKLTVLGGEPKSADKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPS
DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK**

(SEQ ID NO: 20) Signal sequence(1-19), HT1-11 scFv(21-265), linker(266-270), C3E-7085(271-510), linker(511-1512), Hinge(513-527), CH2(528-637), CH3(638-744)

[Fig. 25]

TX3-0003-HC_k

**MKHLWFFLLLVAAPRWVLSGQVQLVQSGAEVKKPGASVKVSCKASGYTFTTAGMQW
VRQAPGGGLEWMGWINTHSGVPKYAEDFKGRVTISADTSTSTAYLQLSSLKSEDTA
VYYCARSGFGSSYWYFDVWGQGLTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLS
ASVGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPSRFSGSGSG
TDFTLTISSLQPEDFAVYYCQQHYITPLTFGQGTKLEIKRTGGGGSEVQLVESGGG
LVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVSKG
RFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWGCGLTVTVSSGGGG
SGGGGSGGGGSGNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTCP
KLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDADYYCQSYSSGFIFGGG
TKLTVLGGEPKSADKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPS
DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK**

**(SEQ ID NO: 21) Signal sequence(1-19), HT1-11 scFv(21-
265), linker(266-270), C3E-7096(271-510), linker(511-
1512), Hinge(513-527), CH2(528-637), CH3(638-744)**

[Fig. 26]

CX3-0001-HC_k

**MKHLWFFLLLVAAAPRWVLSGQVQLVQSGAEVKKPGASVKVSCKASGYAFSNYLIEW
VRQAPGGGLEWMGVINPGSGVTNYNEKFKGRVTITADTSTSTAYMELSSLRSEDTA
VYYCARAEAWFAYWGQGLTVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLAVSLGE
RATINCKSSQSLLYSSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGS
GTDFTLTISSLQAEDVAVYYCQRYYGYPWTFGQGTKVEIKGGGGSEVQLVESGGGL
VQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVKGR
FTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWGQGLTVTVSSGGGG
GGGGSGGGGSNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTAPK
LLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFAEDEADYYCQSYSSGFIFGGGT
KLTVLGGEPKSADKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSD
IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK**

**(SEQ ID NO: 22) Signal sequence(1-19)、hM23-H1L1 scFv(21-
264), linker(265-269), C3E-7085(270-509), linker(510-
511), Hinge(512-526), CH2(527-636), CH3(637-743)**

[Fig. 27]

CX3-0003-HC_k

**MKHLWFFLLLVAAPRWVLSGQVQLVQSGAEVKKPGASVKVSCKASGYAFSNYLIEW
VRQAPGGGLEWMGVINPGSGVTNYNEKFKGRVTITADTSTSTAYMELSSLRSEDTA
VYYCARAEAWFAYWGQGLTVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLAVSLGE
RATINCKSSQSLLYSSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGS
GTDFTLTISSLQAEDVAVYYCQRYYGYPWTFGQGTKVEIKGGGGSEVQLVESGGGL
VQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDSVKGR
FTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWCGTLTVTVSSGGGG
GGGGSGGGGSNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTCPK
LLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFAQEADYYCQSYSSGFIFGGGT
KLTVLGGEPKSADKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSD
IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK**

**(SEQ ID NO: 23) Signal sequence(1-19)、hM23-H1L1 scFv(21-
264), linker(265-269), C3E-7096(270-509), linker(510-
511), Hinge(512-526), CH2(527-636), CH3(637-743)**

[Fig. 28]

RX3-0001-HC_k

**MKHLWFFLLLVAAPRWVLSGQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHW
VRQAPGGGLEWMGRINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSGLRSDDTA
VYYCASGSVRHPWGQGTTLVTVSSGGGGSGGGGSGGGGSQPVLTQPPSASGTPGQRV
TISCSGSRSNIGGNIVSWYQQFPGTAPRLITYADNQRPSGVPDRFSGSKSGTSASL
AISGLQSEDEADYYCAAWDDSLNGVVFGGGTKLTVLGGGGSEVQLVESGGGLVQPG
GSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDSVKGRFTIS
RENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWGQGTTLVTVSSGGGGSGGGG
SGGGGSNFMILTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTAPKLLIY
RDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGGGTKLTV
LGGEPKSADKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVE
WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGK**

(SEQ ID NO: 24) Signal sequence(1-19), C3022 scFv(21-260), linker(261-265), C3E-7085(266-505), linker(506-507), Hinge(508-522), CH2(523-632), CH3(633-739)

[Fig. 29]

RX3-0003-HC_k

**MKHLWFFLLLVAAPRWVLSGQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHW
VRQAPGGGLEWMGRINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSGLRSDDTA
VYYCASGSVRHPWGQGTTLVTVSSGGGGSGGGGSGGGGSQPVLTQPPSASGTPGQRV
TISCSGSRSNIGGNIVSWYQQFPGTAPRLITYADNQRPSGVPDRFSGSKSGTSASL
AISGLQSEDEADYYCAAWDDSLNGVVFGGGTKLTVLGGGGSEVQLVESGGGLVQPG
GSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDSVKGRFTIS
RENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWCGGTLVTVSSGGGGSGGGG
SGGGGSNFMILTQPSSVSGVPGQRTISCTGNTGNIGSNYVNWYQQLPGTCPKLLIY
RDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQSYSSGFIFGGGTKLTV
LGGEPKSADKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
NKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVE
WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGK**

(SEQ ID NO: 25) Signal sequence(1-19), C3022 scFv(21-260), linker(261-265), C3E-7096(266-505), linker(506-507), Hinge(508-522), CH2(523-632), CH3(633-739)

[Fig. 30]

TX3-0002-HC_k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGACAGGTTTCAGCTGGTGCAGTCTGGCGCCGAAGTGAAAAACCTGGCGCCTCCG
TGAAGGTGTCCTGCAAGGCTAGCGGCTACACCTTTACCACAGCCGGCATGCAGTGG
GTCCGACAGGCTCCTGGACAAGGACTCGAGTGGATGGGCTGGATCAATACCCACAG
CGGCGTGGCCAAATACGCCGAGGATTTCAAGGGCAGAGTGACCATCAGCGCCGACA
CCAGCACAAAGCACAGCCTACCTGCAGCTGAGCAGCCTGAAGTCTGAGGACACCGCC
GTGTACTACTGTGCCAGAAGCGGCTTTGGCAGCAGCTACTGGTACTTCGATGTGTG
GGGCCAGGGCACCTGGTCACAGTTTCTAGCGGAGGCGGAGGATCTGGTGGCGGAG
GAAGTGGCGGAGGCGGTTCTGATATCCAGATGACACAGAGCCCCAGCAGCCTGTCT
GCCTCTGTGGGAGACAGAGTGACAATTACATGCAAGGCCAGCCAGGACGTGTCCAC
AGCAGTTGCTTGGTACCAGCAGAAGCCTGGCAAGGCCCTAAGCTGCTGATCTACA
GCGCCAGCTACAGATACACCGGCGTGCCAAGCAGATTTTCCGGCTCTGGCAGCGGC
ACCGATTTACCCCTGACCATATCTAGCCTGCAGCCAGAGGACTTCGCCGTGTATTA
TTGCCAGCAGCACTACATCACCCCTCTGACCTTTGGCCAGGGGACCAAGCTCGAGA
TCAAGAGAACAGGTGGCGGCGGATCTGAGGTGCAGCTGGTTGAAAGCGGCGGAGGA
CTTGTTACGCCTGGCGGATCTCTGAGACTGAGCTGTGCTGCTAGCGGCGTGACCTT
CAACTACTACGGCATGAGCTGGATCCGCCAAGCTCCAGGCAAGGGCCTCGAGTGGG
TTGCCAGCATTACAAGATCTGGCGGCCGCATCTACTACCCCGACTCTGTGAAGGGC
AGATTCACAATCAGCCGCGAGAACACCCAGAAAACCTGTACCTGCAGATGAACTC
CCTGAGAGCCGAGGATACAGCTGTGTACTATTGCACCCTGGACGGCAGAGATGGCT
GGGTTGCATATTGGGGACAGGGAACCCCTCGTGACCGTGTCTCTGCCTCTACAAAG
GGCCCTAGCGTGTTCCCTCTGGCTCCTAGCAGCAAGAGCACAAGCGGAGGAACAGC
CGCTCTGGGCTGTCTGGTCAAGGACTACTTTCCCGAGCCTGTGACAGTGTCTTGG
ACTCTGGCGCTCTGACATCCGGCGTGCACACATTTCCAGCCGTGCTGCAAAGCAGC
GGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCTAGCAGCTCTCTGGGCACCCA
GACCTACATCTGCAATGTGAACCACAAGCCTAGCAACACCAAGGTGGACAAGAGAG
TGGAACCCAAGAGCTGCGACAAGACCCACACCTGTCTCTCCATGTCTGACCTGAA
GCTGCTGGCGGCCCTTCCGTGTTTCTGTTCCCTCCAAAGCCTAAGGACACCCTGAT
GATCAGCAGAACCCCTGAAGTGACCTGCGTGGTGGTGGATGTGTCTCACGAGGACC
CAGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACC
AAGCCTAGAGAGGAACAGTACAACAGCACCTACAGAGTGGTGTCCGTGCTGACAGT
GCTGCACCAGGATTGGCTGAACGGCAAAGAGTACAAGTGAAGGTGTCCAACAAGG
CCCTGCCTGCTCCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAA
CCCCAGGTTTACACCCTTCCCTCCATGCCGGGATGAGCTGACCAAGAACCAGGTGTC
CCTGTGGTGTCTCGTGAAGGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGA
GCAATGGCCAGCCTGAGAACAACACTACAAGACAACCCCTCCTGTGCTGGACAGCGAC
GGCTCATTCTTCTGTACAGCAAGCTGACCGTGGACAAGTCCAGATGGCAGCAGGG
CAACGTGTTTCAAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCACTACACACAGA
AGTCCCTGTCTCTGAGCCCCGGCAAA

(SEQ ID NO: 26) Signal sequence(1-57)、HT1-11 scFv(61-795), linker(796-810), C3E-7085-VH(811-1164), CH1(1165-1458)Hinge(1459-1503), CH2(1504-1833), CH3(1834-2154)

[Fig. 31]

CX3-0002-HC_k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGACAGGTTTCAGCTGGTTCACTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCTG
TGAAGGTGTCCTGCAAGGCCTCTGGCTACGCCTTCAGCAACTACCTGATCGAGTGG
GTCCGACAGGCCCTGGACAAGGACTTGAATGGATGGGCGTGATCAACCCTGGCAG
CGGCGTGACCAACTACAACGAGAAGTTCAAGGGCAGAGTGACCATCACCGCCGACA
CCAGCACAAAGCACCGCCTACATGGAAGTGAAGCAGCCTGAGAAGCGAGGACACCGCC
GTGTACTATTGTGCCAGAGCCGAGGCTTGGTTTGCCTATTGGGGACAGGGCACCCCT
GGTCACCGTTAGCTCTGGTGGAGGCGGTTCAAGGCGGAGGTGGCAGCGGCGGTGGCG
GGAGTGATATTGTGATGACACAGAGCCCCGACAGCCTGGCCGTGTCTCTTGAGAA
AGAGCCACCATCAACTGCAAGAGCAGCCAGAGCCTGCTGTACTCCAGCAACCAGAA
GAACTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGCCTCCTAAGCTGCTGATCT
ACTGGGCCAGCACCCAGAGAAAGCGGCGTGCCCGATAGATTTTCTGGCTCTGGCAGC
GGCACCGACTTCACCCCTGACAATTTCTAGCCTGCAAGCCGAGGACGTGGCCGTGTA
CTACTGCCAGAGATATTACGGCTACCCCTGGACCTTTGGCCAGGGCACCAAGGTGG
AAATCAAGggaggcggaggatctGAGGTGCAGCTTGTGAATCAGGTGGCGGACTT
GTGCAGCCTGGCGGAAGCCTCAGACTTAGCTGTGCTGCTTCCGGCGTGACCTTCAA
CTACTACGGCATGAGCTGGATCAGGCAGGCACCTGGAAAGGGCCTCGAGTGGGTTG
CCTCTATCACAAGAAGCGGCGGCAGAATCTACTACCCCGACTCTGTGAAAGGCCGG
TTCACCATCTCCAGAGAGAACACCCAGAAAACACTCTATCTCCAGATGAACTCTCT
GCGCGCCGAAGATACAGCCGTCTATTACTGCACCCTGGACGGCAGAGATGGCTGGG
TTGCATATTGGGGACAGGGAACCCCTCGTGACCGTGTCTCTGCCTCTACAAAGGGC
CCTAGCGTGTTCCCTCTGGCTCCTAGCAGCAAGTCTACCAGCGGAGGAACAGCCGC
TCTGGGCTGTCTGGTCAAGGACTACTTTCCCGAGCCAGTGACAGTGTCTTGAACT
CTGGCGCTCTGACATCCGGCGTGCACACATTTCCAGCCGTGCTGCAAAGCTCCGGC
CTGTACTCTCTGAGCAGCGTGGTCACAGTGCCAAGCTCTAGCCTGGGCACCCAGAC
CTACATCTGCAATGTGAACCACAAGCCTAGCAACACCAAGGTGACAAGAGAGTGG
AACCCAAGAGCTGCGACAAGACCCACACCTGTCCTCCATGTCCTGCTCCAGAAGCT
GCAGGCGGCCCTTCCGTGTTTCTGTTCCCTCCAAAGCCTAAGGACACCCTGATGAT
CAGCCGGACACCTGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGATCCCG
AAGTGAAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAG
CCTAGAGAGGAACAGTACAACAGCACCTACAGAGTGGTGTCTGTGCTGACAGTGCT
GCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCC
TGCTGCTCCTATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCC
CAGGTTTACACCCTGCCTCCATGCAGGGATGAGCTGACCAAGAACCAGGTGTCCCT
GTGGTGCCTGGTTAAGGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCA
ATGGCCAGCCAGAGAACAACTACAAGACAACCCCTCCTGTGCTGGACTCCGACGGC
TCATTCTTCCTGTACAGCAAGCTGACCGTGGACAAGAGCAGATGGCAGCAGGGCAA
CGTGTTCACTGTCAGCGTGATGCACGAGGCCCTGCACAACCACTACACACAGAAGT
CCCTGTCTCTGAGCCCCGGCAA

(SEQ ID NO: 27) Signal sequence(1-57), hM23-H1L1 scFv(61-792), linker(793-807), C3E-7085-VH(808-1161), CH1(1162-1455)Hinge(1458-1500), CH2(1501-1830), CH3(1831-2151)

[Fig. 32]

RX3-0002-HC_k

ATGAAGCACCTGTGGTTCTTTCTGCTGCTGGTGGCCGCTCCTAGATGGGTGCTGTC
TGGACAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCAGGCGCCAGCG
TGAAGGTGTCCTGCAAGGCCAGCGGCTACACCTTTACCGGCTACTACATGCACTGG
GTGCGCCAGGCTCCAGGCCAGGGACTGGAATGGATGGGCGGATCAACCCCAATAG
CGGCGGCACCAACTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACA
CCAGCATCAGCACCGCCTACATGGAAGTGAAGCGGCCTGAGAAGCGACGACACCGCC
GTGTACTACTGTGCCTCTGGCTCTGTGCGGCACCCTTGGGGACAGGGAACACTCGT
GACCGTGTCCAGCGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGCGGTGGCGGGA
GTCAGCCTGTGCTGACACAGCCTCCAAGCGCCTCTGGCACACCTGGCCAGAGAGTG
ACAATCAGCTGCAGCGGCAGCAGAAGCAACATCGGCGGCAACATCGTGTCTGGTA
TCAGCAGTTCCCCGGCACCGCCCCCTAGACTGCTGACCTACGCCGACAACCAGAGGC
CTAGCGGCGTGCCCGATAGATTCAGCGGCTCTAAGAGCGGCACCAGCGCCAGCCTG
GCCATCTCTGGCCTGCAGTCTGAGGACGAGGCCGACTACTATTGCGCCGCCTGGGA
CGACAGCCTGAACGGCGTGGTGTGTTGGCGGAGGCACCAAGCTGACAGTGCTGGGAG
GCGGAGGATCTGAGGTGCAGCTTGTGTAATCAGGTGGCGGACTTGTGCAGCCTGGC
GGAAGCCTCAGACTTAGCTGTGCTGCTTCCGGCGTGACCTTCAACTACTACGGCAT
GAGCTGGATCAGGCAGGCACCTGGAAAGGGCCTCGAGTGGGTGCTCTATCACAA
GAAGCGGCGGCAGAATCTACTACCCCGACTCTGTGAAAGGCCGTTTACCATCTCC
AGAGAGAACACCCAGAAAACACTCTATCTCCAGATGAACTCTCTGCGCGCCGAAGA
TACAGCCGTCTATTACTGCACCCTGGACGGCAGAGATGGCTGGGTTGCATATTGGG
GACAGGGAACCCTCGTGACCGTGTCTCTGCTCTACAAAGGGCCCTAGCGTGTTT
CCTCTGGCTCCTAGCAGCAAGTCTACCAGCGGAGGAACAGCCGCTCTGGGCTGTCT
GGTCAAGGACTACTTTCCCGAGCCAGTGACAGTGTCTGGAAGTCTGGCGCTCTGA
CATCCGGCGTGCACACATTTCCAGCCGTGCTGCAAAGCTCCGGCCTGTACTCTCTG
AGCAGCGTGGTACAGTGCCAAGCTCTAGCCTGGGCACCCAGACCTACATCTGCAA
TGTGAACCACAAGCCTAGCAACACCAAGGTGACAAGAGAGTGGAACCCAAGAGCT
GCGACAAGACCCACACCTGTCTCCATGTCTGCTCCAGAAGCTGCAGGCGGCCCT
TCCGTGTTTCTGTTCCCTCCAAAGCCTAAGGACACCCTGATGATCAGCCGGACACC
TGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGATCCCGAAGTGAAGTTCA
ATTGGTACGTGGACGGCGTGGAAGTGACAACGCCAAGACCAAGCCTAGAGAGGAA
CAGTACAACAGCACCTACAGAGTGGTGTCTGTGCTGACAGTGCTGCACCAGGACTG
GCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTGCTCCTA
TCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCTAGGGAACCCAGGTTTACACC
CTGCCTCCATGCAGGGATGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGCCTGGT
TAAGGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAATGGCCAGCCAG
AGAACAACCTACAAGACAACCCCTCCTGTGCTGGACTCCGACGGCTCATTCTTCTG
TACAGCAAGCTGACCGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTTACGCTG
CAGCGTGATGCACGAGGCCCTGCACAACCACTACACACAGAAGTCCCTGTCTCTGA
GCCCCGGCAAA

(SEQ ID NO: 28) Signal sequence(1-57), C3022 scFv(61-780), linker(781-795), C3E-7085-VH(796-1149), CH1(1150-1443)Hinge(1444-1488), CH2(1489-1818), CH3(1819-2139)

[Fig. 33]

TX3-0002-HC_k

**MKHLWFFLLLVAAPRWVLSGQVQLVQSGAEVKKPGASVKVSCKASGYTFTTAGMQW
VRQAPGGGLEWMGWINTHSGVPKYAEDFKGRVTISADTSTSTAYLQLSSLKSEDTA
VYYCARSGFGSSYWFVDVWGQGLTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLS
ASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYTGVPSTRFSGSGSG
TDFTLTISSLQPEDFAVYYCQQHYITPLTFGQGTKLEIKRTGGGGSEVQLVESGGG
LVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDsvKG
RFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWGQGLTVTVSSASTK
GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE
AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD
GSFFLYSKLTVDKSRWQQGNVFSVMHEALHNHYTQKSLSLSPGK**

**(SEQ ID NO: 29) Signal sequence(1-19)、HT1-11 scFv(21-
265), linker(266-270), C3E-7085-VH(271-388), CH1(389-
486)Hinge(487-501), CH2(502-611), CH3(612-718)**

[Fig. 34]

CX3-0002-HC_k

**MKHLWFFLLLVAAPRWVLSGQVQLVQSGAEVKKPGASVKVSCKASGYAFSNYLIEW
VRQAPGGGLEWMGVINPGSGVTNYNEKFKGRVTITADTSTSTAYMELSSLRSEDTA
VYYCARAEAWFAYWGQGLTVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLAVSLGE
RATINCKSSQSLLYSSNQKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGS
GTDFTLTISSLQAEDVAVYYCQRYYGYPWTFGQGTKVEIKGGGGSEVQLVESGGGL
VQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDVKGR
FTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVWAYWGQGLTVTVSSASTKG
PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEA
AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK**

**(SEQ ID NO: 30) Signal sequence(1-19)、hM23-H1L1 scFv(21-
264), linker(265-269), C3E-7085-VH(270-387), CH1(388-
485)Hinge(486-500), CH2(501-610), CH3(611-717)**

[Fig. 35]

RX3-0002-HC_k

**MKHLWFFLLLVAAPRWVLSGQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHW
VRQAPGGGLEWMGRINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSGLRSDDTA
VYYCASGSVRHPWGQGTTLTVSSGGGGSGGGGSGGGGSQPVLTQPPSASGTPGQRV
TISCSGSRSNIGGNIVSWYQQFPGTAPRLLTYADNQRPSGVPDRFSGSKSGTSASL
AISGLQSEDEADYYCAAWDDSLNGVVFGGGTKLTVLGGGGSEVQLVESGGGLVQPG
GSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITRSGGRIYYPDsvKGRFTIS
RENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGWVAYWGQGTTLTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGGP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
LPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK**

**(SEQ ID NO: 31) Signal sequence(1-19), C3022 scFv(21-
260), linker(261-265), C3E-7085-VH(266-383), CH1(384-
481)Hinge(482-496), CH2(497-606), CH3(607-713)**

[Fig. 36]

Amino acid sequence of C3E-7085 heavy chain CDR1
GVTFNYYG
(SEQ ID NO: 32)

Amino acid sequence of C3E-7085 heavy chain CDR2
ITRSGGRI
(SEQ ID NO: 33)

Amino acid sequence of C3E-7085 heavy chain CDR3
TLDGRDGWVAY
(SEQ ID NO: 34)

Amino acid sequence of C3E-7085 light chain CDR1
TGNIGSNY
(SEQ ID NO: 35)

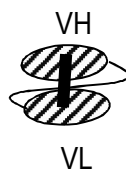
Amino acid sequence of C3E-7085 light chain CDR2
RDD
(SEQ ID NO: 36)

Amino acid sequence of C3E-7085 light chain CDR3
QSYSSGFI
(SEQ ID NO: 37)

[Fig. 37]

GGGGS linker
GGGGS
(SEQ ID NO: 38)

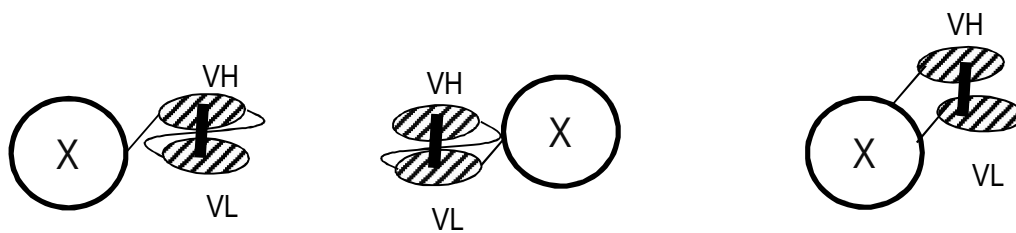
[Fig. 38A]



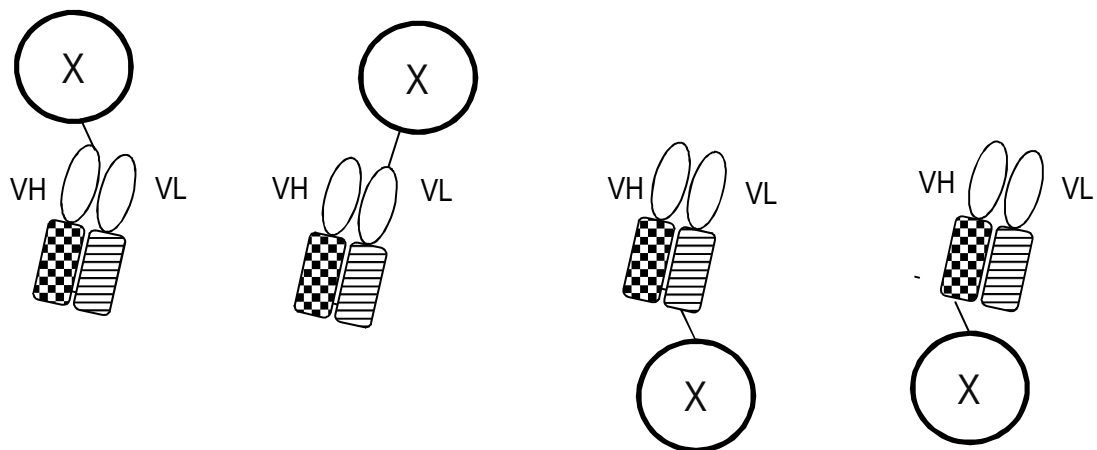
[Fig. 38B]



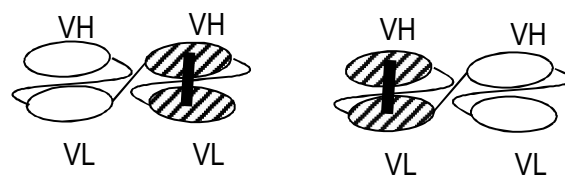
[Fig. 38C]



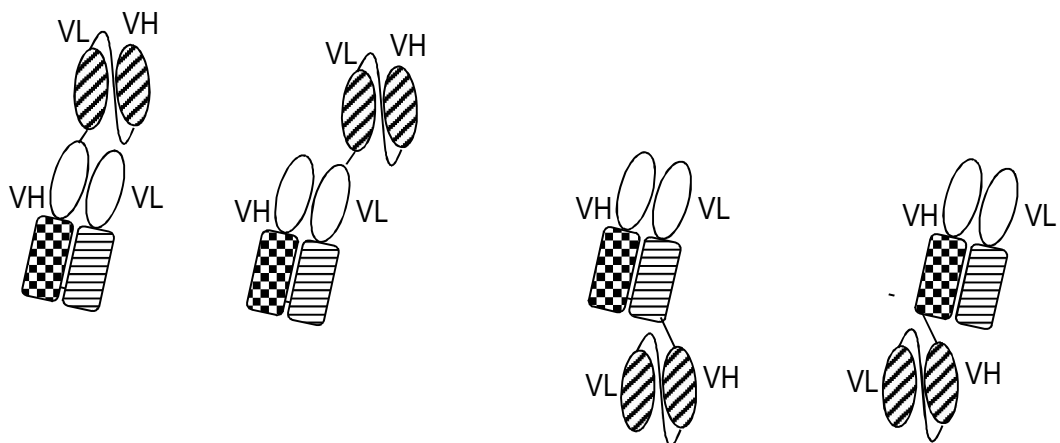
[Fig. 38D]



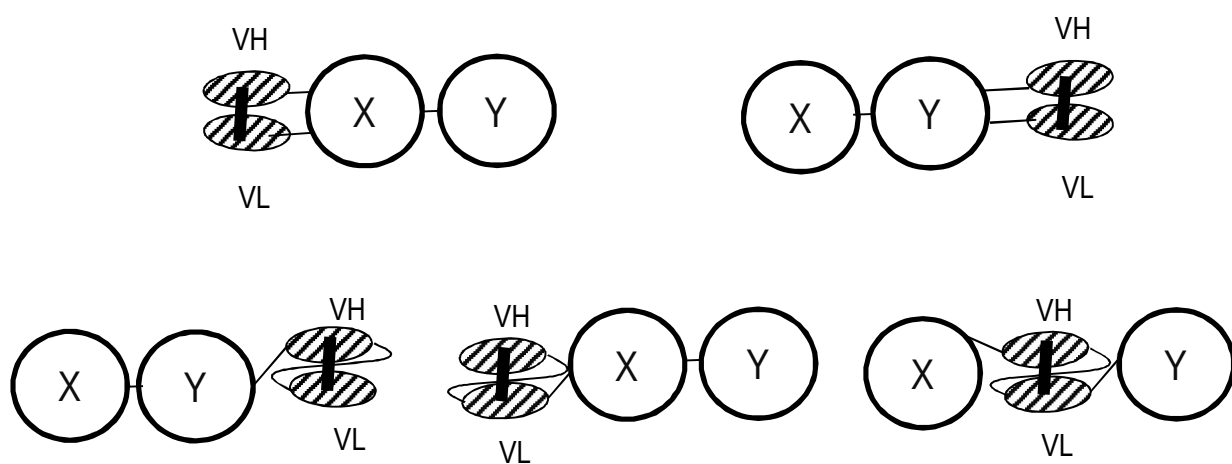
[Fig. 38E]



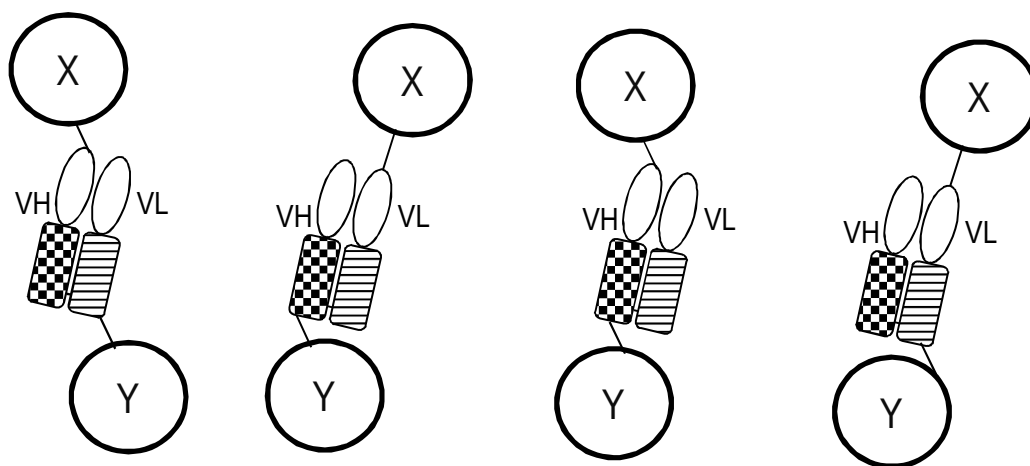
[Fig. 38F]



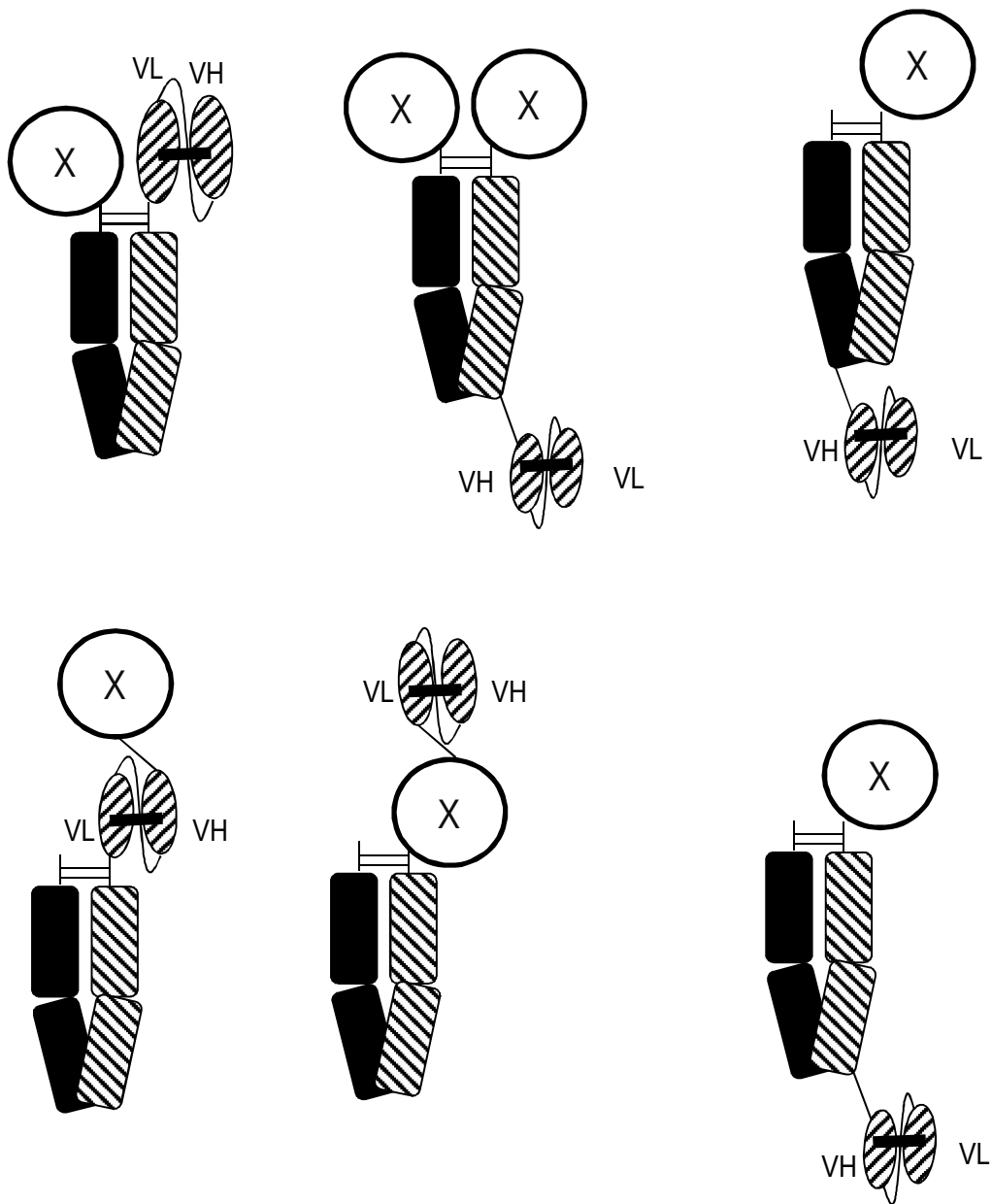
[Fig. 39A]



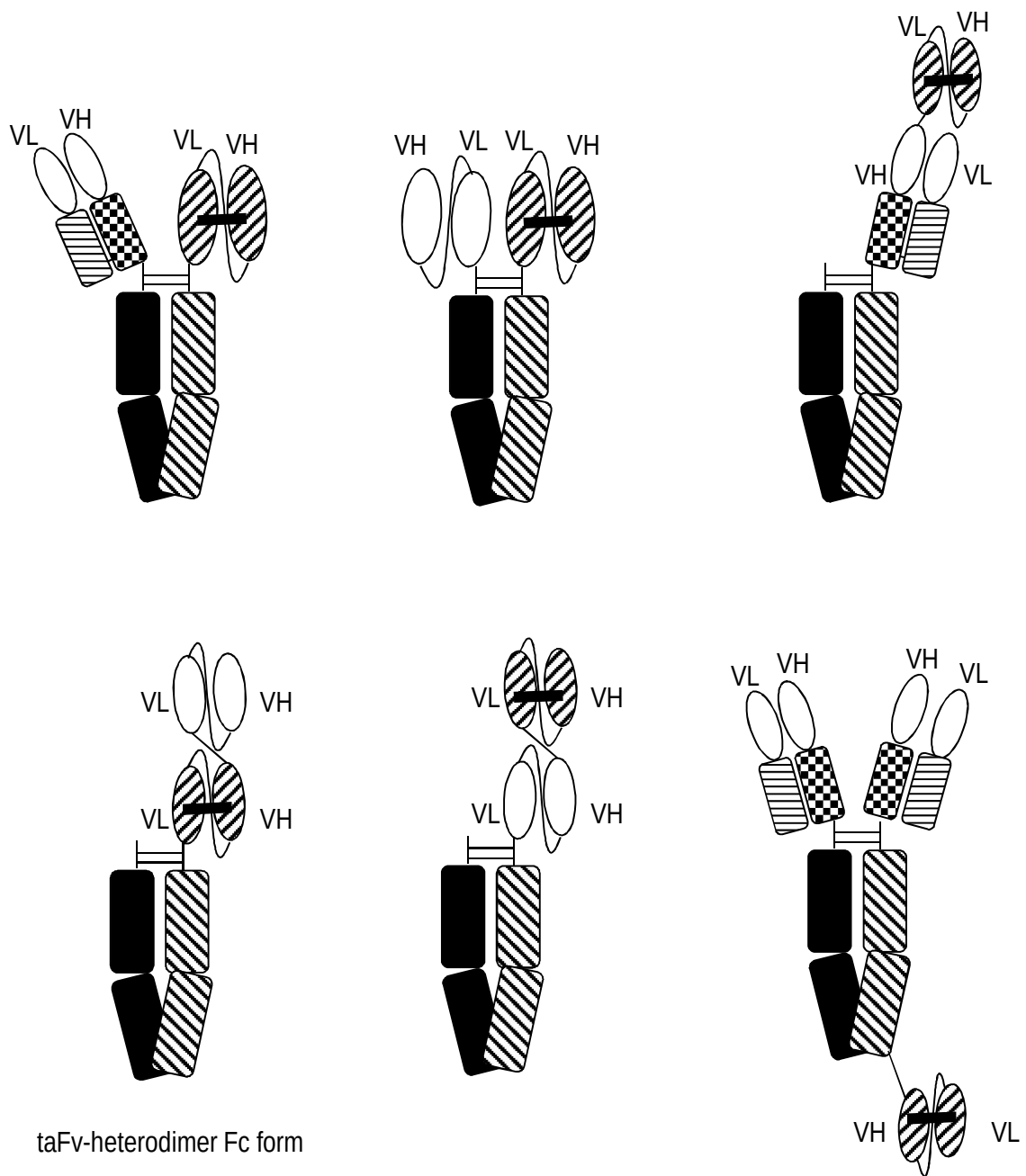
[Fig. 39B]



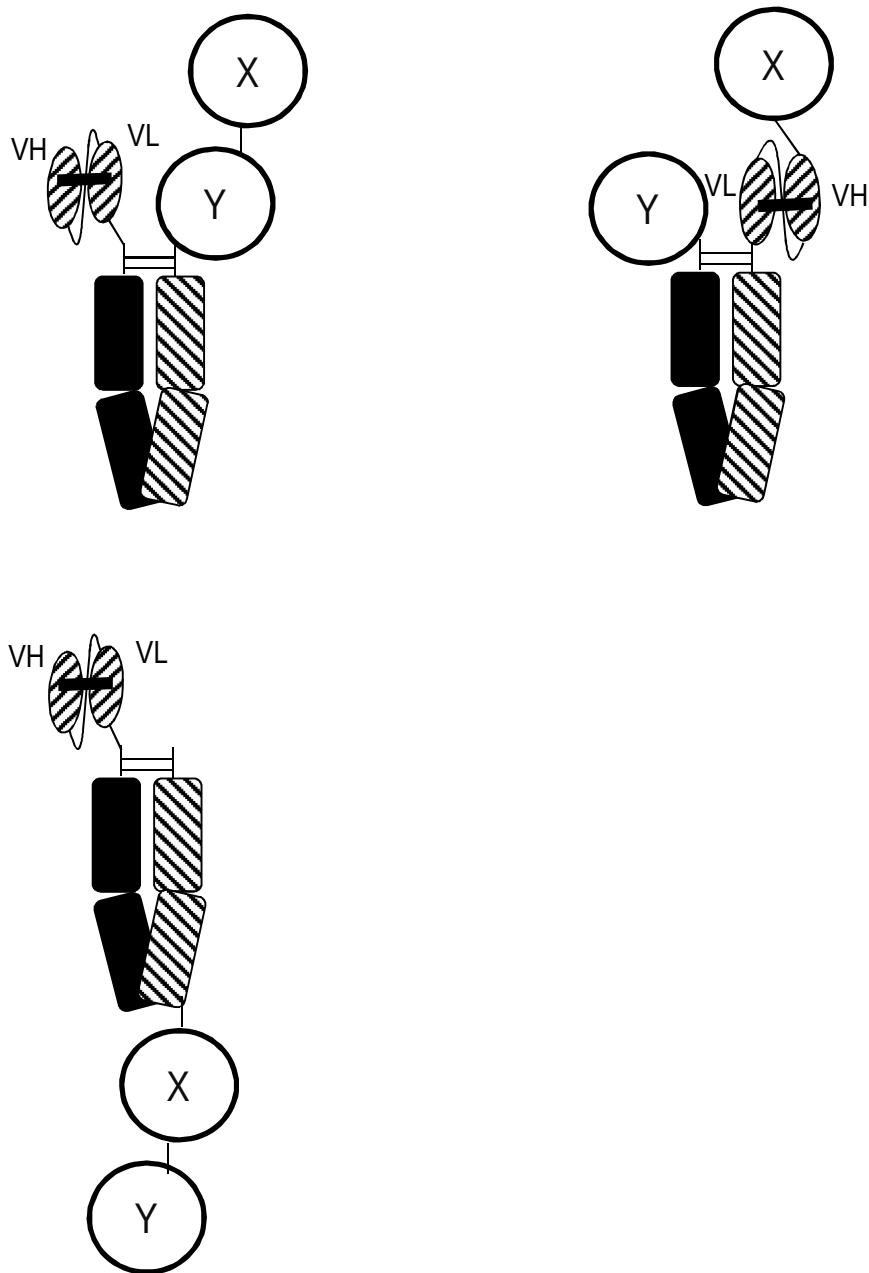
[Fig. 40A]



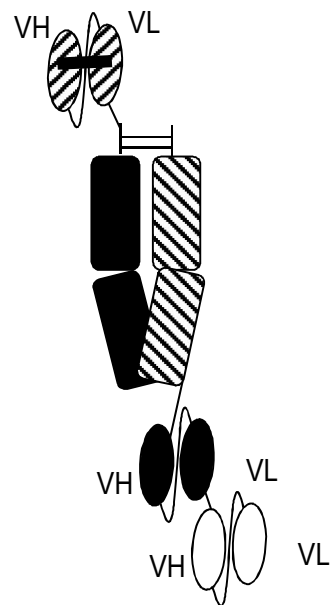
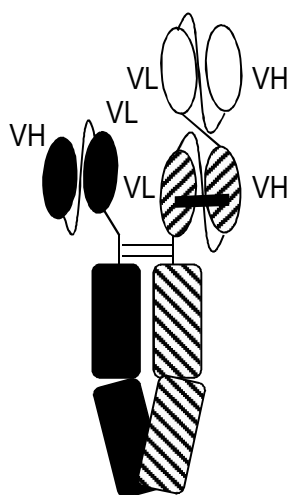
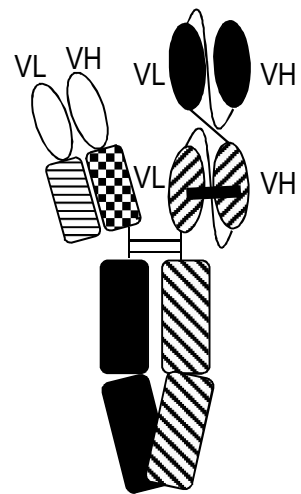
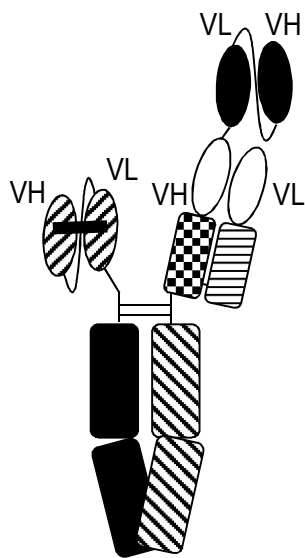
[Fig. 40B]



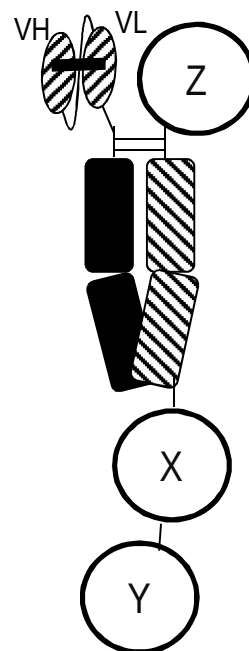
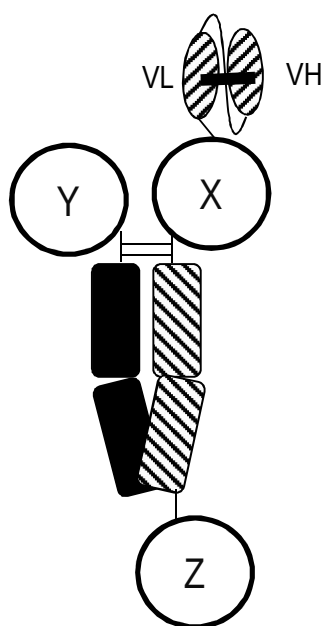
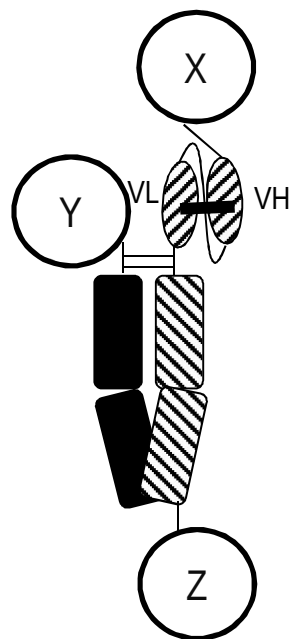
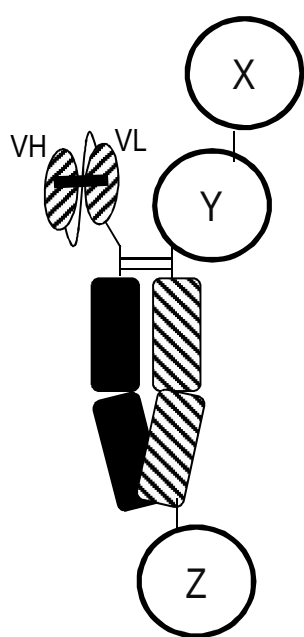
[Fig. 41A]



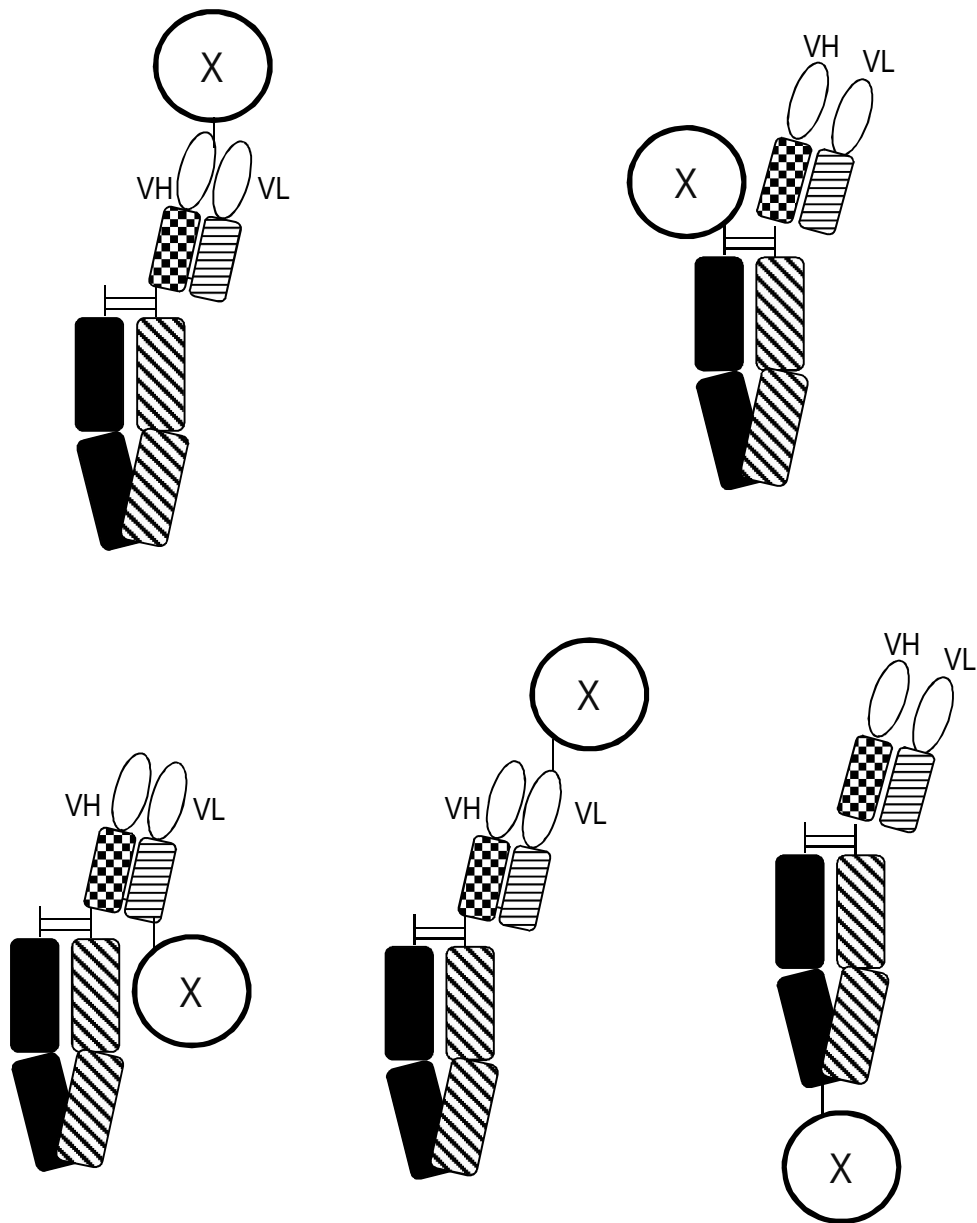
[Fig. 41B]



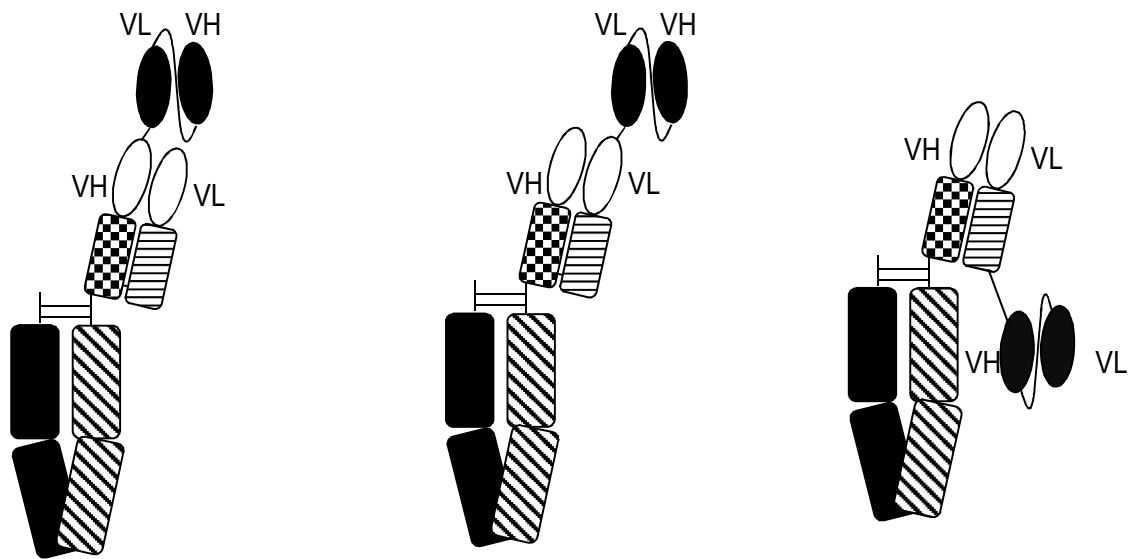
[Fig. 42]



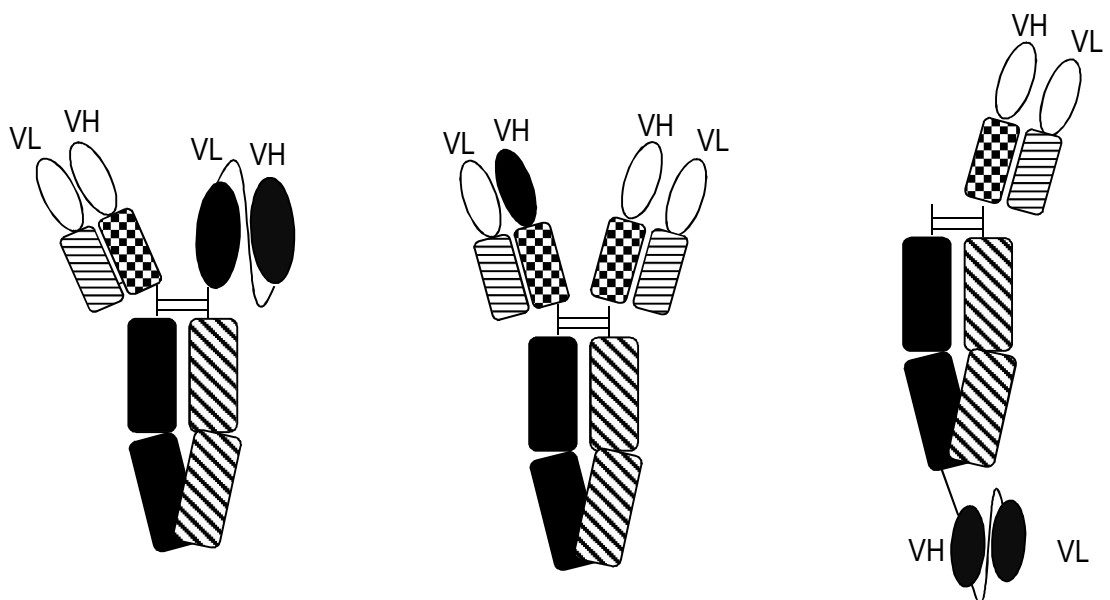
[Fig. 43A]



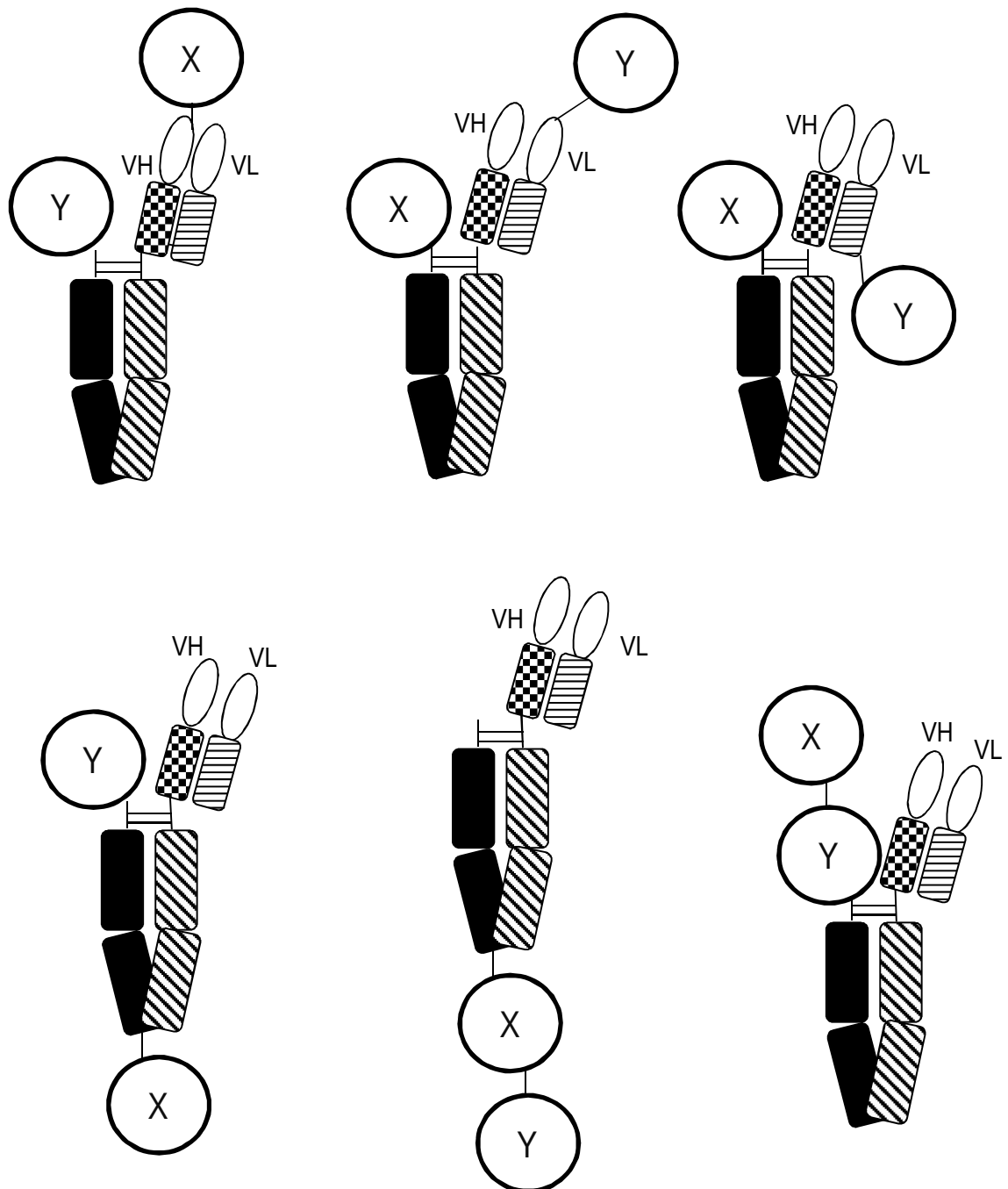
[Fig. 43B]



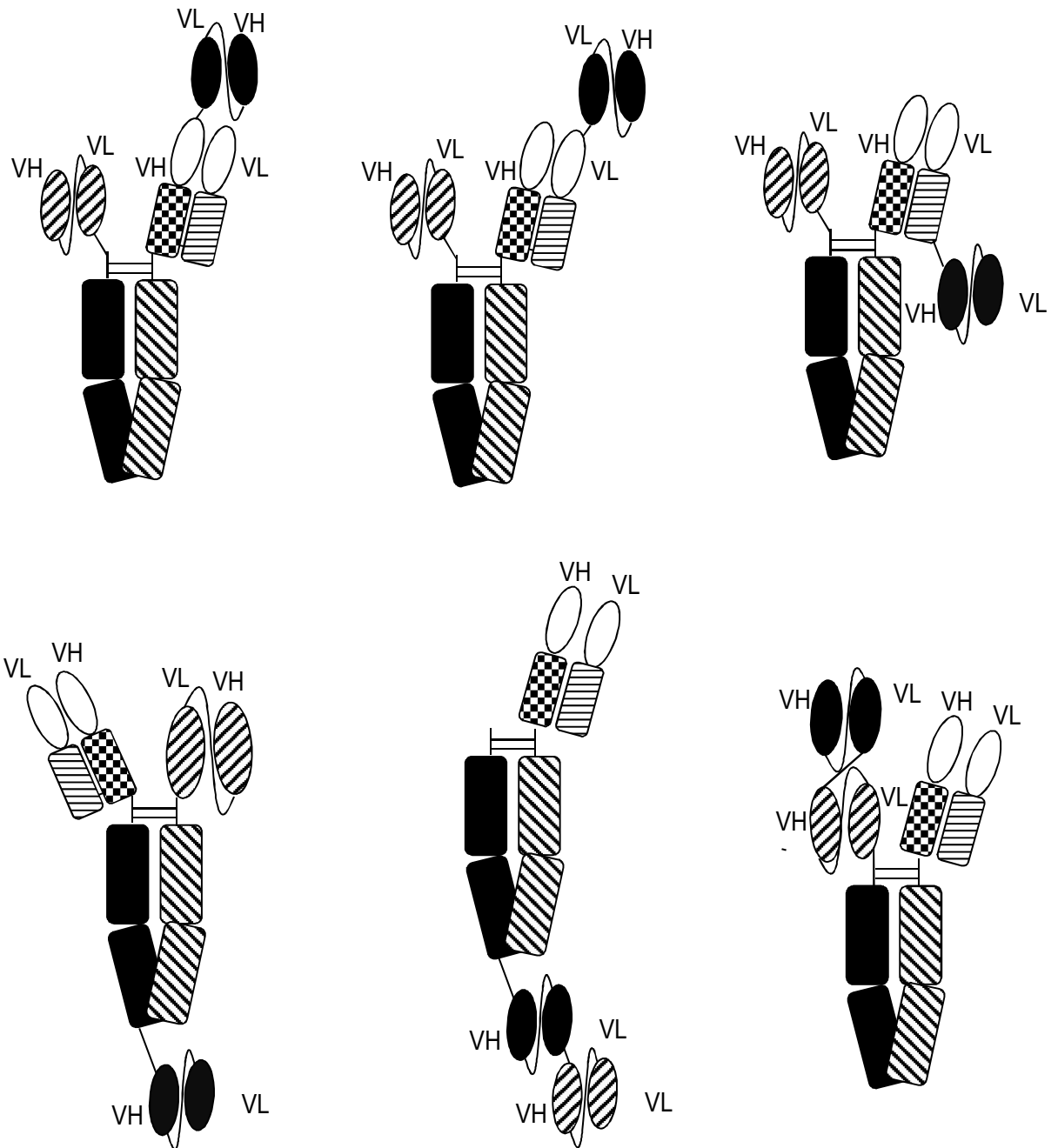
scFv-Fab-heterodimer Fc format



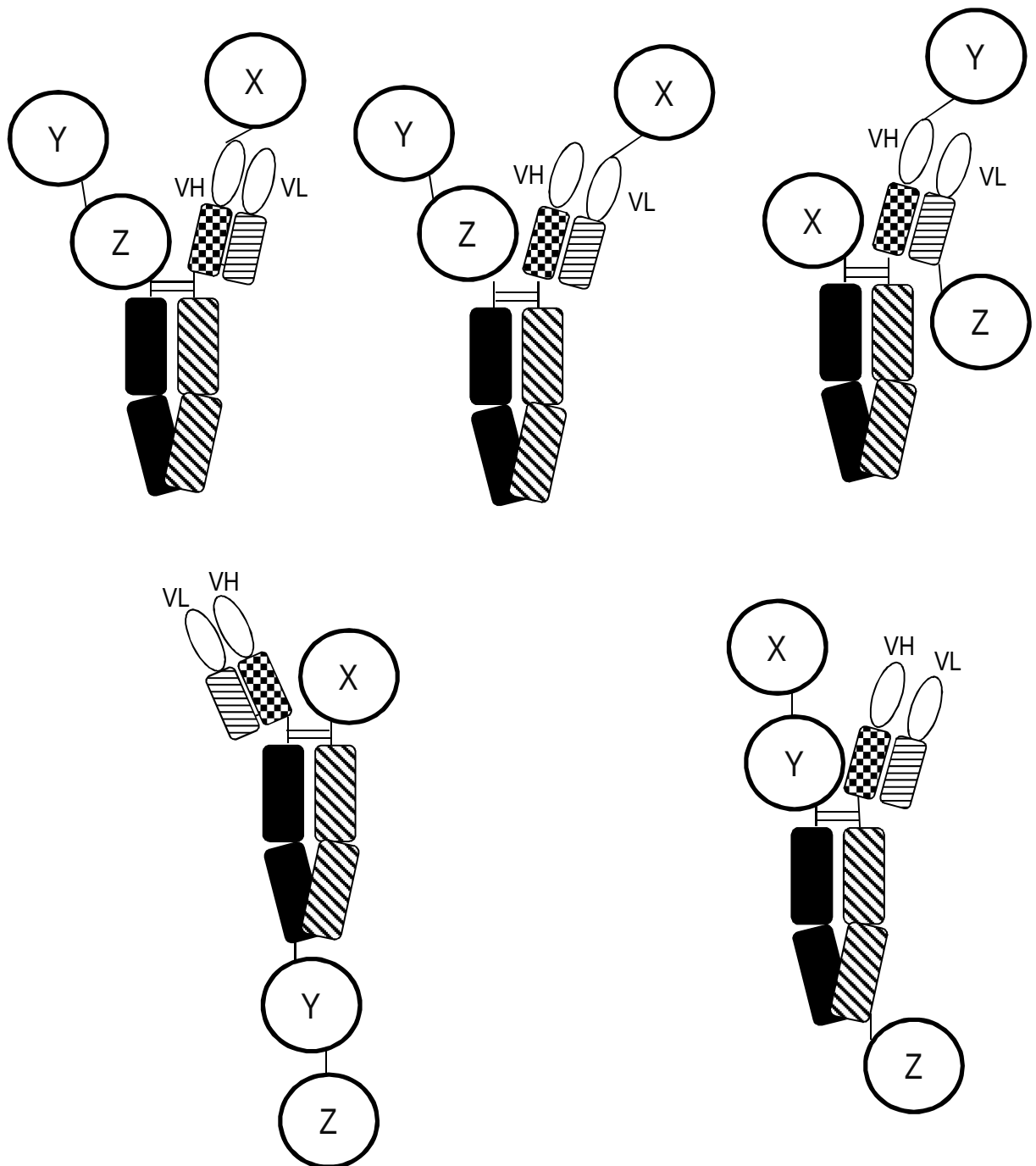
[Fig. 44A]



[Fig. 44B]



[Fig. 45]



[Fig. 46]

C3E - 7097

**EVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKCLEWVASITRSGG
RIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVAYWGQGT
LVTVSSGGGGSGGGGSGGGGSNFMLTQPSSVSGVPGQRTISCTGNTGNIGSNYVN
WYQQLPGTAPKLLIYRDDKRPSGVPDRFSGSKSGTSASLAITGFQAEDEADYYCQS
YSSGFIFGCGTKLTVL
(SEQ ID NO: 39)**

[Fig. 47]

Amino acid sequence of heavy chain CDR1 of C3E-7093
GVTFNYYG
(SEQ ID NO: 40)

Amino acid sequence of heavy chain CDR2 of C3E-7093
ITSSGGRI
(SEQ ID NO: 41)

Amino acid sequence of heavy chain CDR3 of C3E-7093
TLDGRDGWVAY
(SEQ ID NO: 42)

Amino acid sequence of light chain CDR1 of C3E-7093
TGNIGSNY
(SEQ ID NO: 43)

Amino acid sequence of light chain CDR2 of C3E-7093
RND
(SEQ ID NO: 44)

Amino acid sequence of light chain CDR3 of C3E-7093
QSYSSGFI
(SEQ ID NO: 45)

[Fig. 48]

C3E-7093-Fab

**EVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITSSGG
RIIYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVAYWGQGT
LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRV
(SEQ ID NO: 46)**

[Fig. 49]

C3E-7093-LC

**NFMLTQPHSVSESPGKTVTISCKRNTGNIGSNYVNWYQQHEGSSPTTIIYRNDKRP
DGVSDRFSGSIDRSSKSASLTISNLKTEDEADYFCQSYSSGFIFGGGTKLTVLGQP
KAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPS
KQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
(SEQ ID NO: 47)**

[Fig. 50]

C3E - 7098

**EVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKGLEWVASITSSGG
RIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVVAYWGCGT
LVTVSSGGGGSGGGGSGGGGSNFMLTQPHSVSESPGKTVTISCKRNTGNIGSNYVN
WYQQHEGSCPTTIIYRNDKRPDGVSDRFSGSIDRSSKSASLTISNLKTEDEADYFC
QSYSSGFIFGGGTKLTVL
(SEQ ID NO: 48)**

[Fig. 51]

C3E - 7099

**EVQLVESGGGLVQPGGSLRLSCAASGVTFNYYGMSWIRQAPGKCLEWVASITSSGG
RIYYPDSVKGRFTISRENTQKTLYLQMNSLRAEDTAVYYCTLDGRDGVAYWGQGT
LVTVSSGGGGSGGGGSGGGGSNFMLTQPHSVSESPGKTVTISCKRNTGNIGSNYVN
WYQQHEGSSPTTIIYRNDKRPDGVSDRFSGSIDRSSKSASLTISNLKTEDEADYFC
QSYSSGFIFGCGTKLTVL
(SEQ ID NO: 49)**