

FIGURE 1

SEQ ID NO: 1

MF3370-VH:

QVQLVQSGAEVKKPGASVKVSCKASGYFTSYGISWVRQAPGQGLEWMGWISAYNGNTNYAQKLQGRVTM
TTDSTSTAYMELRSLRSDDTAVYYCAKDRHWHWWLDAFDYWGQGTLLTVSS

SEQ ID NO: 2

MF3370-VH-CDR1:

SYGIS

SEQ ID NO: 3

MF3370-VH-CDR2:

WISAYNGNTNYAQKLQG

SEQ ID NO: 4

MF3370-VH-CDR3:

DRHWHWWLDAFDY

SEQ ID NO: 5

MF3755-VH:

QVQLVQSGSELKKPGASVKISCKASGYDFTNYAMNWVRQAPGHGLEWMGWINANTGDPTYAQGFTGRFVFSLDTSV
STAYLQISSLKAEDSAVYYCTRERFLEWLHFDYWGQGTLLTVSS

SEQ ID NO: 6

MF3755-VH-CDR1:

NYAMN

SEQ ID NO: 7

MF3755-VH-CDR2:

WINANTGDPTYAQGFTG

SEQ ID NO: 8

MF3755-VH-CDR3:

ERFLEWLHFDY

SEQ ID NO: 9

MF4280-VH:

QVQLVQSGAEVKKPGASVKVSCKVSGYTLT~~ELSMH~~WVRQAPGKGLEWMGGFDPEYGKTFFAQNFQGRVTMTEDTS
ADTAYMELSSLRSEDTAVYYCATEGY~~YETTTYYN~~LFD~~SWGQGTLLTVSS~~

SEQ ID NO: 10

MF4280-VH-CDR1:

ELSMH

(FIGURE 1 continued)

SEQ ID NO: 11
MF4280-VH-CDR2:
GFDPEYGKTFFAQNFQG

SEQ ID NO: 12
MF4280-VH-CDR3:
EGYYETTTYYNLFDS

SEQ ID NO: 13
MF4289-VH:
QVQLVQSGSELKKPGASVKVSCKTSGYFTDYAMTWVRQAPGQGLEWMGWITNTGDPTYAPGFTGRFVFSLDTSVS
TAYLQISSLKAEDTAVYYCARVYHWIRGFEFWGQGTLVTVSS

SEQ ID NO: 14
MF4289-VH-CDR1:
DYAMT

SEQ ID NO: 15
MF4289-VH-CDR2:
WITNTGDPTYAPGFTG

SEQ ID NO: 16
MF4289-VH-CDR3:
VYHWIRGFEF

Underlining indicates consecutive CDR1, CDR2 and CDR3 sequences according to KABAT. E.g. CDR1 for sequence MF3370 is SYGIS, CDR2 is WISAYNGNTNYAQKLQG and CDR3 is DRHWHWWLDAFDY.

FIGURE 2

SEQ ID NO: 17

MF5790-VH

QVQLQESGPGLVKPSSETLSLTCTVSGGSFSSSSYWGWIRQPPGKGLEWIGSFYYSGNTYYNPSLKSRVTISEDTSKNQFS
LKLSSVTAADTAVYYCARQTYSSSWDGVLYYFDYWQGGLTVTVSS

SEQ ID NO: 18

MF5790-VH-CDR1

SSSSYWG

SEQ ID NO: 19

MF5790-VH-CDR2

SFYYSGNTYYNPSLKS

SEQ ID NO: 20

MF5790-VH-CDR3

QTYSSSWDGVLYYFDY

SEQ ID NO: 21

MF5803-VH:

QVQLQESGPGLVKPSSETLSLTCTVSNGSISTYYWSWIRQPPGKGLEWIGYVYYTGRTKYNPSLKSRVTISVDTSKNQFSLN
LSSVTAADTAVYYCARGGIVVPAARDYVMDVWGKGTTVTVSS

SEQ ID NO: 22

MF5803-VH-CDR1:

TYYWS

SEQ ID NO: 23

MF5803-VH-CDR2:

YVYYTGRTKYNPSLKS

SEQ ID NO: 24

MF5803-VH-CDR3:

GGIVVPAARDYVMDV

SEQ ID NO: 25

MF5805-VH:

EVQLVQSGAEVKKPGESLKIAACKGSGFSFTSHWIGWVRQKPGRGLEWMGVYIPGDS DTRYSPSFQGGQVTVSADKSINT
AYLQWNSLKASDTAIYYCARPN SGSPRYFEFWGRGTLTVTVSS

SEQ ID NO: 26

MF5805-VH-CDR1:

(FIGURE 2 continued)

SHWIG

SEQ ID NO: 27

MF5805-VH-CDR2:

VIYPGDS DTRYSPSFQG

SEQ ID NO: 28

MF5805-VH-CDR3:

PNSGSPRYFEF

SEQ ID NO: 29

MF5808-VH:

QVQLQESGPGLVKPSSETLSLTCTVSGGSISSSSYWG WIRQPPGKGLEWIGSFYYSGNTYYNPSLKS RVTISVDTSKNQFS
LKLSVTAADTAVYYCAR QEYYYGSGSPSYFDYWGQGT LVTVSS

SEQ ID NO: 30

MF5808-VH-CDR1:

SSSYWG

SEQ ID NO: 31

MF5808-VH-CDR2:

SFYYSGNTYYNPSLKS

SEQ ID NO: 32

MF5808-VH-CDR3:

QEYYYGSGSPSYFDY

SEQ ID NO: 33

MF5809-VH:

EVQLVQSGAEVKKPGESLKISCKGSGDSFISHWIAWVRQMPGKGLEWMGIVYPGDS DTRYSPSFQG QVTISADKSITTA
YLQWSSLKASDTAMYYCAR HEWELLGPFDYWGQGT LVTVSS

SEQ ID NO: 34

MF5809-VH-CDR1:

SHWIA

SEQ ID NO: 35

MF5809-VH-CDR2:

IVYPGDS DTRYSPSFQG

SEQ ID NO: 36

MF5809-VH-CDR3:

(FIGURE 2 continued)

HEWELLGPFDY

SEQ ID NO: 37

MF5814-VH:

EVQLVQSGAEVKKPGSSVKVSKASGGTSTNDAISWVRQTPGQGLEWMGSIIPILDTTDHAQKFQGRVTITADKSTNT
AYMELNSLRSDDTAVYYCAREHIAARQDYFDYWGQGLTVTVSS

SEQ ID NO: 38

MF5814-VH-CDR1:

NDAIS

SEQ ID NO: 39

MF5814-VH-CDR2:

SIIPILDTTDHAQKFQG

SEQ ID NO: 40

MF5814-VH-CDR3:

EHIAARQDYFDY

SEQ ID NO: 41

MF5816-VH:

EVQLVQSGSKLKKPGASVKVSKASGYTFTSYTMNWVRQAPGQGLEWMGWINTDTGDPTYAQGFTGRFVFSLDTSV
STAFLLQINSLKAEDTAVYYCARGDCDSTSCYRYSYGIEDYWGQGLTVTVSS

SEQ ID NO: 42

MF5816-VH-CDR1:

SYTMN

SEQ ID NO: 43

MF5816-VH-CDR2:

WINTDTGDPTYAQGFTG

SEQ ID NO: 44

MF5816-VH-CDR3:

GDCDSTSCYRYSYGIEDY

SEQ ID NO: 45

MF5817-VH:

QVQLVQSGAEVKKPGSSVKVSKVSGGTFRSYAISWVRQAPGQGLEWMGGIIPIDTRNYAQILQGRVTITADLSTSTA
YMEINSLRSEDTAIYYCARGSDEGDWFDPWGQGLTVTVSS

SEQ ID NO: 46

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(FIGURE 2 continued)

MF5817-VH-CDR1:
SYAIS

SEQ ID NO: 47
MF5817-VH-CDR2:
GIIPFDTRNYAQILQG

SEQ ID NO: 48
MF5817-VH-CDR3:
GSDEGDWFDP

SEQ ID NO: 49
MF5818-VH:
EVQLVQSGTEVRKPGSSVKVSCASGGTFSNYAISWVRQAPGQGLEWMGSIIPILGTTDHAQKFQDRVTITADKSSNTT
YMESSLRSDDTAVYYCAREEYIAARLDYFDSWGQGTLVTVSS

SEQ ID NO: 50
MF5818-VH-CDR1:
NYAIS

SEQ ID NO: 51
MF5818-VH-CDR2:
SIIPILGTTDHAQKFQD

SEQ ID NO: 52
MF5818-VH-CDR3:
EYIAARLDYFDS

Underlining indicates consecutive CDR1, CDR2 and CDR3 sequences according to KABAT.

FIGURE 3

SEQ ID NO: 53

VL:

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAAASLQSGVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQQSYSTPPTFGQGTKVEIK

SEQ ID NO: 54

VL-CDR1:

QSISSY

SEQ ID NO: 55

VL-CDR2:

AAS

SEQ ID NO: 56

VL-CDR3:

QQSYSTPPT

SEQ ID NO: 57

CL:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

Underlining indicates consecutive CDR1, CDR2 and CDR3 sequences of the common light chain according to IMGT.

FIGURE 4

SEQ ID NO: 58

CH1:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
CNVNHKPSNTKVDKRV

SEQ ID NO: 59

Hinge:

EPKSCDKTHTCPPCP

SEQ ID NO: 60

CH2:

APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAK

SEQ ID NO: 61

CH3-DE:

GQPREPQVYTDPPSREEMTKNQVSLTCEVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 62

CH3-KK:

GQPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 5a

SEQ ID NO: 63

MF3755x5816:

QVQLVQSGSELKKPGASVKISCKASGYDFTNYAMNWVRQAPGHGLEWMGWINANTGDPTYAQGFTGRFVFSLDTSV
STAYLQISSLKAEDSAVYYCTRERFLEWLHFDYWGGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL
GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTDPPSREEMTKNQVSLTCEVKGFPYSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVQSGSKLKKPGASVKVSKAS
GYTFTSYTMNWVRQAPGQGLEWMGWINTDTGDPTYAQGFTGRFVFSLDTSVSTAFLQINSLKAEDTAVYYCARGDC
DSTSCYRYSYGEDYWGGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 5b

SEQ ID NO: 64

MF3755x5790:

QVQLVQSGSELKKPGASVKISKASGYDFTNYAMNWVRQAPGHGLEWMGWINANTGDPTYAQGFTGRFVFSLDTSV
STAYLQISSLKAEDSAVYYCTRERFLEWLHFDYWGGTGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL
GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTDPPSREEMTKNQVSLTCEVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKQVQLQESGPGLVKPSETLSLTCTVS
GGSFSSSSSYWGWIRQPPGKLEWIGSFYYSGNTYYNPSLKSRTISEDTSKNQFSLKLSVTAADTAVYYCARQTYSSS
WDGVLYYFDYWGGTGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
ISKAKGQPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 5c

SEQ ID NO: 65

MF3755x5818:

QVQLVQSGSELKKPGASVKISCKASGYDFTNYAMNWVRQAPGHGLEWMGWINANTGDPTYAQGFTGRFVFSLDTSV
STAYLQISSLKAEDSAVYYCTRERFLEWLHFDYWGGTGLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL
GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTDPPSREEMTKNQVSLTCEVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVQSGTEVRKPGSSVKVSCKAS
GGTFSNYAISWVRQAPGQGLEWMGSIIPILGTTDHAQKFQDRVITADKSSNTTYMELSSLRSDDTAVYYCAREYIAARL
DYFDSWGQGTGLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
LSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 5d

SEQ ID NO: 66

MF4280x5790:

QVQLVQSGAEVKKPGASVKVSCKVSGYLTLSMHWVRQAPGKGLEWMGGFDPEYGKTFFAQNFQGRVTMTEDTS
ADTAYMELSSLRSEDTAVYYCATEGYYETTTYYNLFDSWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTDPPSREEMTKNQVSLTCEVKGFYPSDIAVEWESNGQPE
NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKQVQLQESGPGLVKPSETLSL
TCTVSGGSFSSSSSYWGWIQQPGKLEWIGSFYYSGNTYYNPSSLKSRVTISEDTSKNQFSKLSSVTAADTAVYYCARQT
YSSSWDGLVYYFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP
AVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPA
PIEKTISKAKGQPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 5e

SEQ ID NO: 67

MF4280x5816:

QVQLVQSGAEVKKPGASVKVSCKVSGYLTLSMHWVRQAPGKGLEWMGGFDPEYGKTFFAQNFQGRVTMTEDTS
ADTAYMELSSLRSEDTAVYYCATEGYYETTTYYNLFDSWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTDPPSREEMTKNQVSLTCEVKGFYPSDIAVEWESNGQPE
NNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVQSGSKLKKPGASVKV
SCKASGYFTSYTMNWVRQAPGQGLEWMGWINTDGDPTYAQGFTGRFVFSLDTSVSTAFLQINSLKAEDTAVYYCA
RGDCDSTSCYRYSYGYEDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
VHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPIEKTISKAKGQPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 5f

SEQ ID NO: 68

MF4280x5818:

QVQLVQSGAEVKKPGASVKVSCKVSGYLTLSMHWVRQAPGKGLEWMGGFDPEYGKTFFAQNFQGRVTMTEDTS
ADTAYMELSSLRSEDTAVYYCATEGYYETTTYYNLFDSWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVL
HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTDPPSREEMTKNQVSLTCEVKGFYPSDIAVEWESNGQPE
NNYKTTTPVLDSGGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVQSGTEVRKPGSSVK
VSCKASGGTFSNYAISWVRQAPGQGLEWMGSIIPILGTTDHAQKFQDRVITADKSSNTTYMELSSLRSDDTAVYYCAR
EYIAARLDYFDSWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT
PEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
TISKAKGQPREPQVYTKPPSREEMTKNQVSLKCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain sequences from six exemplary bispecific antibodies composed of two different MF clones, a hinge, CH1, CH2 and CH3-DE and CH3-KK domains