

FIG. 1A**CL25_hu_10-4 VH**

EVQLVQSGAEVKKPGESLKISCKGSGYTFTSYGLSWVRQMPGKGLEWMGEIYPGSG
NTYYNEKFKGQVTISADKSISTAYLQWSSLKASDTAMYICARYDYLGSSYGFDYWG
AGTTVTVSS (SEQ ID NO:22)

CL25_hu_10-4 VL

DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLLYSASYRYS
GVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:80)

H_zCL25 VH

EVQLVQSGAEVKKPGESLKISCKGSGYTFTSYGLSWVRQMPGKGLEWMGEIYPGSG
NTYYNEKFKGQVTISADKSISTAYLQWSSLKASDTAMYICARYDYLGSSYGFDYWG
AGTTVTVSS (SEQ ID NO:22)

H_zCL25 VL

DIVMTQSPDSLAVSLGERATINCKASQDVSTAVAWYQQKPGQPPKLLIYSASYRYS
GVPDRFSGSGSGTDFTLTISLQAEDEVAVYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:23)

CL25_hu_10-6 VH

EVQLVQSGAEVKKPGESLKISCKGSGYTFTSYGLSWVRQMPGKGLEWMGEIYPGSG
NTYYNEKFKGQVTISADKSISTAYLQWSSLKASDTAMYICARYDYLGSSYGFDYWG
AGTTVTVSS (SEQ ID NO:22)

CL25_hu_10-6 VL

AIRMTQSPSSFSASTGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYS
GVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:81)

CL25_hu_11-4 VH

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSG
NTYYNEKFKGRVTMTANTSISTAYMELSSLRSEDTAVYYCARYDYLGSSYGFDYWG
AGTTVTVSS (SEQ ID NO:82)

CL25_hu_11-4 VL

DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLLYSASYRYS
GVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:80)

FIG. 1B**CL25_hu_11-5_VH**

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSG
NTYYNEKFKGRVTMTANTSISTAYMELSSLRSED TAVYYCARYDYL GSSYGF DYWG
AGTTVTVSS (SEQ ID NO:82)

CL25_hu_11-5_VL

DIVMTQSPDSLAVSLGERATINCKASQDVSTAVAWYQQKPGQPPKLLIYSASYRYS
GVPDRFSGSGSGTDFTLTISLQAEDVAVYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:23)

CL25_hu_11-6_VH

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSG
NTYYNEKFKGRVTMTANTSISTAYMELSSLRSED TAVYYCARYDYL GSSYGF DYWG
AGTTVTVSS (SEQ ID NO:82)

CL25_hu_11-6_VL

AIRMTQSPSSFSASTGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYS
GVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:81)

CL25_hu_8-4_VH

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSG
NTYYNEKFKGRVTMTRNTSISTAYMELSSLRSED TAVYYCARYDYL GSSYGF DYWG
AGTTVTVSS (SEQ ID NO:83)

CL25_hu_8-4_VL

DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYS
GVPSRFSGSGSGTDYTLTISLQPEDFATYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:80)

CL25_hu_8-5_VH

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSG
NTYYNEKFKGRVTMTRNTSISTAYMELSSLRSED TAVYYCARYDYL GSSYGF DYWG
AGTTVTVSS (SEQ ID NO:83)

CL25_hu_8-5_VL

DIVMTQSPDSLAVSLGERATINCKASQDVSTAVAWYQQKPGQPPKLLIYSASYRYS
GVPDRFSGSGSGTDFTLTISLQAEDVAVYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:23)

FIG. 1C**CL25_hu_8-6 VH**

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSG
NTYYNEKFKGRVTMTRNTSISTAYMELSSLRSED TAVYYCARYDYL GSSYGF DYWG
AGTTVTVSS (SEQ ID NO:83)

CL25_hu_8-6 VL

AIRMTQSPSSFSASTGDRV TITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYS
GVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:81)

CL25_hu_9-4 VH

QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYGLSWVRQAPGQGLEWMGEIYPGSG
NTYYNEKFKGRVTITADESTSTAYMELSSLRSED TAVYYCARYDYL GSSYGF DYWG
AGTTVTVSS (SEQ ID NO:84)

CL25_hu_9-4 VL

DIQMTQSPSSLSASVGDRTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYS
GVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:80)

CL25_hu_9-5 VH

QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYGLSWVRQAPGQGLEWMGEIYPGSG
NTYYNEKFKGRVTITADESTSTAYMELSSLRSED TAVYYCARYDYL GSSYGF DYWG
AGTTVTVSS (SEQ ID NO:84)

CL25_hu_9-5 VL

DIVMTQSPDSLAVSLGERATINCKASQDVSTAVAWYQQKPGQPPKLLIYSASYRYS
GVPDRFSGSGSGTDFTLTISLQAEDEVAVYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:23)

CL25_hu_9-6 VH

QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYGLSWVRQAPGQGLEWMGEIYPGSG
NTYYNEKFKGRVTITADESTSTAYMELSSLRSED TAVYYCARYDYL GSSYGF DYWG
AGTTVTVSS (SEQ ID NO:84)

CL25_hu_9-6 VL

AIRMTQSPSSFSASTGDRV TITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYS
GVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQHYNTPYTFGGGTKLEIK (SEQ
ID NO:81)

FIG. 1D

```
CL25      QVQLVQSGAELARPGASVKLSCKASGYTFTSYGLSWVRQRTGQGLEWIGEIYPGSGNTYY 60
CL_hu_10-4 EVQLVQSGAEVKKPGESLKISCKGSGYTFTSYGLSWVRQMPGKGLEWMGEIYPGSGNTYY 60
HzCL25     EVQLVQSGAEVKKPGESLKISCKGSGYTFTSYGLSWVRQMPGKGLEWMGEIYPGSGNTYY 60
CL25_hu_10-6 EVQLVQSGAEVKKPGESLKISCKGSGYTFTSYGLSWVRQMPGKGLEWMGEIYPGSGNTYY 60
CL25_hu_9-4  QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYGLSWVRQAPGQGLEWMGEIYPGSGNTYY 60
CL25_hu_9-5  QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYGLSWVRQAPGQGLEWMGEIYPGSGNTYY 60
CL25_hu_9-6  QVQLVQSGAEVKKPGSSVKVSKASGYTFTSYGLSWVRQAPGQGLEWMGEIYPGSGNTYY 60
CL25_hu_11-4 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSGNTYY 60
CL25_hu_11-5 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSGNTYY 60
CL25_hu_11-6 QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSGNTYY 60
CL25_hu_8-4  QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSGNTYY 60
CL25_hu_8-5  QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSGNTYY 60
CL25_hu_8-6  QVQLVQSGAEVKKPGASVKVSKASGYTFTSYGLSWVRQATGQGLEWMGEIYPGSGNTYY 60
          :*** :*****: :** *:***:*****:*****:*****:*****:*****:*****
          :*****:*****:*****:*****:*****:*****:*****:*****:*****:*****

CL25      NEKFKGKATLTADKSSSTAYMELRSLTSEDSAVYFCARYDYLGSSEYGFYDWGQGTTLTVS 120
CL_hu_10-4 NEKFKGQVTISADKSIISTAYLQWSSSLKASDTAMYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
HzCL25     NEKFKGQVTISADKSIISTAYLQWSSSLKASDTAMYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_10-6 NEKFKGQVTISADKSIISTAYLQWSSSLKASDTAMYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_9-4  NEKFKGRVTITADESTSTAYMELSSLRSEDTAVYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_9-5  NEKFKGRVTITADESTSTAYMELSSLRSEDTAVYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_9-6  NEKFKGRVTITADESTSTAYMELSSLRSEDTAVYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_11-4 NEKFKGRVTMTANTSISTAYMELSSLRSEDTAVYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_11-5 NEKFKGRVTMTANTSISTAYMELSSLRSEDTAVYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_11-6 NEKFKGRVTMTANTSISTAYMELSSLRSEDTAVYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_8-4  NEKFKGRVTMTANTSISTAYMELSSLRSEDTAVYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_8-5  NEKFKGRVTMTANTSISTAYMELSSLRSEDTAVYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
CL25_hu_8-6  NEKFKGRVTMTANTSISTAYMELSSLRSEDTAVYYCARYDYLGSSEYGFYDWGAGTTTVTS 120
          *****:*****:*****:*****:*****:*****:*****:*****:*****:*****
          *****:*****:*****:*****:*****:*****:*****:*****:*****:*****

CL25      S 120 (SEQ ID NO:26)
CL_hu_10-4 S 121 (SEQ ID NO:22)
HzCL25     S 121 (SEQ ID NO:22)
CL25_hu_10-6 S 121 (SEQ ID NO:22)
CL25_hu_9-4  S 121 (SEQ ID NO:84)
CL25_hu_9-5  S 121 (SEQ ID NO:84)
CL25_hu_9-6  S 121 (SEQ ID NO:84)
CL25_hu_11-4 S 121 (SEQ ID NO:82)
CL25_hu_11-5 S 121 (SEQ ID NO:82)
CL25_hu_11-6 S 121 (SEQ ID NO:82)
CL25_hu_8-4  S 121 (SEQ ID NO:83)
CL25_hu_8-5  S 121 (SEQ ID NO:83)
CL25_hu_8-6  S 121 (SEQ ID NO:83)
```

FIG. 1E

```
CL25      DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYRYNGVPD 60
HzCL25    DIVMTQSPDSLAVSLGERATINCKASQDVSTAVAWYQQKPGQPPKLLIYSASYRYSGVPD 60
CL25_hu_11-5 DIVMTQSPDSLAVSLGERATINCKASQDVSTAVAWYQQKPGQPPKLLIYSASYRYSGVPD 60
CL25_hu_8-5  DIVMTQSPDSLAVSLGERATINCKASQDVSTAVAWYQQKPGQPPKLLIYSASYRYSGVPD 60
CL25_hu_9-5  DIVMTQSPDSLAVSLGERATINCKASQDVSTAVAWYQQKPGQPPKLLIYSASYRYSGVPD 60
CL25_hu_10-4 DIQMTQSPSSLSASVGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYSGVPS 60
CL25_hu_11-4 DIQMTQSPSSLSASVGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYSGVPS 60
CL25_hu_8-4  DIQMTQSPSSLSASVGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYSGVPS 60
CL25_hu_9-4  DIQMTQSPSSLSASVGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYSGVPS 60
CL25_hu_10-6 AIRMTQSPSSFSASTGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYSGVPS 60
CL25_hu_11-6 AIRMTQSPSSFSASTGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYSGVPS 60
CL25_hu_8-6  AIRMTQSPSSFSASTGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYSGVPS 60
CL25_hu_9-6  AIRMTQSPSSFSASTGDRVITITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYSGVPS 60
          * ***** . :.:* *:*.*****: *****:****,****,
          * ***** . :.:* *:*.*****: *****:****,****,

CL25      RFTSGSGSGTDFTFTISSVQAEDLAVYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:27)
HzCL25    RFTSGSGSGTDFTLTISSLQAEDVAVYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:23)
CL25_hu_11-5 RFTSGSGSGTDFTLTISSLQAEDVAVYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:23)
CL25_hu_8-5  RFTSGSGSGTDFTLTISSLQAEDVAVYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:23)
CL25_hu_9-5  RFTSGSGSGTDFTLTISSLQAEDVAVYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:23)
CL25_hu_10-4 RFTSGSGSGTDYTLTISSLQPEDFATYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:80)
CL25_hu_11-4 RFTSGSGSGTDYTLTISSLQPEDFATYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:80)
CL25_hu_8-4  RFTSGSGSGTDYTLTISSLQPEDFATYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:80)
CL25_hu_9-4  RFTSGSGSGTDYTLTISSLQPEDFATYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:80)
CL25_hu_10-6 RFTSGSGSGTDFTLTISCLQSEDFATYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:81)
CL25_hu_11-6 RFTSGSGSGTDFTLTISCLQSEDFATYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:81)
CL25_hu_8-6  RFTSGSGSGTDFTLTISCLQSEDFATYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:81)
CL25_hu_9-6  RFTSGSGSGTDFTLTISCLQSEDFATYYCQQHYNTPYTFGGGTKLEIK 107 (SEQ ID NO:81)
          **:*****:*.***.:* **.*.*****
```

FIG. 2A

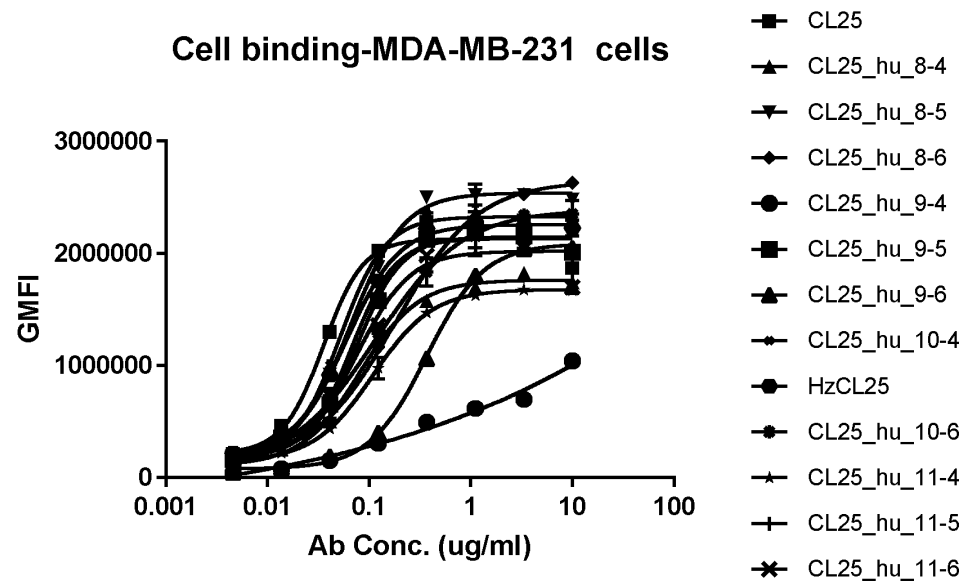


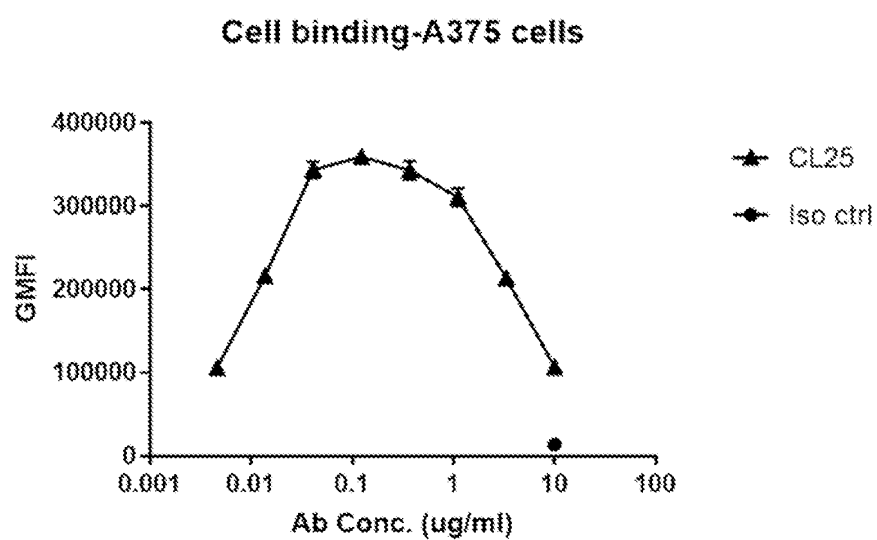
FIG. 2B

FIG. 3A

Cellular CD73 inhibition - A375 cells

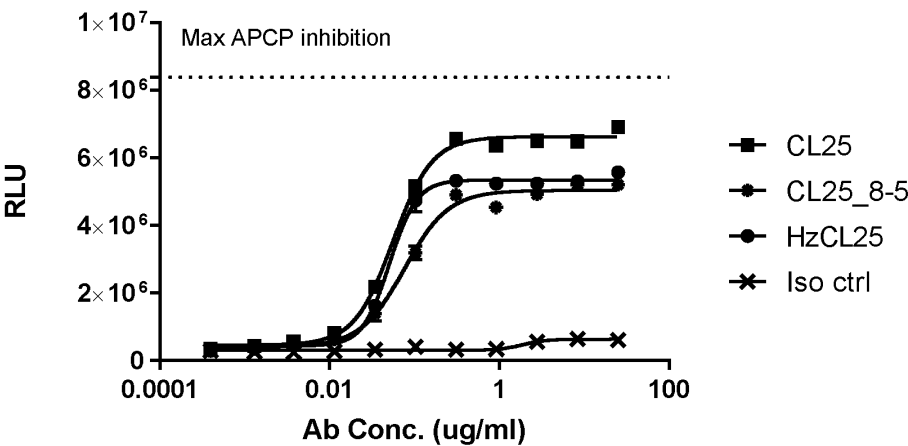


FIG. 3B

Cellular CD73 inhibition - MDA-MB-231 cells

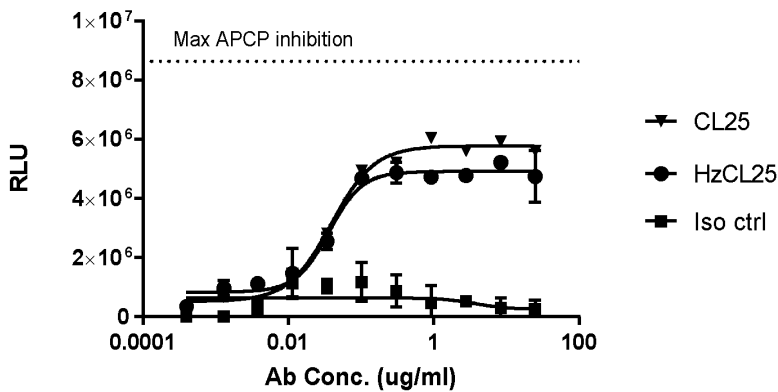


FIG. 3C

Cellular CD73 inhibition - MDA-MB-231 cells

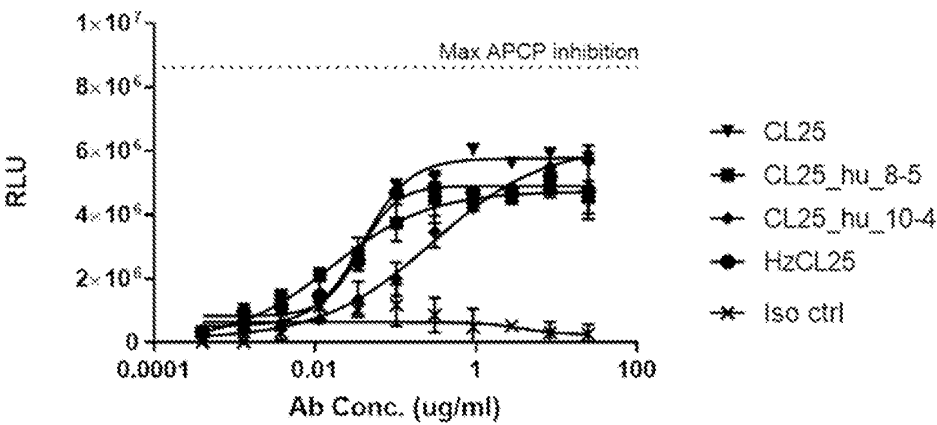


FIG. 4

Recombinant CD73 inhibition

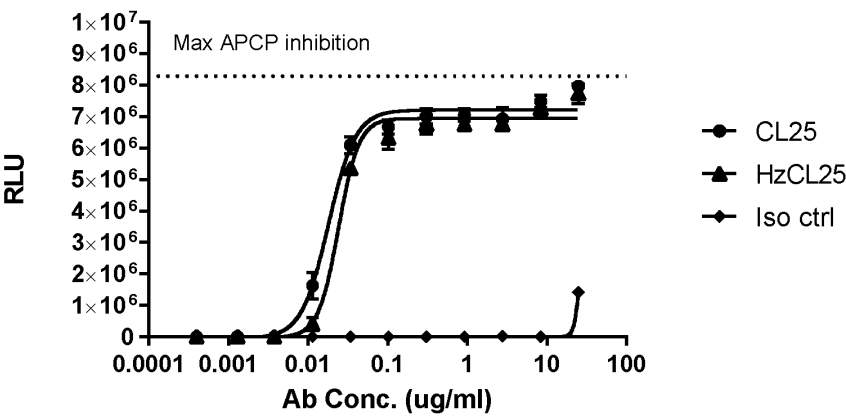


FIG. 5

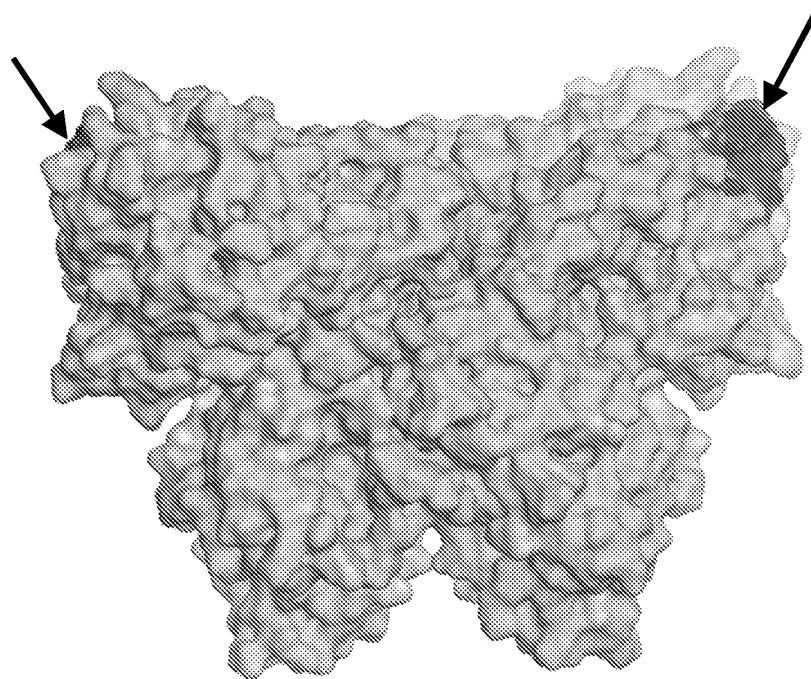


FIG. 6

Surface CD73 after 24 hour antibody incubation

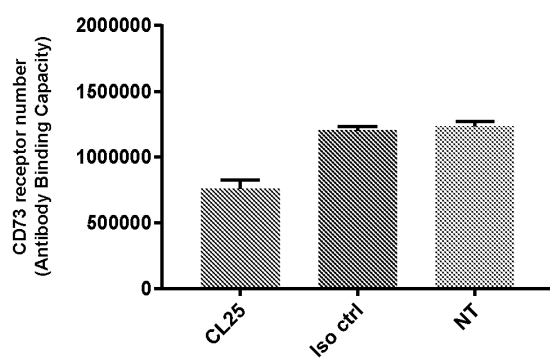


FIG. 7A

Cell binding-MDA-MB-231cells

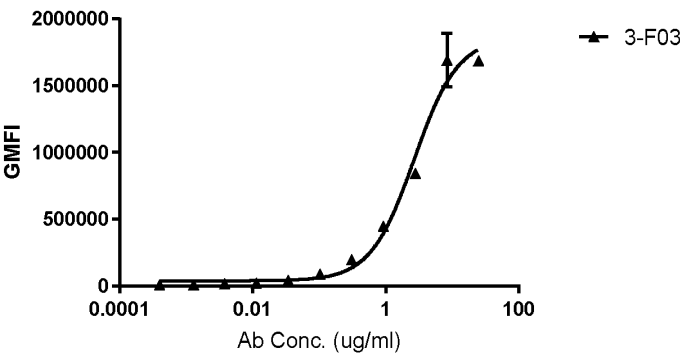


FIG. 7B

Cell binding-A375 cells

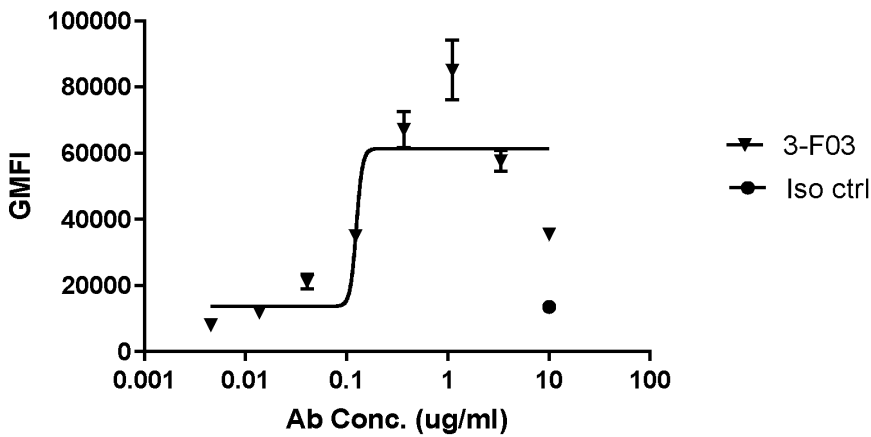


FIG. 8A

Cellular CD73 inhibition - A375 cells

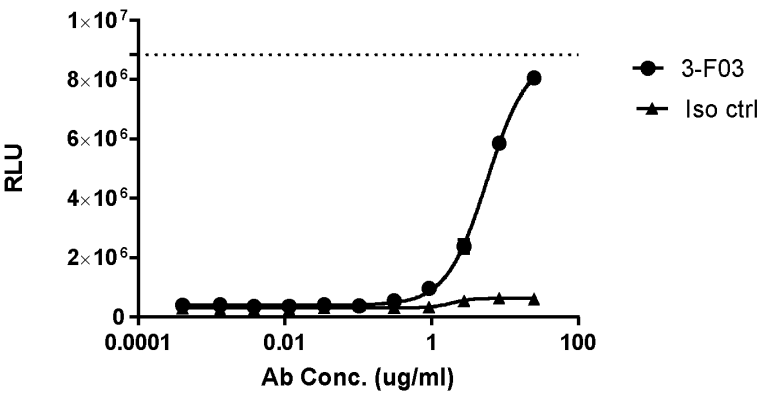


FIG. 8B

Cellular CD73 Inhibition- MDA-MB-231 cells

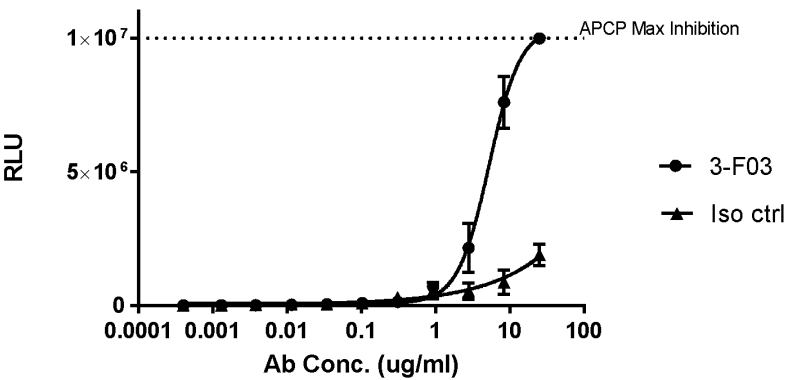


FIG. 9

Recombinant CD73 inhibition

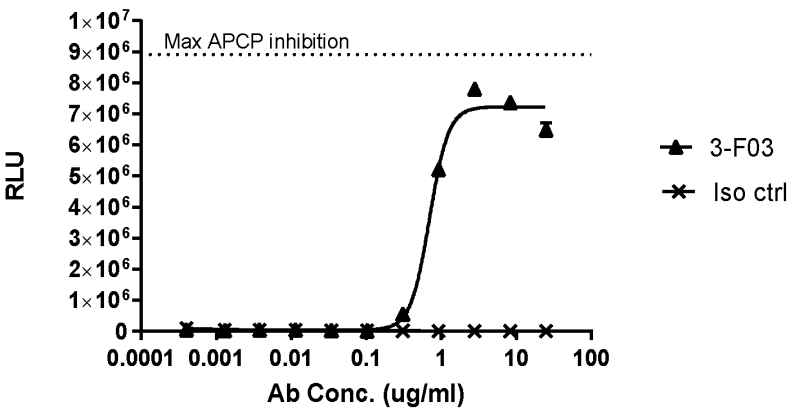


FIG. 10

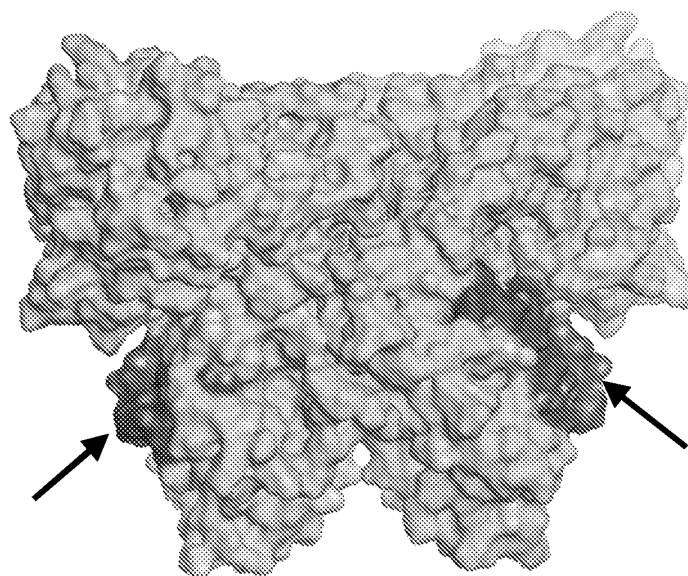


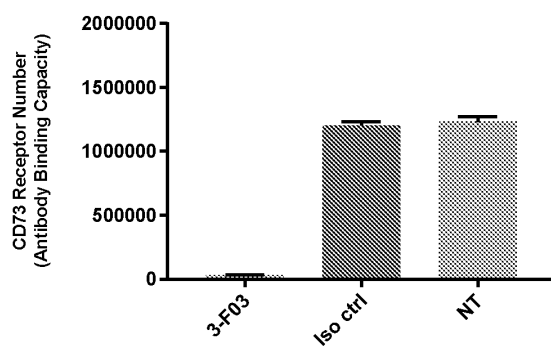
FIG. 11**Surface CD73 after 24 hour antibody incubation**

FIG. 12A**3-F03_VH_yeast**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:77)

3-F03_VL_yeast

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:65)

3-F03_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:60)

3-F03_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:61)

3-F03_411_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:62)

3-F03_411_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:61)

3-F03_413_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGS
NKYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:63)

3-F03_413_LC

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:61)

FIG. 12B**3-F03_396_VH**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:77)

3-F03_396_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:65)

3-F03_408_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:77)

3-F03_408_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
VPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:61)

3-F03_402_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:85)

3-F03_402_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:65)

3-F03_384_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:77)

3-F03_384_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:64)

FIG. 12C**3-F03_399_VH**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:62)

3-F03_399_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:65)

3-F03_414_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:85)

3-F03_414_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:61)

3-F03_390_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:85)

3-F03_390_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:64)

3-F03_398_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:86)

3-F03_398_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:65)

FIG. 12D**3-F03_387_VH**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:62)

3-F03_387_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTREIK (SEQ
ID NO:64)

3-F03_386_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEG
S
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:86)

3-F03_386_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTREIK (SEQ
ID NO:64)

3-F03_401_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEG
S
NKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:63)

3-F03_401_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTREIK (SEQ
ID NO:65)

3-F03_410_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEG
S
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:86)

3-F03_410_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSG
VPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTREIK (SEQ
ID NO:61)

FIG. 12E**3-F03_389_VH**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGS
NKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:63)

3-F03_389_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:64)

3-F03_392_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGS
NKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:87)

3-F03_392_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:64)

3-F03_404_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGS
NKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:87)

3-F03_404_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:65)

3-F03_419_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGS
NKKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:88)

3-F03_419_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:61)

FIG. 12F**3-F03_416_VH**

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGSN
KYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:87)

3-F03_416_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:61)

3-F03_407_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGSN
KYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:88)

3-F03_407_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:65)

3-F03_395_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGSN
KYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:88)

3-F03_395_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:64)

3-F03_388_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGS
NKYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:69)

3-F03_388_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:64)

FIG. 12G**3-F03_397_VH**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:68)

3-F03_397_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:65)

3-F03_385_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:68)

3-F03_385_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:64)

3-F03_400_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGS
NKYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:69)

3-F03_400_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:65)

3-F03_409_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGS
NKYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:69)

3-F03_409_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSG
VPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:61)

FIG. 12H**3-F03_403_VH**

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGSN
KYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LV TVSS (SEQ ID NO:32)

3-F03_403_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:65)

3-F03_415_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGSN
KYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LV TVSS (SEQ ID NO:32)

3-F03_415_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:61)

3-F03_391_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGSN
KYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LV TVSS (SEQ ID NO:32)

3-F03_391_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:64)

3-F03_406_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGSN
KYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LV TVSS (SEQ ID NO:67)

3-F03_406_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:65)

FIG. 12I**3-F03_412_VH**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGS
NKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:69)

3-F03_412_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:61)

3-F03_394_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSG
SNKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:67)

3-F03_394_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:64)

3-F03_418_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSG
SNKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:67)

3-F03_418_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:61)

3_F03_417_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:60)

3_F03_417_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:61)

FIG. 12J**3_F03_393_VH**

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGSN
KYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:60)

3_F03_393_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:64)

3_F03_405_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGSN
KYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:60)

3_F03_405_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:65)

FIG. 13

Cell binding-MDA-MB-231 cells

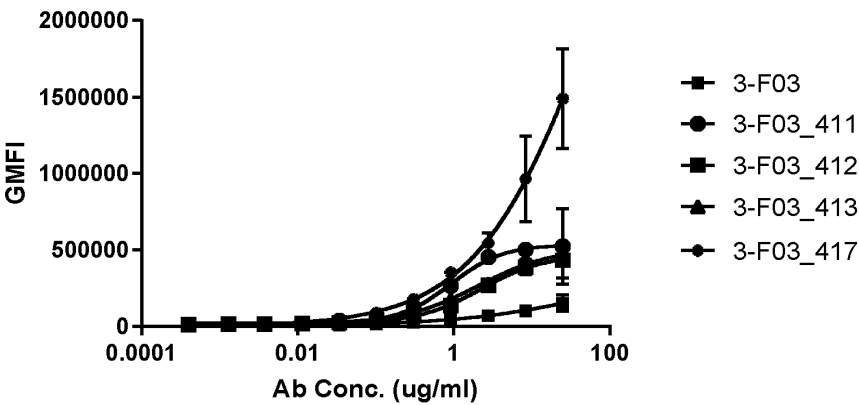


FIG. 14

Cellular CD73 inhibition - MDA-MB-231 cells

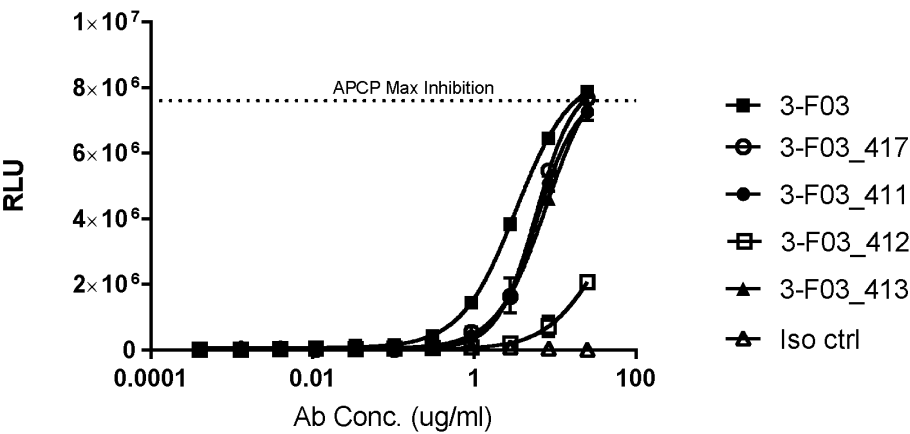


FIG. 15**Human IgG1 heavy chain CH1-hinge-CH2-CH3, with N297A mutation**

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG (SEQ
ID NO:73)

Human IgG1 heavy chain CH1-hinge-CH2-CH3, with N297A mutation with C-terminal lysine

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK (SEQ
ID NO:75)

Human kappa light chain constant region

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ
ID NO:74)

FIG. 16A

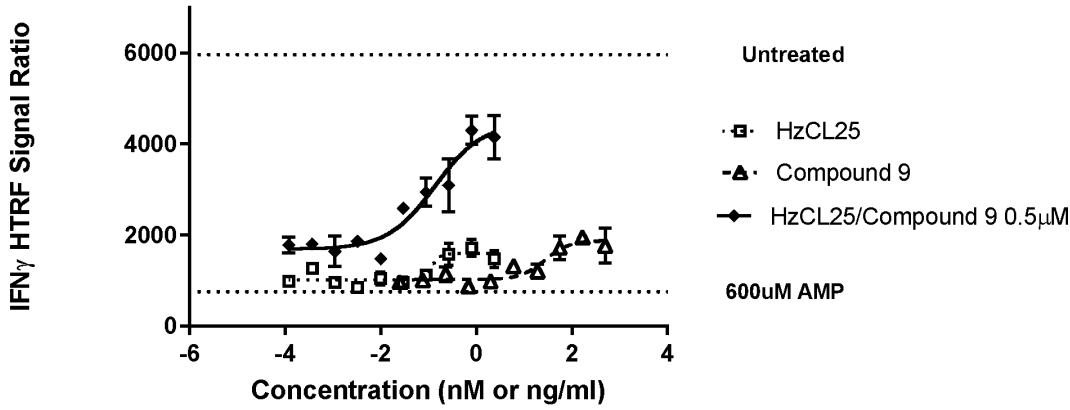


FIG. 16B

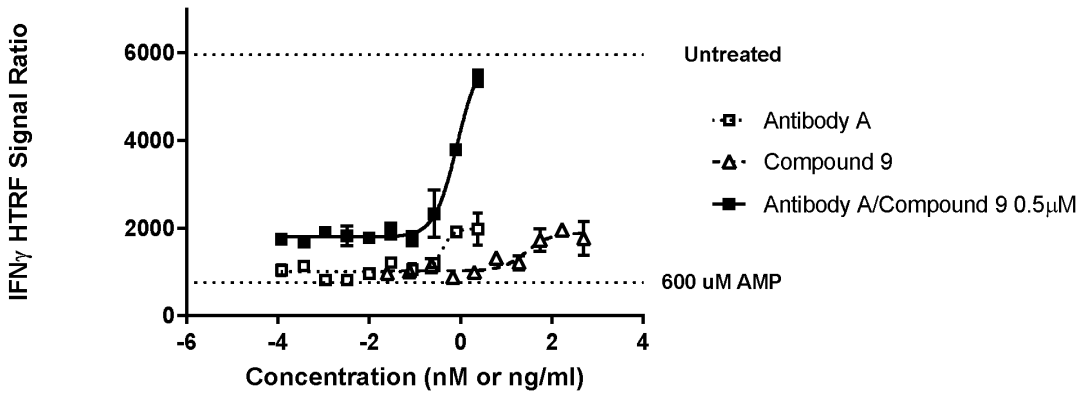


FIG. 16C

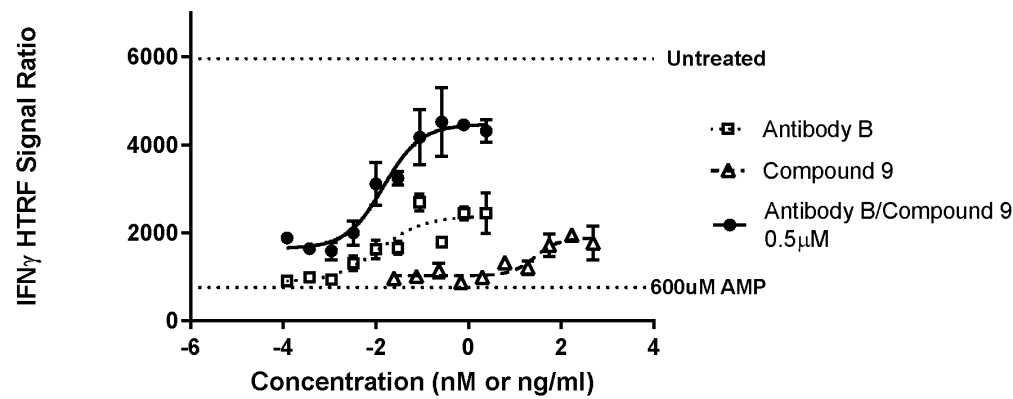


FIG. 17A

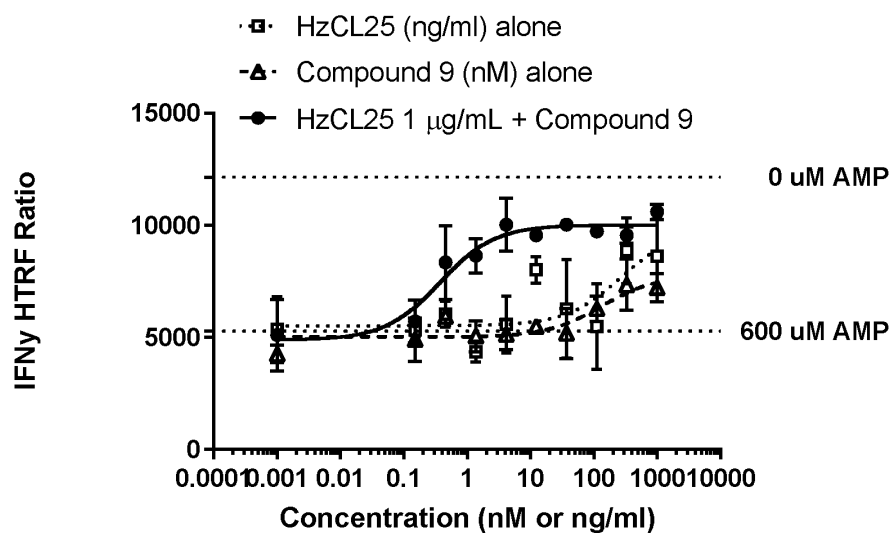


FIG. 17B

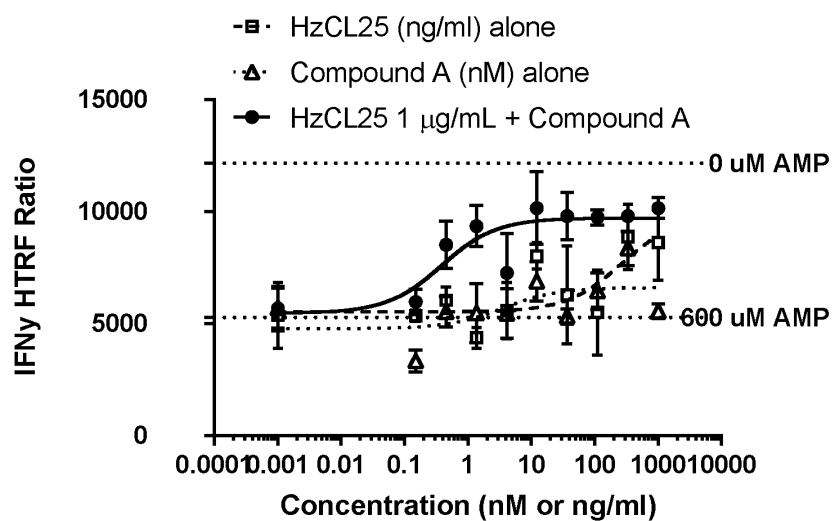


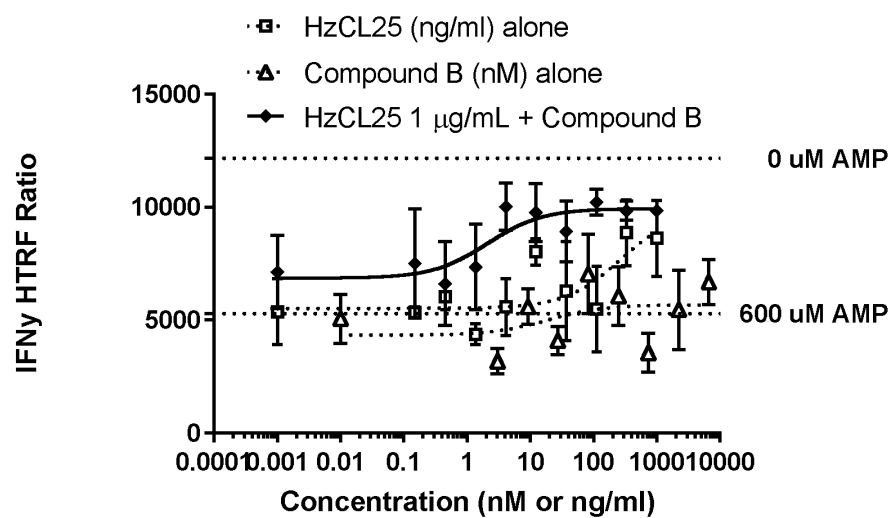
FIG. 17C

FIG. 18A

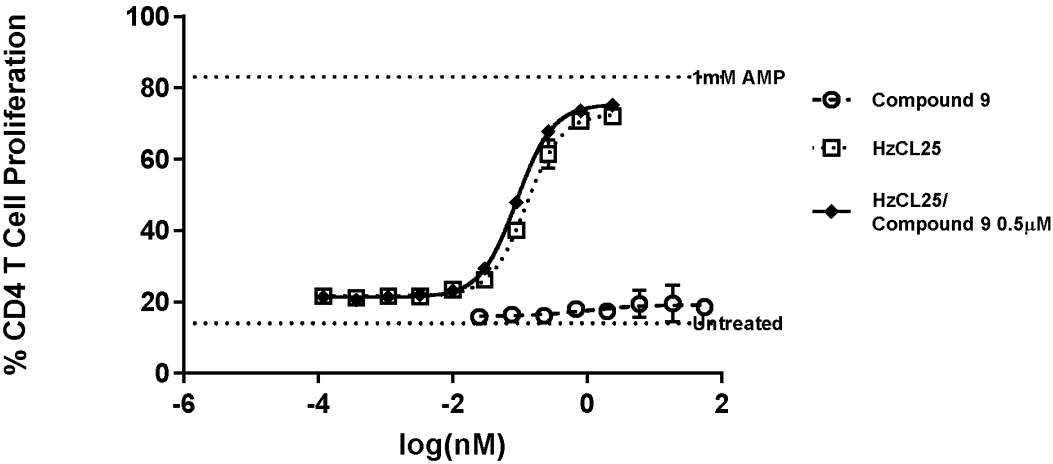


FIG. 18B

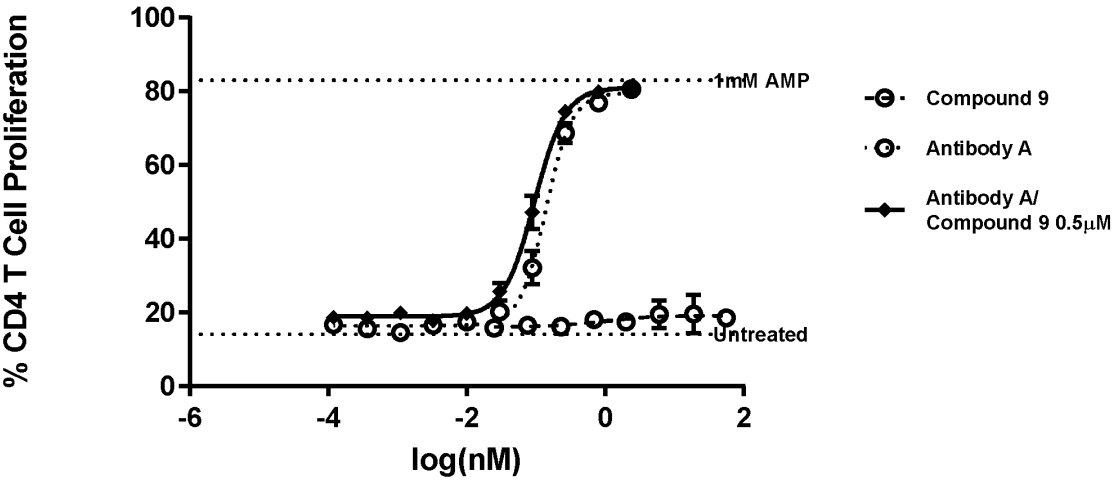


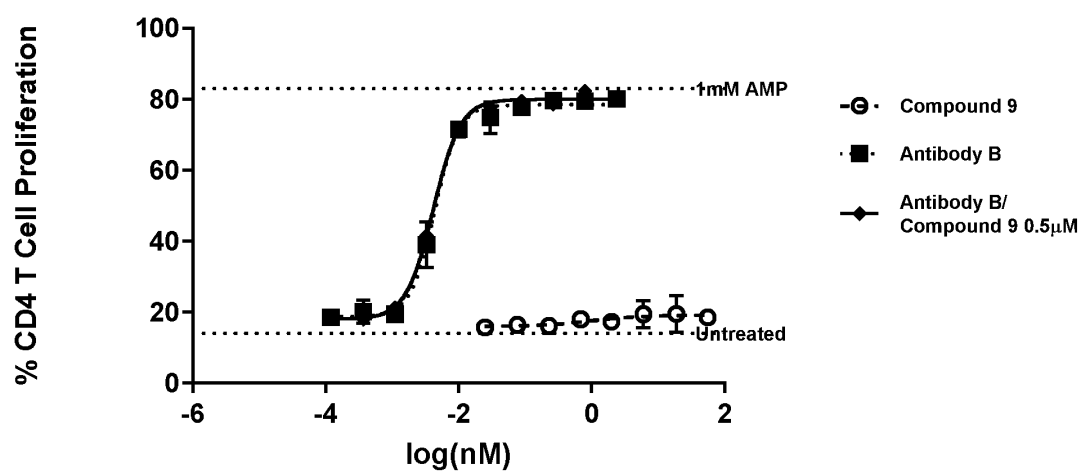
FIG. 18C

FIG. 19A

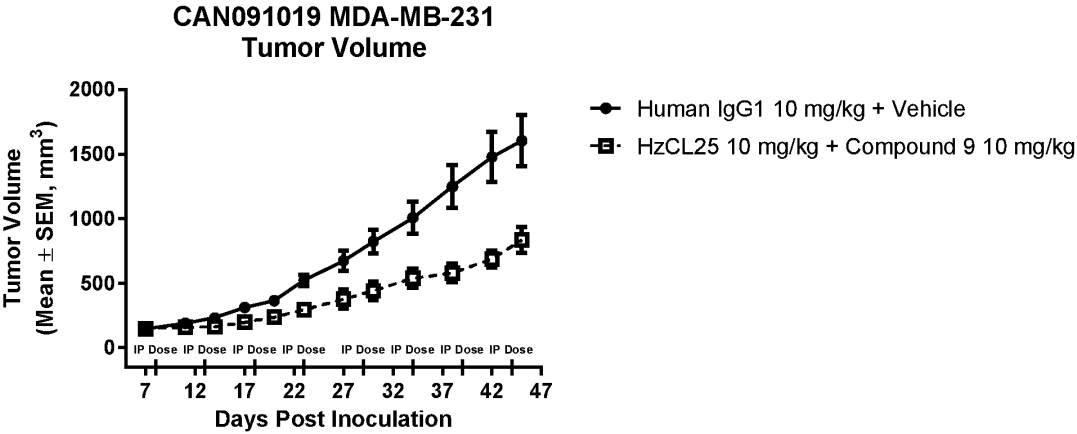


FIG. 19B

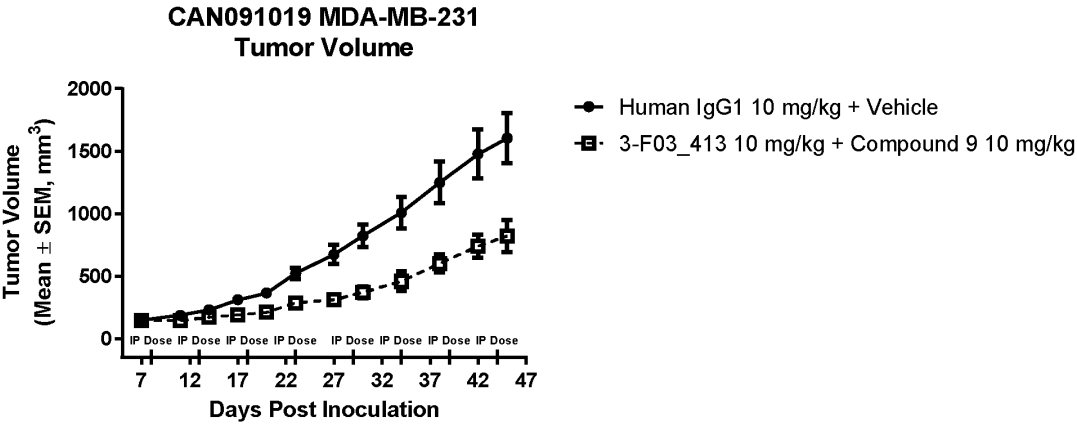


FIG. 20A**HzCL25 heavy chain DNA sequence**

GAAGTGCAGCTCGTGCAGTCCGGAGCCGAAGTGAAAAAGCCTGGAGAGTCCCTGAAGATC
AGCTGCAAGGGTTCCGGCTATACATTACCTCCTACGGGCTCAGCTGGGTCAGACAGATG
CCGGGAAAGGGTCTTGAGTGGATGGGAGAGATCTACCCGGGCTCCGGCAACACCTACTAC
AACGAAAAGTTCAAGGGCCAGGTCACCATTTCCGCCGACAAGTCAATCTCCACCGCTTAC
CTCCAATGGTTCGAGCCTGAAGGCATCGGATACCGCGATGTACTACTGCGCCCGCTACGAC
TACCTGGGCTCGTCATACGGCTTCGATTACTGGGGGGCGGGAACCTACCGTGACTGTGTCC
TCCGCCCTCCACTAAGGGACCCTCAGTGTTCCCCCTTGCCCCGAGCTCCAAGAGCACTTCG
GGCGGAACCGCTGCCCTGGGTTGCCTCGTGAAGGATTACTTCCCCGAGCCTGTGACCGTG
TCCTGGAACCTCCGGGGCCTTGACCAGCGGAGTCCACACCTTCCCGGCCGTGCTGCAATCA
TCCGGTCTGTACAGTCTGTCTCCGTGGTACGGTGCCCTCGTCTCTACTGGGGACTCAG
ACTTACATCTGTAACGTGAACCATAAGCCATCGAACACCAAAGTCGACAAACGGGTGGAA
CCTAAGTCATGCGACAAGACCCACACGTGCCACCTTGCCCCGCCCCCGAGCTCCTGGGG
GGGCGGAGCGTGTTCTCTTCCCGCCGAAACCGAAGGACACCCTGATGATCTCGAGGACT
CCTGAAGTCACTTGCGTGGTCTGTGGACGTGTGCGACGAGGACCCCGAAGTCAAGTTCAAT
TGGTACGTGGACGGAGTCGAAGTGCACAACGCTAAGACCAAACCCCGCGAGGAGCAGTAC
GCAAGCACCTACCGCGTTGTGACGCTGCTACCGTGCTGCATCAGGATTGGCTGAATGGA
AAGGAGTACAAGTGCAAAGTGTCCAACAAGGCCCTGCCTGCACCAATTGAAAAGACCATC
TCCAAGGCCAAGGGCCAGCCCCGGGAGCCCCAAGTCTACACTCTGCCGCCGTGAGAGAA
GAAATGACCAAGAACCAAGTGTCCCTGACTTGTCTGGTCAAGGGCTTCTATCCTTCGGAC
ATCGCGGTGGAATGGGAGAGCAACGGCCAGCCGAGACAACAATTACAAGACTACGCCACCC
GTGCTGGACTCTGACGGCTCCTTTTTCTGTATTCCAAGCTACCGTGGACAAGAGCCGC
TGGCAACAGGGAAACGTGTTGAGCTGCTCCGTGATGCACGAAGCCCTGCACAACCACTAC
ACCCAGAAGTCCCTGAGCTTGTCCCCTGGT (SEQ ID NO:89)

HzCL25 light chain DNA sequence

GACATCGTGATGACCCAGTCCCCGGATTCACTCGCGGTGTCTTTGGGGGAGAGGGCAACC
ATTAAGTCAAGGCCTCACAGGATGTGTCCACTGCTGTGCGCTGGTACCAGCAGAAGCCT
GGGCAGCCGCCCAAGCTGCTGATCTACTCGGCCTCCTACCGCTATTCCGGAGTCCCCGAC
CGGTTCTCCGGCTCGGGTTCCGGAACCTGATTTACCCCTGACAATTTCTGCTGCTGCAAGCC
GAGGACGTGGCCGTGTACTACTGCCAACAGCATTACAACACTCCTTACACTTTTGGTGGC
GGAACCTAAGCTCGAGATCAAGCGGACGGTGGCAGCTCCGTCAGTGTTTCATCTTCCCTCCA
TCGGACGAACAGCTGAAGTCCGGCACCGCGTCCGTGCTGTGTCTGTTGAACAACCTTCTAC
CCGCGGGAAGCCAAGGTCCAGTGGAAAGTCGACAACGCGCTGCAGTCCGGAAATAGCCAG
GAAAGCGTGACCGAACAGGACTCCAAGGACAGCACCTACTCCCTGAGCTCAACCCTGACC
CTGAGCAAGGCCGACTATGAGAAGCACAAAGTGACGCTGCGAAGTGACCCACCAAGGC
CTGAGCAGCCCAGTGACCAAGTCCTTCAACCGCGGGGAGTGT (SEQ ID NO:90)

FIG. 20B**3-F03_411 heavy chain DNA sequence**

GAAGTGCAGTTGGTGGAGAGCGGGGGCGGACTGGTGCAGCCGGGGGGCTCGCTGCG
GCTGTCCTGCGCCGCGTCCGGTTTCACTTTTTTCGAGCTACGACATGCACTGGGTCC
GCCAAGCACCGGGGAAGGGTCTGGAATGGGTGGCCGTGATGTCGTACGACGGCTCC
AACAAGTACTACGCCGACTCCGTGAAGGGACGGTTCACCATCTCCCGCGACAACAG
CAAGAACGCCCTTTACCTCCAAATGAACAGCCTGAGGGCCGAGGACACAGCCGTAT
ACTACTGCGCGACCGAGATCGCCGCCAAGGGGGACTACTGGGGTCAAGGCACTCTG
GTCACCGTGTCCTCCGCCTCCACTAAGGGACCCCTCAGTGTTCCCCCTTGCCCCGAG
CTCCAAGAGCACTTCGGGCGGAACCGCTGCCCTGGGTTCCTCGTGAAGGATTACT
TCCCCGAGCCTGTGACCGTGTCCTGGAACCTCCGGGGCCTTGACCAGCGGAGTCCAC
ACCTTCCCGGCCGTGCTGCAATCATCCGGTCTGTACAGTCTGTCTCCGTGGTCAC
GGTGCCCTCGTCCTCACTGGGGACTCAGACTTACATCTGTAACGTGAACCATAAGC
CATCGAACACCAAAGTCGACAAACGGGTGGAACCTAAGTCATGCGACAAGACCCAC
ACGTGCCCACCTTGCCCCGCCCCCGAGCTCCTGGGGGGCCGAGCGTGTTCTCTT
CCCGCCGAAACCGAAGGACACCCTGATGATCTCGAGGACTCCTGAAGTCACTTGCG
TGGTCGTGGACGTGTGCGACGAGGACCCCGAAGTCAAGTTCAATTGGTACGTGGAC
GGAGTCGAAGTGCAACACGCTAAGACCAAACCCCGCGAGGAGCAGTACGCAAGCAC
CTACCGCGTTGTCAGCGTGCTCACCGTGCTGCATCAGGATTGGCTGAATGGAAAGG
AGTACAAGTGCAAAGTGTCACAACAAGGCCCTGCCTGCACCAATTGAAAAGACCATC
TCCAAGGCCAAGGGCCAGCCCCGGGAGCCCCAAGTCTACACTCTGCCGCCGTGAG
AGAAGAAATGACCAAGAACCAAGTGTCCTGACTTGTCTGGTCAAGGGCTTCTATC
CTTCGGACATCGCGGTGGAATGGGAGAGCAACGGCCAGCCGGAGAACAATTACAAG
ACTACGCCACCCGTGCTGGACTCTGACGGCTCCTTTTTCTGTATTCCAAGCTCAC
CGTGGACAAGAGCCGCTGGCAACAGGGAAACGTGTTCAAGCTGCTCCGTGATGCACG
AAGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCTTGTCCTCTGGT (SEQ
ID NO: 91)

FIG. 20C**3-F03_411 and 3-F03_413 light chain DNA sequence**

ATCCAGATGACTCAGTCCCCTTCCTCGTTGTCCGCTTCCGTGGGTGATCGGGTCAC
AATCACTTGCCGGGCCAGCCAGGGAATTTCCAACCTACCTCGCCTGGTACCAGCAGA
AGCCCGGAAAGGCACCGAAGCTGCTGATCTACGCCGCGTCCACTCTGCAATCCGGA
GTGCCTTCTCGGTTCTCGGGCTCGGGAAGCGGCACCGACTTTACCCTGACCATTAG
CAGCCTGCAGCCCGAGGACTTCGCAACCTACTACTGTCAGCAGTCTACTCAACCC
CTCACTTCGGACAGGGTACTAGACTCGAGATCAAGAGGACTGTGGCCGCGCCGTCG
GTGTTTCATCTTCCCACCCTCGGACGAGCAGCTGAAGTCCGGCACCGCCAGCGTGGT
CTGCCTGCTGAACAACCTTCTATCCGCGCGAAGCCAAGGTCCAGTGGAAAGTGGATA
ATGCGCTGCAGAGCGGGAACCTCCAAGAGTCCGTGACGGAACAGGACTCCAAAGAC
TCCACCTACTCACTGTCATCCACCCTGACCCTGTCAAAGGCCGACTACGAGAAGCA
TAAGGTCTACGCCTGCGAAGTGACCCACCAAGGGCTGAGCTCGCCCCGTGACCAAGT
CCTTCAACCGGGGCGAATGC (SEQ ID NO:92)

3-F03_413 heavy chain DNA sequence

GAAGTGCAGTTGGTGGAGAGCGGGGGCGGACTGGTGCAGCCGGGGGGCTCGCTGCG
GCTGTCCTGCGCCGCGTCCGGTTTCACTTTTTTCGAGCTACGACATGCACTGGGTCC
GCCAAGCACCGGGGAAGGGTCTGGAATGGGTGGCCGTGATGTCGTACGAAGGCTCC
AACAAGTACTACGCCGACTCCGTGAAGGGACGGTTCACCATCTCCCGCGACAACAG
CAAGAACGCCCTTTACCTCCAAATGAACAGCCTGAGGGCCGAGGACACAGCCGTAT
ACTACTGCGCGACCGAGATCGCCGCCAAGGGGGACTACTGGGGTCAAGGCACTCTG
GTCACCGTGTCCTCCGCCTCCACTAAGGGACCCTCAGTGTTCCCCCTTGCCCCGAG
CTCCAAGAGCACTTCGGGCGGAACCGCTGCCCTGGGTGTCCTCGTGAAGGATTACT
TCCCCGAGCCTGTGACCGTGTCCTGGAACCTCCGGGGCCTTGACCAGCGGAGTCCAC
ACCTTCCCGGCCGTGCTGCAATCATCCGGTCTGTACAGTCTGTCTCCGTGGTCAC
GGTGCCCTCGTCCTCACTGGGGACTCAGACTTACATCTGTAACGTGAACCATAAGC
CATCGAACACCAAAGTCGACAAACGGGTGGAACCTAAGTCATGCGACAAGACCCAC
ACGTGCCCACCTTGCCCCGCCCCCGAGCTCCTGGGGGGGCCGAGCGTGTTCTCTT
CCCGCCGAAACCGAAGGACACCCTGATGATCTCGAGGACTCCTGAAGTCACTTGCG
TGGTCGTGGACGTGTCGCACGAGGACCCCGAAGTCAAGTTCAATTGGTACGTGGAC
GGAGTCGAAGTGCACAACGCTAAGACCAAACCCCGCGAGGAGCAGTACGCAAGCAC
CTACCGCGTTGTCAGCGTGCTCACCGTGCTGCATCAGGATTGGCTGAATGGAAAGG
AGTACAAGTGCAAAGTGTCCAACAAGGCCCTGCCTGCACCAATTGAAAAGACCATC
TCCAAGGCCAAGGGCCAGCCCCGGGAGCCCCAAGTCTACACTCTGCCGCCGTGAG
AGAAGAAATGACCAAGAACCAAGTGTCCCTGACTTGTCTGGTCAAGGGCTTCTATC
CTTCGACATCGCGGTGGAATGGGAGAGCAACGGCCAGCCGGAGAACAATTACAAG
ACTACGCCACCCGTGCTGGACTCTGACGGCTCCTTTTTCTGTATTCCAAGCTCAC
CGTGGACAAGAGCCGCTGGCAACAGGGAAACGTGTTTCAAGCTGCTCCGTGATGCACG
AAGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCTTGTCCCCTGGT (SEQ
ID NO:93)