

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

EVQLVQSGAEVKKPGESLKISCKGSGYTFTSYGLSWVRQMPGKGLEWMGEIYPGSG
NTYYNEKFKGQVTISADKSISTAYLQWSSLKASDTAMYICARYDYLGSSYGFDYWG
AGTTVTVSS (SEQ ID NO:22)

CL25_hu_10-4 VL

DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYS
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

DIQMTQSPSSLSASVGDRVTITCKASQDVSTAVAWYQQKPGKAPKLLIYSASYRYS
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      RFTSGSGSGTDFTLTISSVQAEDLAVYYCQQHYNTPYTFGGGTKLEIK 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

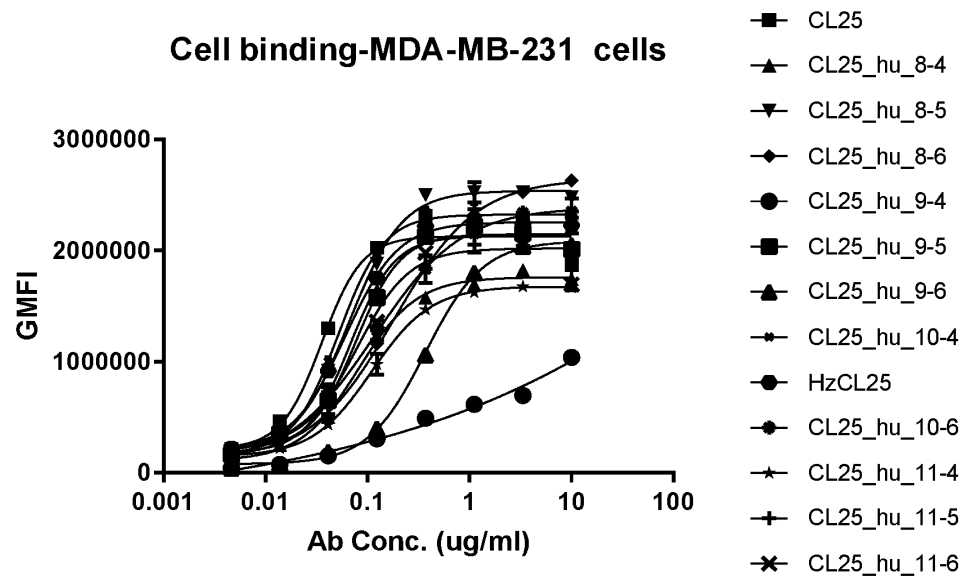


FIG. 2B

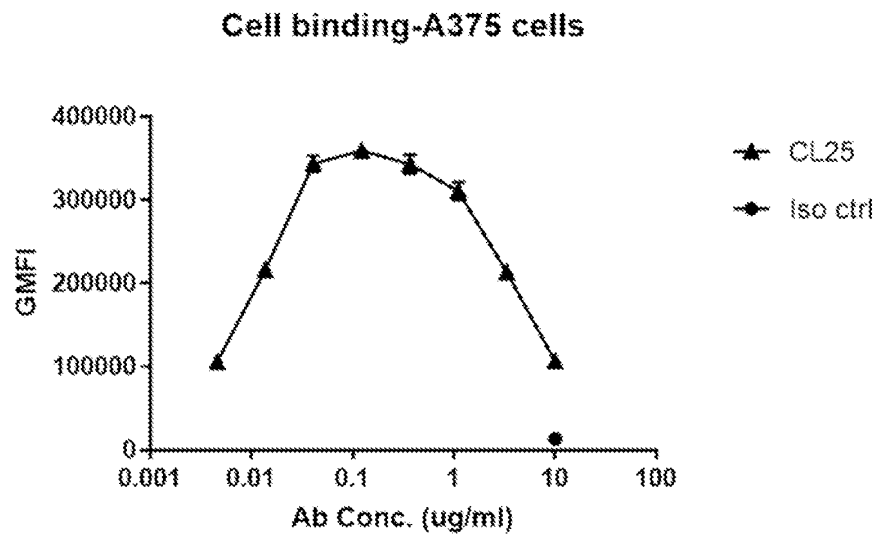


FIG. 3A

Cellular CD73 inhibition - A375 cells

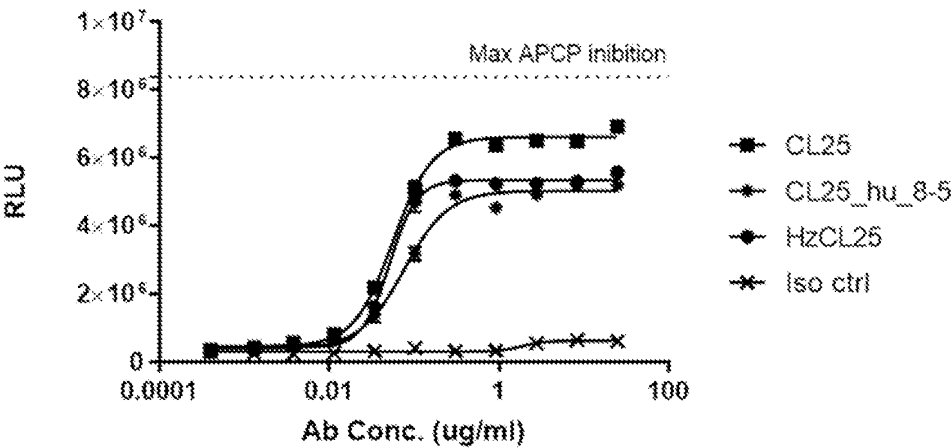


FIG. 3B

Cellular CD73 inhibition - MDA-MB-231 cells

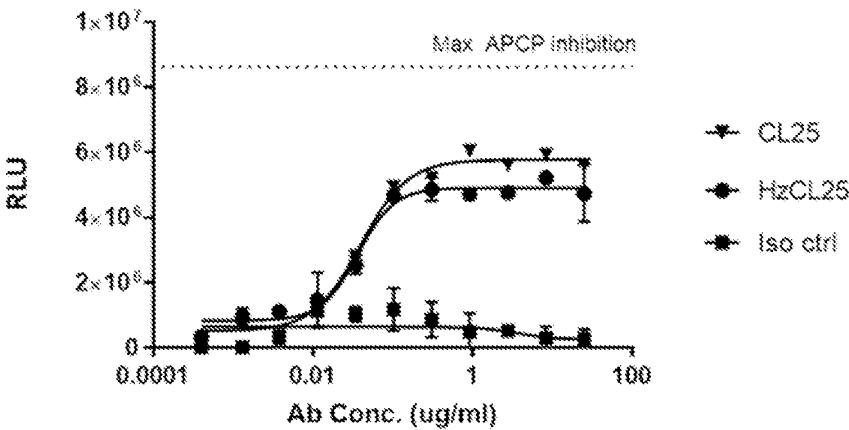


FIG. 3C

Cellular CD73 inhibition - MDA-MB-231 cells

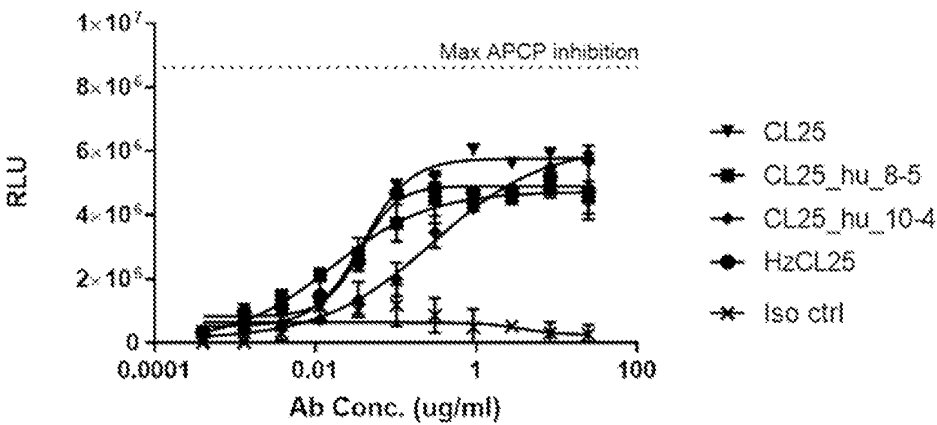


FIG. 4

Recombinant CD73 inhibition

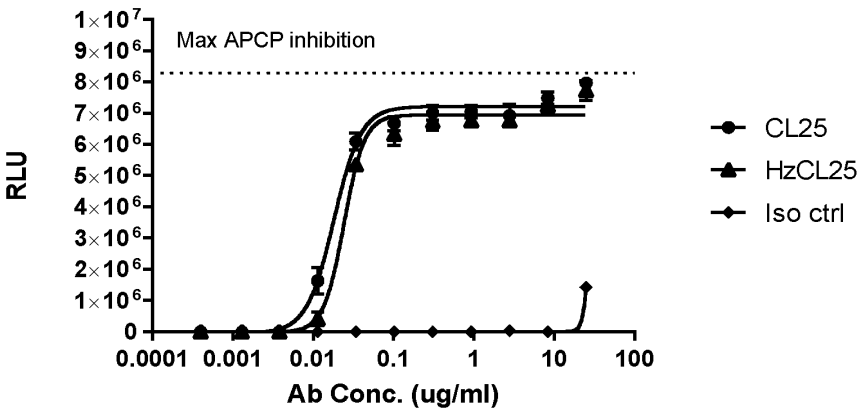


FIG. 5A

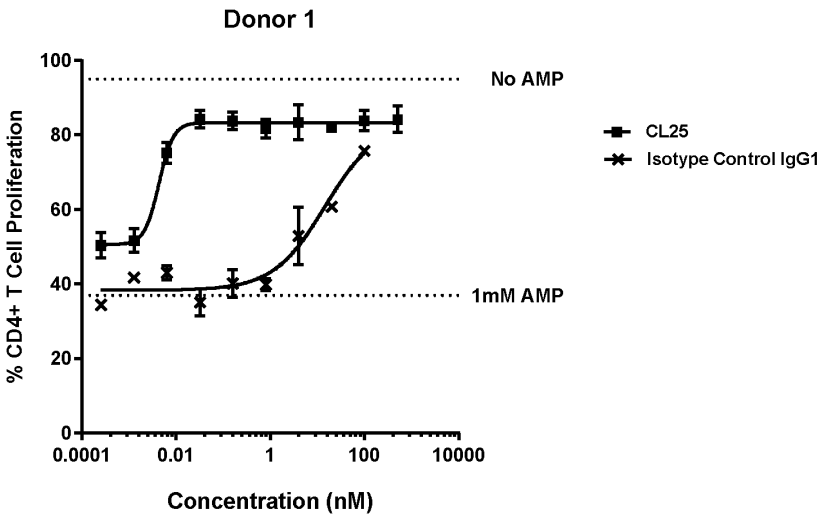


FIG. 5B

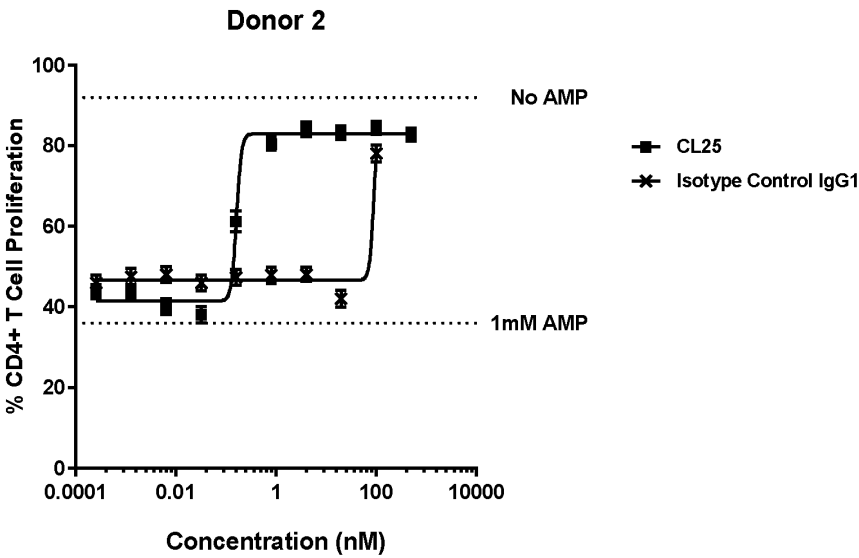


FIG. 5C

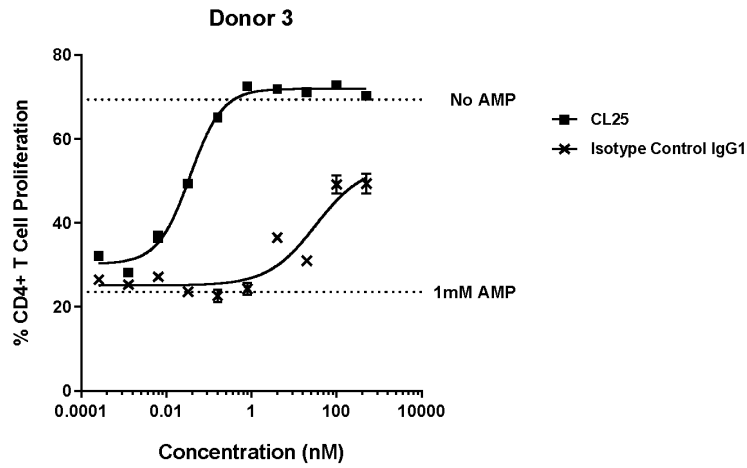


FIG. 5D

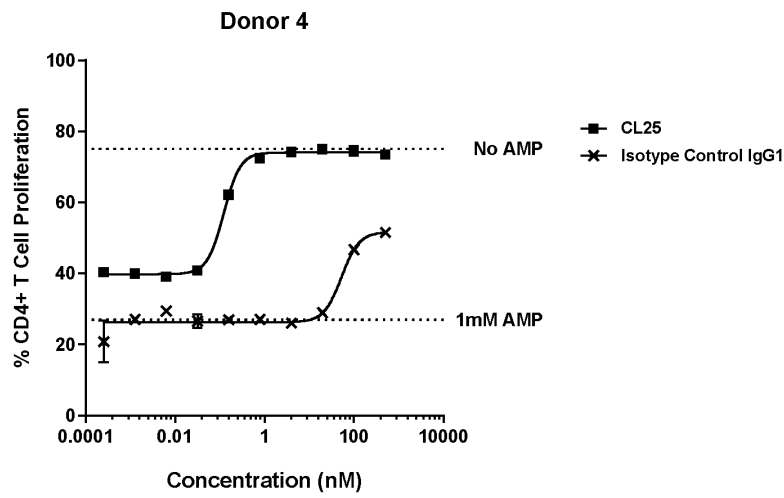


FIG. 5E

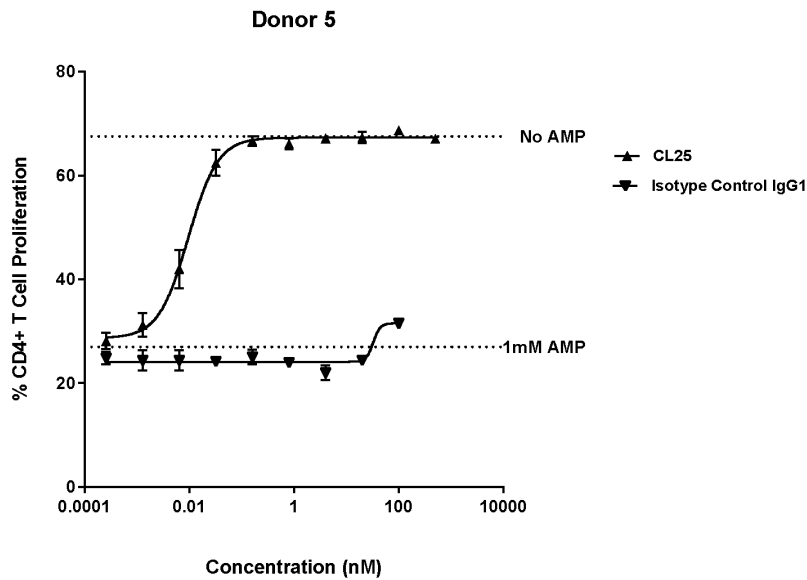


FIG. 5F

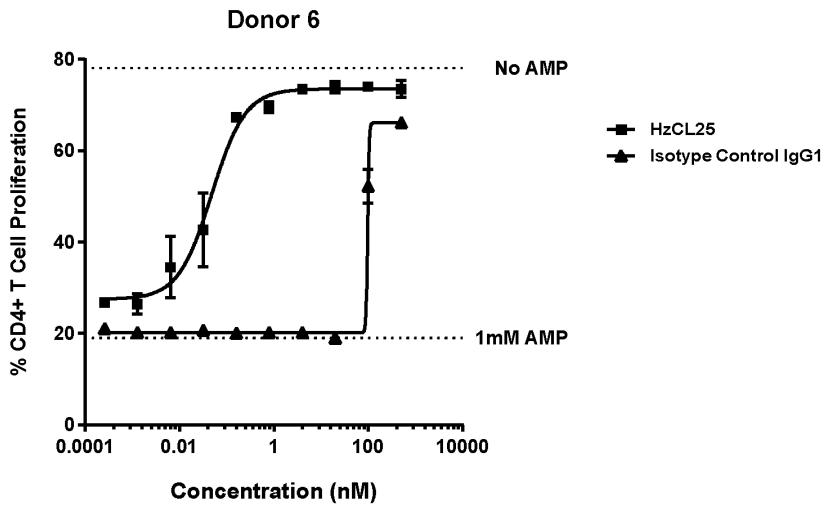


FIG. 5G

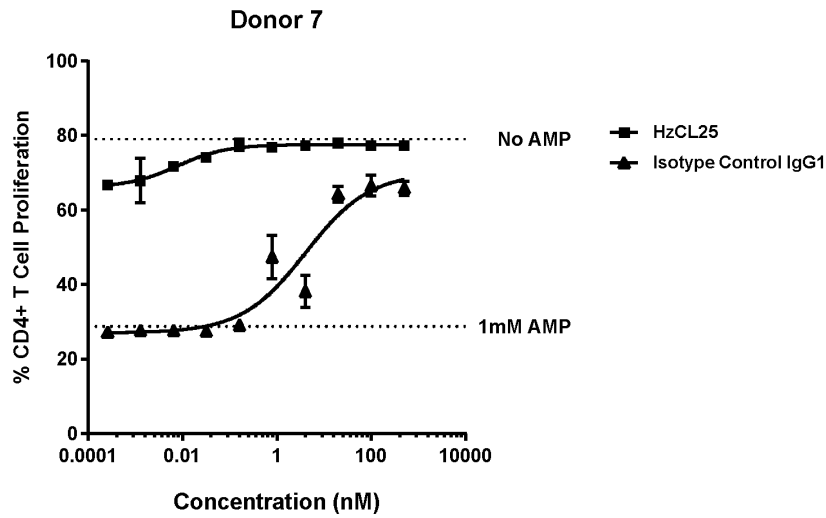


FIG. 5H

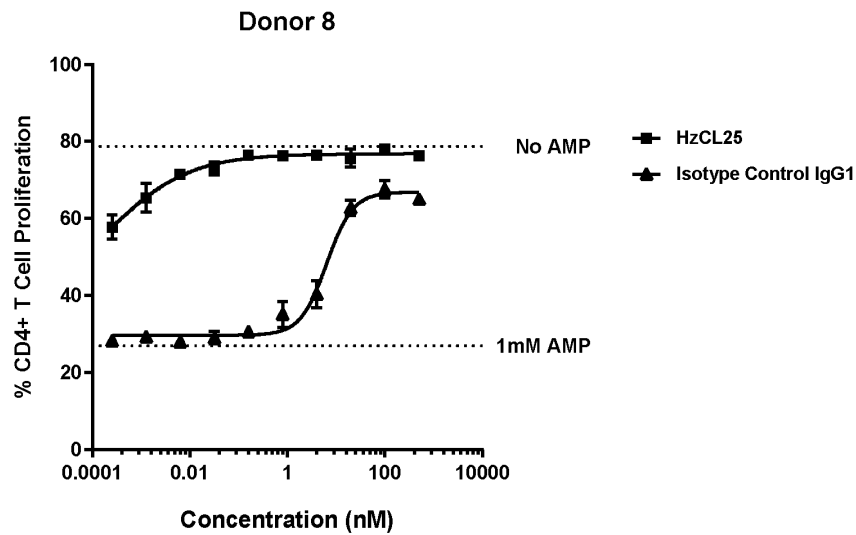


FIG. 5I

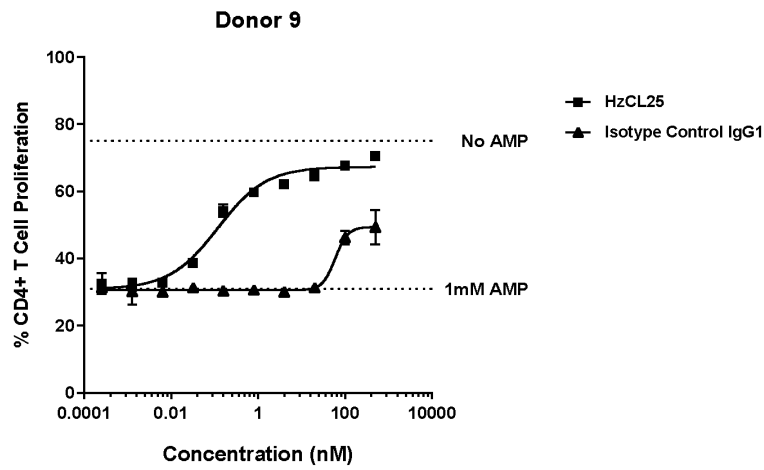


FIG. 5J

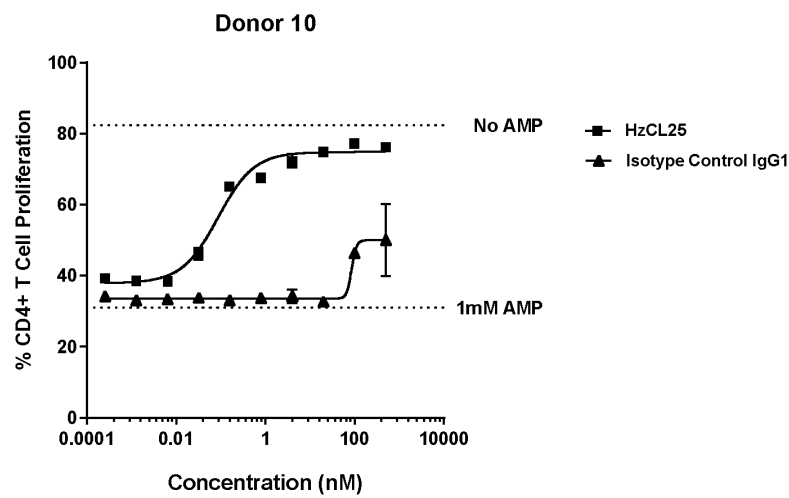


FIG. 5K

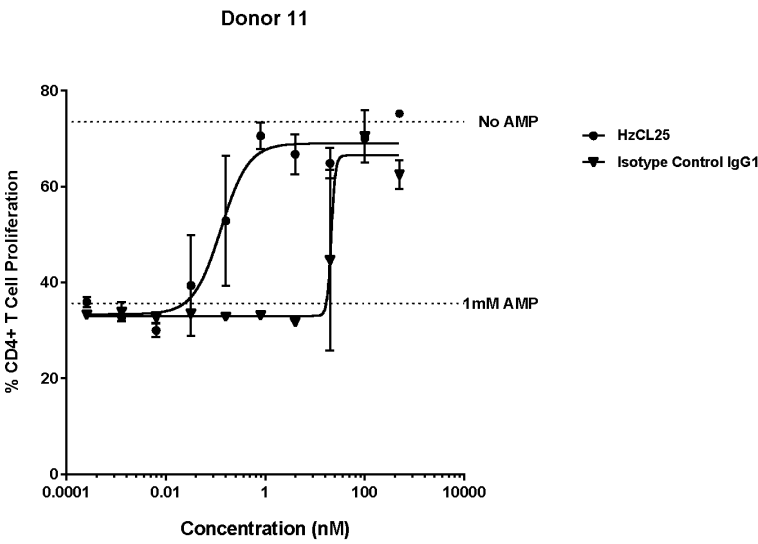


FIG. 5L

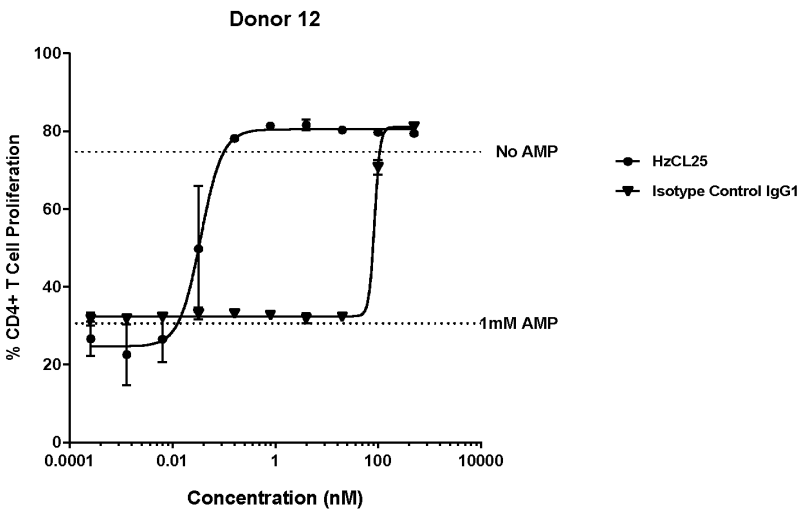


FIG. 5M

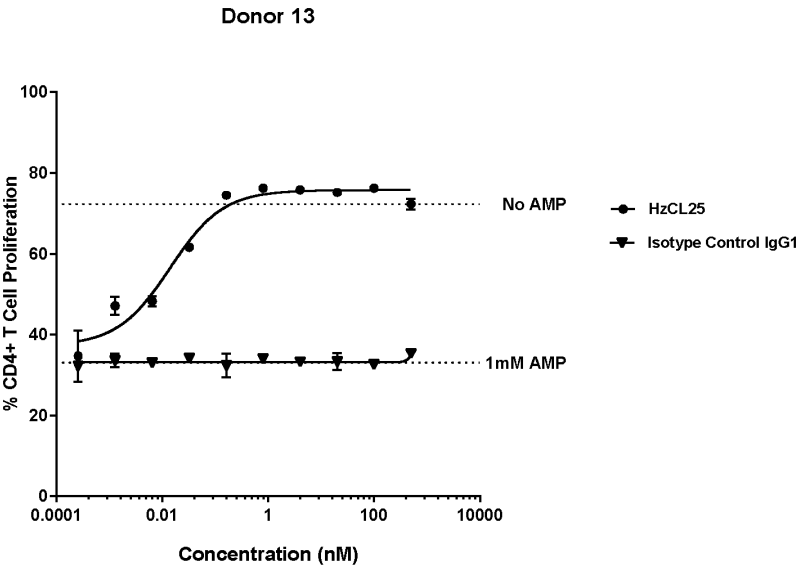


FIG. 5N

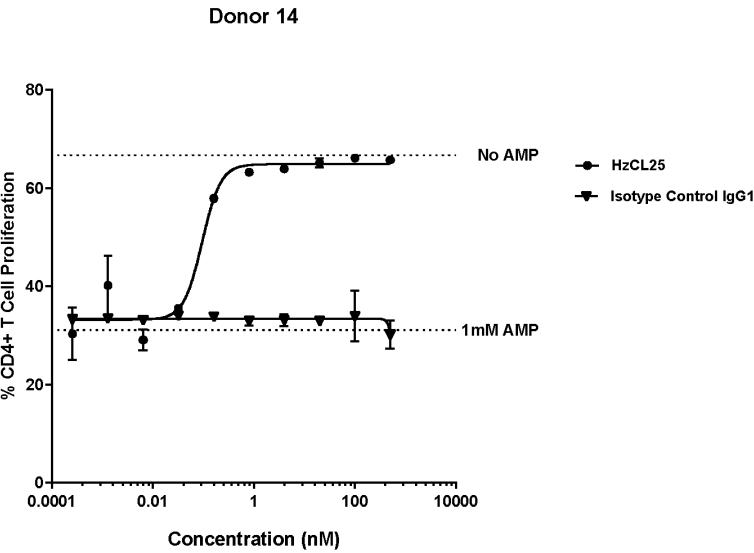


FIG. 6

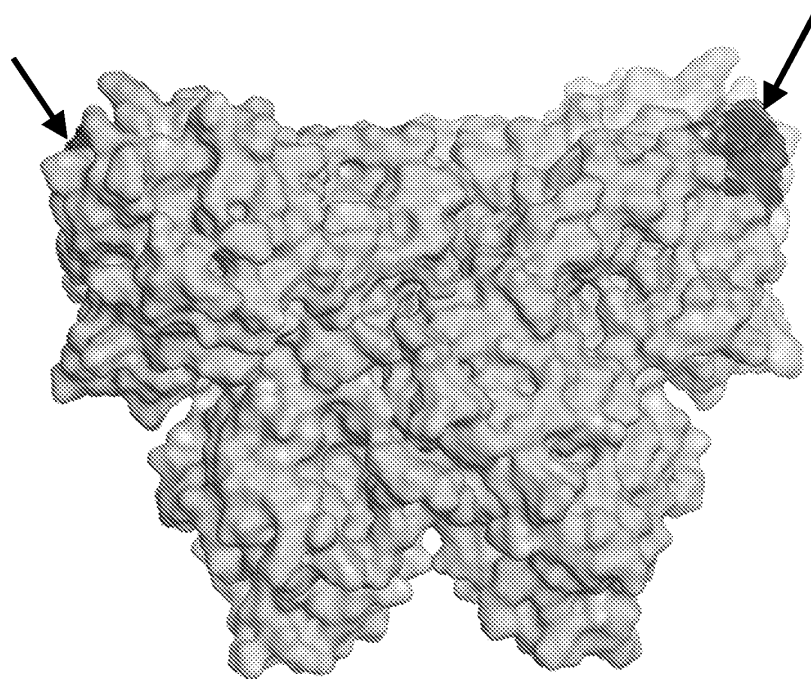


FIG. 7

Surface CD73 after 24 hour antibody incubation

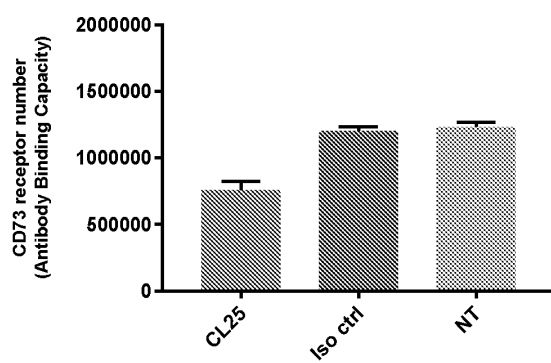


FIG. 8

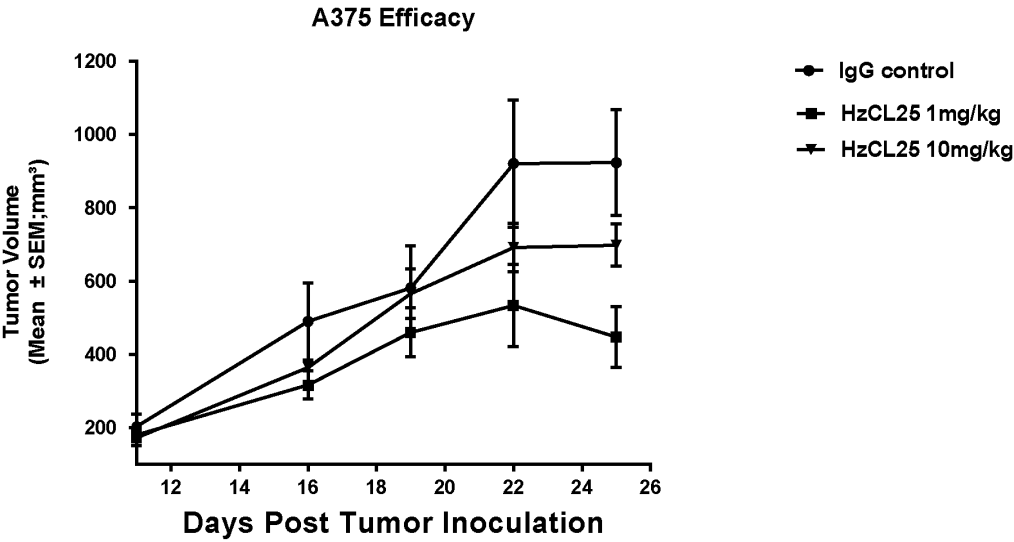


FIG. 9

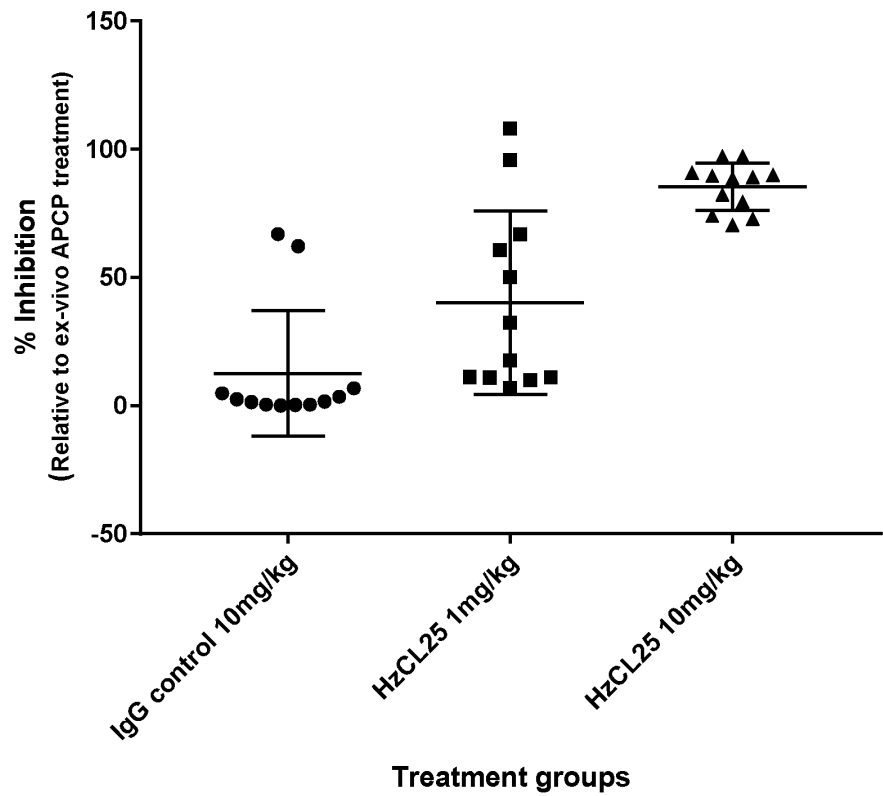


FIG. 10A

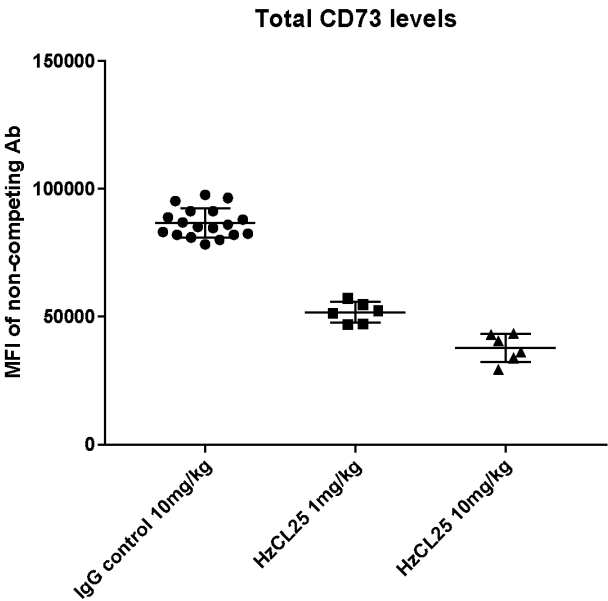


FIG. 10B

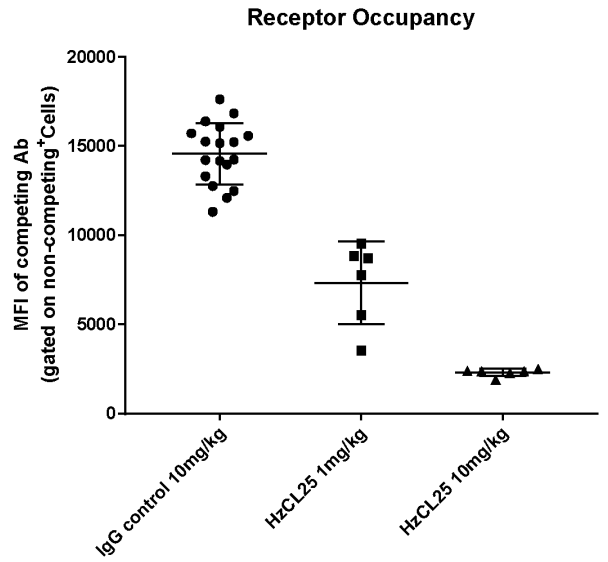


FIG. 11A

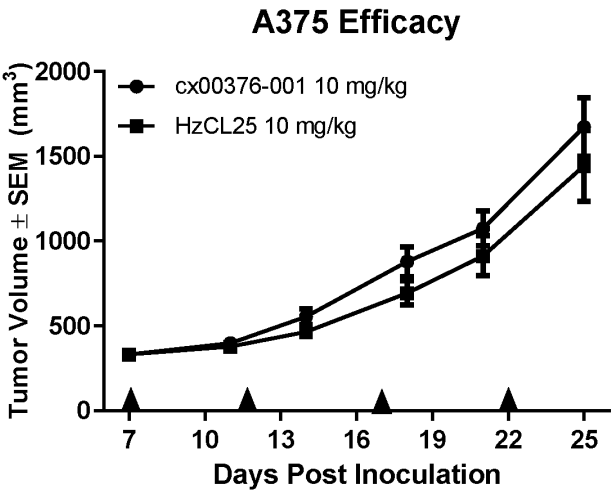


FIG. 11B

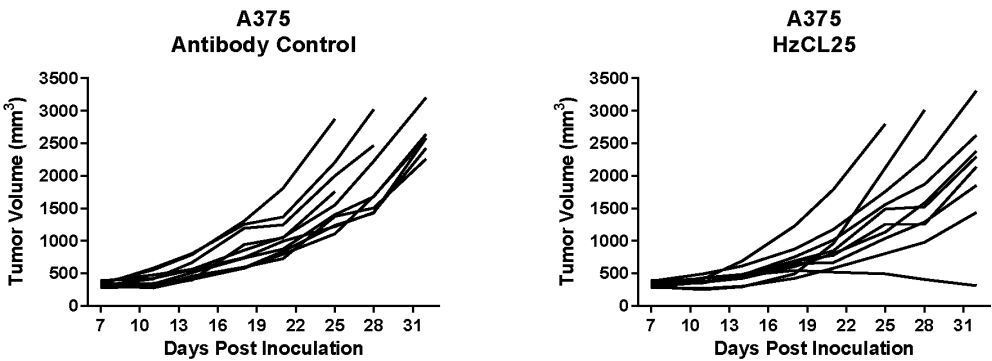
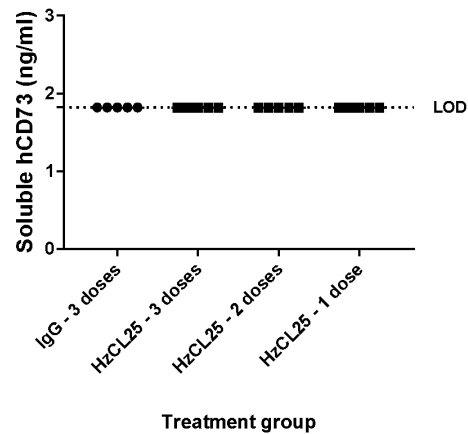


FIG. 12

Free soluble hCD73 in mouse sera following antibody treatment
Detection w /competing Ab



Total soluble hCD73 in mouse sera following antibody treatment
Detection with non-competing Ab

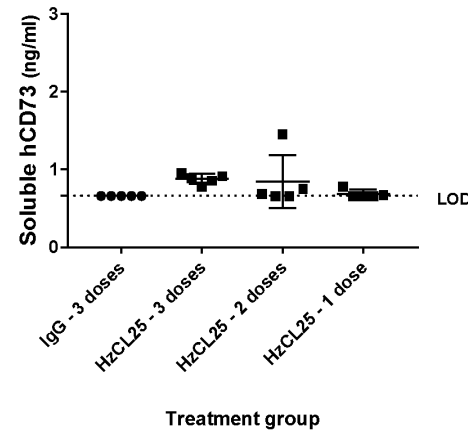


FIG. 13A

Cell binding-MDA-MB-231cells

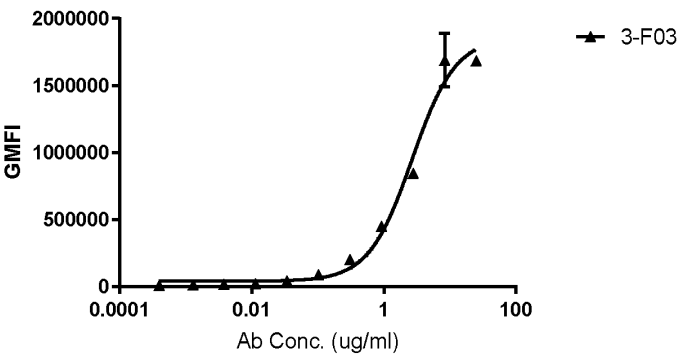


FIG. 13B

Cell binding-A375 cells

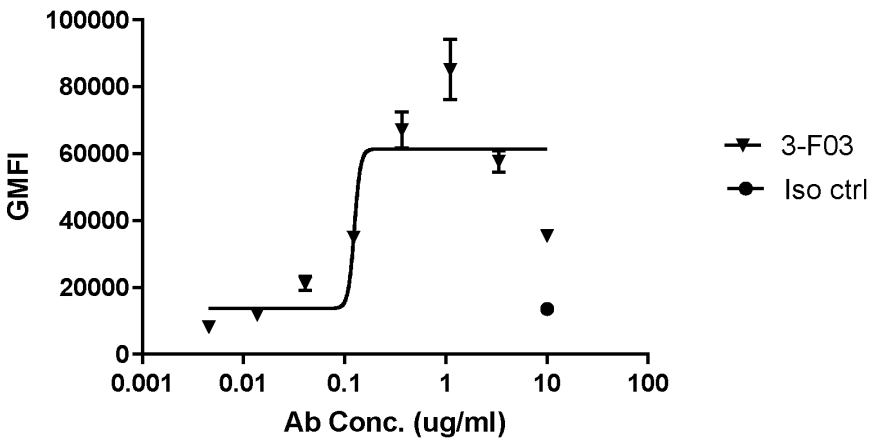


FIG. 14A

Cellular CD73 inhibition - A375 cells

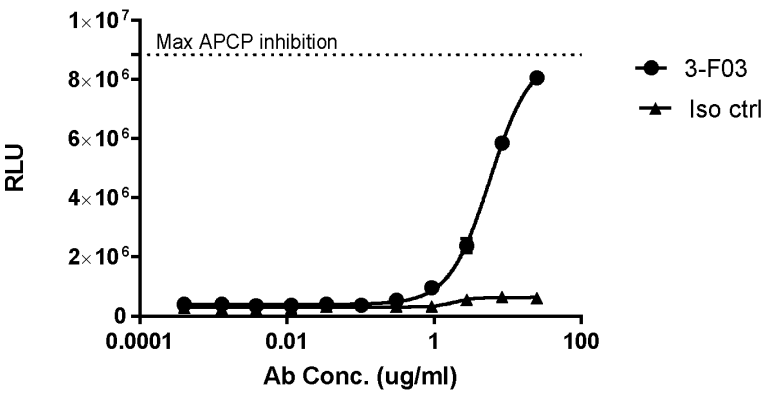


FIG. 14B

Cellular CD73 Inhibition- MDA-MB-231 cells

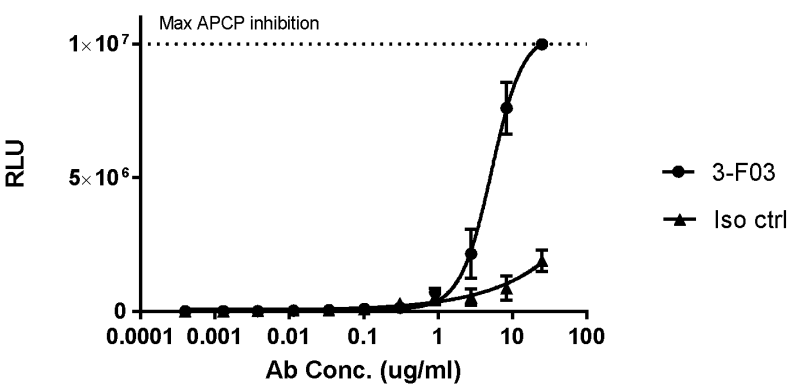


FIG. 15

Recombinant CD73 inhibition

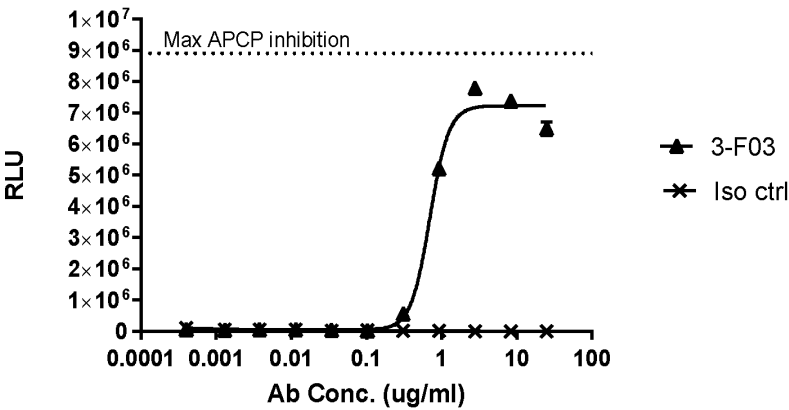


FIG. 16A

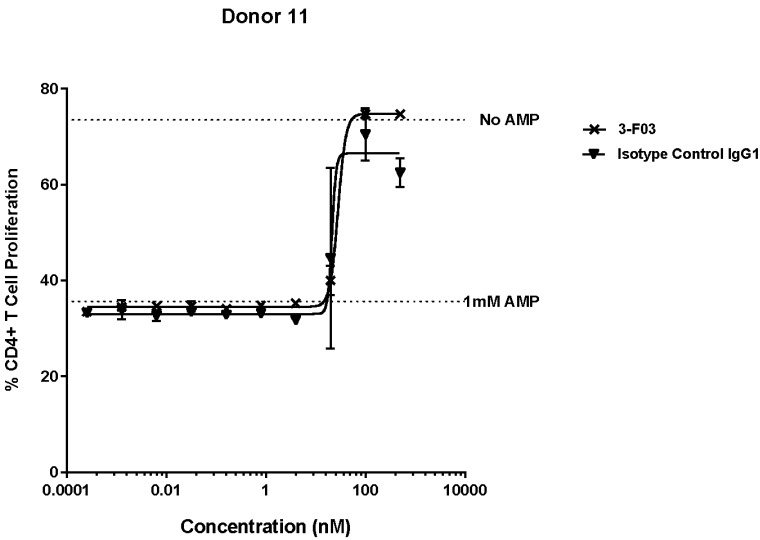


FIG. 16B

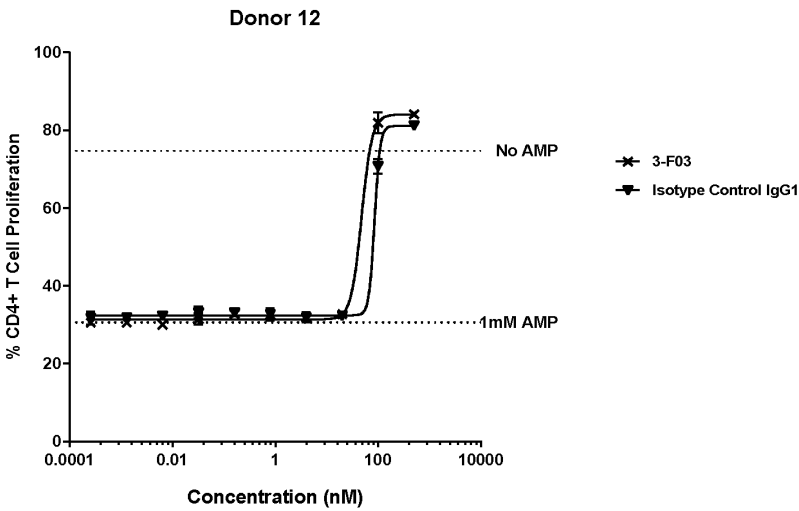


FIG. 16C

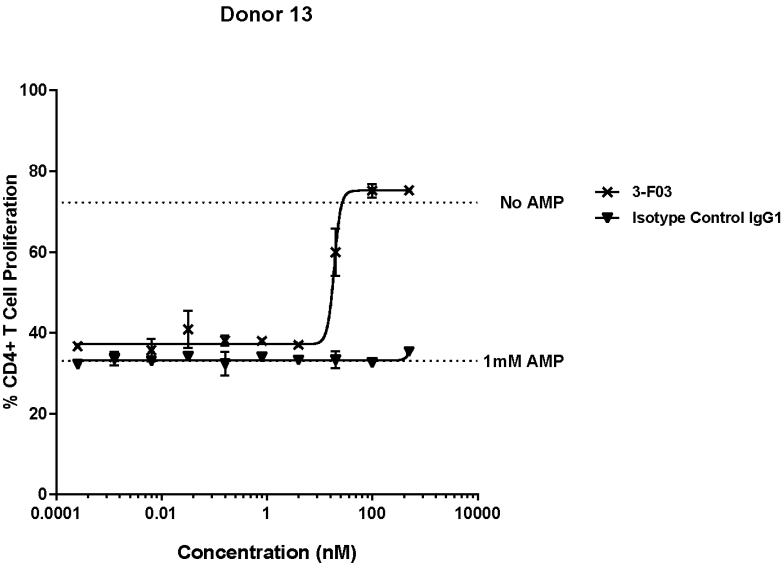


FIG. 16D

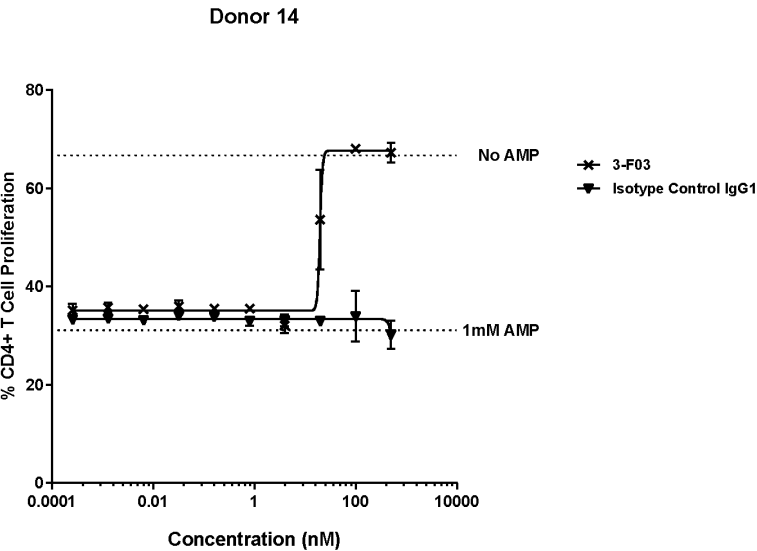


FIG. 17

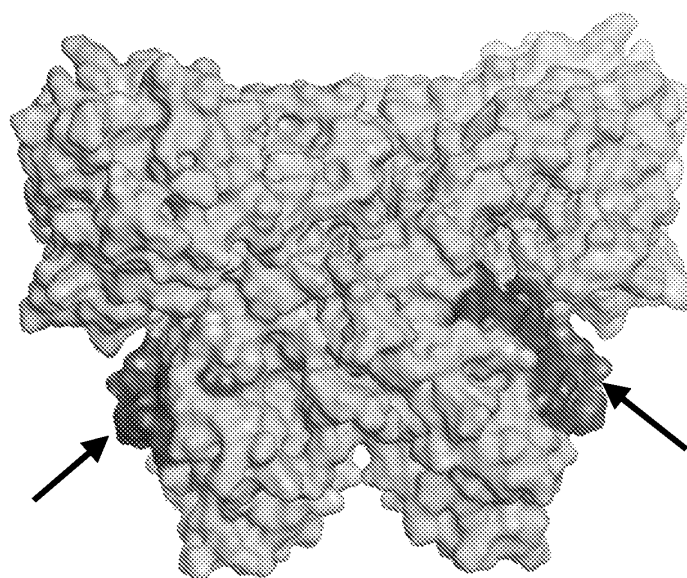


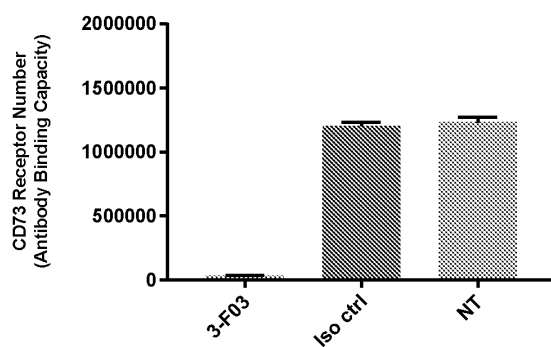
FIG. 18**Surface CD73 after 24 hour antibody incubation**

FIG. 19A

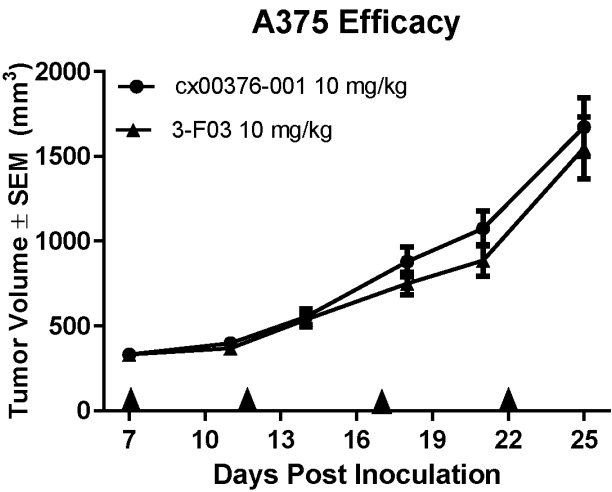


FIG. 19B

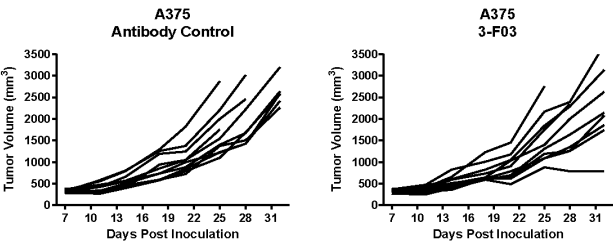
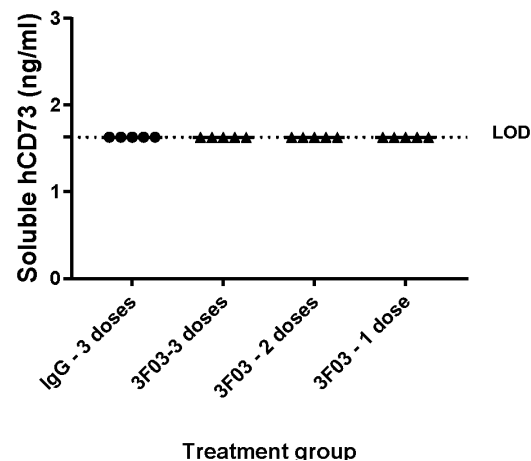


FIG. 20

Total soluble hCD73 in mouse sera following antibody treatment
Detection with non-competing Ab



Free soluble hCD73 in mouse sera following antibody treatment
Detection with competing Ab

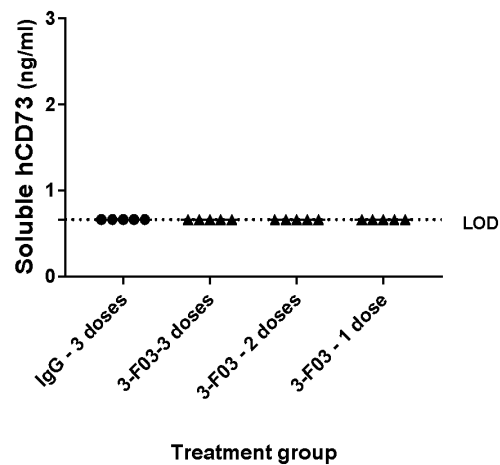


FIG. 21A**3-F03_VH_yeast**

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. 21B**3-F03_396_VH**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:77)

3-F03_396_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:65)

3-F03_408_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:77)

3-F03_408_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
VPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:61)

3-F03_402_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:85)

3-F03_402_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:65)

3-F03_384_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:77)

3-F03_384_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:64)

FIG. 21C**3-F03_399_VH**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:62)

3-F03_399_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:65)

3-F03_414_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:85)

3-F03_414_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:61)

3-F03_390_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:85)

3-F03_390_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:64)

3-F03_398_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGS
NKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:86)

3-F03_398_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:65)

FIG. 21D**3-F03_387_VH**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGS
NKYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTSS (SEQ ID NO:62)

3-F03_387_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:64)

3-F03_386_VH

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

3-F03_386_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:64)

3-F03_401_VH

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

3-F03_401_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS
GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:65)

3-F03_410_VH

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

3-F03_410_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSG
VPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:61)

FIG. 21E**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

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGSN
KYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:87)

3-F03_392_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:64)

3-F03_404_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGSN
KYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:87)

3-F03_404_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:65)

3-F03_419_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGSN
KYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:88)

3-F03_419_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:61)

FIG. 21F**3-F03_416_VH**

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGSN
KYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:87)

3-F03_416_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:61)

3-F03_407_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGSN
KYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:88)

3-F03_407_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:65)

3-F03_395_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYEGSN
KYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:88)

3-F03_395_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:64)

3-F03_388_VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGS
NKYYADSVKGRFTISRDN SKNLYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:69)

3-F03_388_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:64)

FIG. 21G**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. 21H**3-F03_403_VH**

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

3-F03_403_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:65)

3-F03_415_VH

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

3-F03_415_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSG VPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:61)

3-F03_391_VH

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

3-F03_391_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:64)

3-F03_406_VH

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

3-F03_406_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQS GVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPHFGQGT
RLEIK (SEQ ID NO:65)

FIG. 21I**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

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGSN
KYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:67)

3-F03_394_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:64)

3-F03_418_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYSGSN
KYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:67)

3-F03_418_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:61)

3_F03_417_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGSN
KYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LTVSS (SEQ ID NO:60)

3_F03_417_VL

IQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK (SEQ
ID NO:61)

FIG. 21J**3_F03_393_VH**

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGSN
KYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:60)

3_F03_393_VL

DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:64)

3_F03_405_VH

VQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVMSYDGSN
KYYADSVKGRFTISRDN SKNALYLQMNSLRAEDTAVYYCATEIAAKGDYWGQGT
LVTVSS (SEQ ID NO:60)

3_F03_405_VL

AIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKAPKLLIYAAS
TLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPHFGQGTRLEIK
(SEQ ID NO:65)

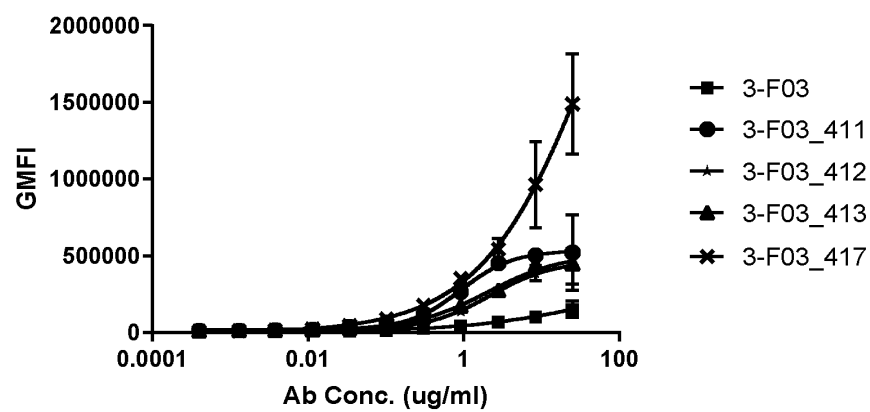
FIG. 22**Cell binding-MDA-MB-231 cells**

FIG. 23

Cellular CD73 inhibition - MDA-MB-231 cells

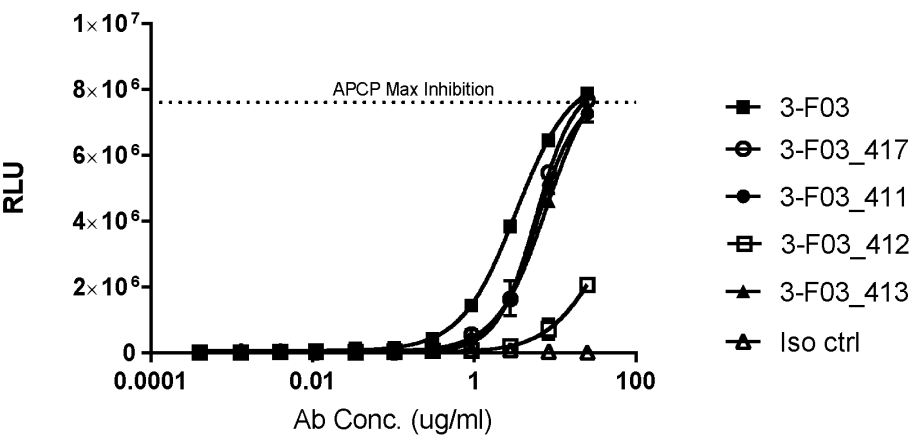


FIG. 24**Human IgG1 heavy chain CH1-hinge-CH2-CH3, with N297A mutation**

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. 25A**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
CGGTTCTCCGGCTCGGGTTCCGGAACCTGATTTACCCTGACAATTTCTGCTGCTGCAAGCC
GAGGACGTGGCCGTGTACTACTGCCAACAGCATTACAACACTCCTTACACTTTTGGTGGC
GGAACCTAAGCTCGAGATCAAGCGGACGGTGGCAGCTCCGTCAGTGTTTCATCTTCCCTCCA
TCGGACGAACAGCTGAAGTCCGGCACCGCGTCCGTGCTGTGTCTGTTGAACAACCTTCTAC
CCGCGGGAAGCCAAGGTCCAGTGGAAAGTCGACAACGCGCTGCAGTCCGGAAATAGCCAG
GAAAGCGTGACCGAACAGGACTCCAAGGACAGCACCTACTCCCTGAGCTCAACCCTGACC
CTGAGCAAGGCCGACTATGAGAAGCACAAAGTGACGCTGCGAAGTGACCCACCAAGGC
CTGAGCAGCCCAGTGACCAAGTCCTTCAACCGCGGGGAGTGT (SEQ ID NO:90)

FIG. 25B**3-F03_411 heavy chain DNA sequence**

GAAGTGCAGTTGGTGGAGAGCGGGGGCGGACTGGTGCAGCCGGGGGGCTCGCTGCG
GCTGTCCTGCGCCGCGTCCGGTTTCACTTTTTTCGAGCTACGACATGCACTGGGTCC
GCCAAGCACCGGGGAAGGGTCTGGAATGGGTGGCCGTGATGTCGTACGACGGCTCC
AACAAGTACTACGCCGACTCCGTGAAGGGACGGTTCACCATCTCCCGCGACAACAG
CAAGAACGCCCTTTACCTCCAAATGAACAGCCTGAGGGCCGAGGACACAGCCGTAT
ACTACTGCGCGACCGAGATCGCCGCCAAGGGGGACTACTGGGGTCAAGGCACTCTG
GTCACCGTGTCTCCGCCTCCACTAAGGGACCCTCAGTGTTCCCCCTTGCCCCGAG
CTCCAAGAGCACTTCGGGCGGAACCGCTGCCCTGGGTTCCTCGTGAAGGATTACT
TCCCCGAGCCTGTGACCGTGTCTTGGAACCTCCGGGGCCTTGACCAGCGGAGTCCAC
ACCTTCCCGGCCGTGCTGCAATCATCCGGTCTGTACAGTCTGTCTCCGTGGTCAC
GGTGCCCTCGTCTCACTGGGGACTCAGACTTACATCTGTAACGTGAACCATAAGC
CATCGAACACCAAAGTCGACAAACGGGTGGAACCTAAGTCATGCGACAAGACCCAC
ACGTGCCCACCTTGCCCCGCCCCCGAGCTCCTGGGGGGCCGAGCGTGTTCTCTT
CCCGCCGAAACCGAAGGACACCCTGATGATCTCGAGGACTCCTGAAGTCACTTGCG
TGGTTCGTGGACGTGTGCGACGAGGACCCCGAAGTCAAGTTCAATTGGTACGTGGAC
GGAGTCGAAGTGCAACGCTAAGACCAAACCCGCGAGGAGCAGTACGCAAGCAC
CTACCGCGTTGTCAGCGTGCTCACCGTGCTGCATCAGGATTGGCTGAATGGAAAGG
AGTACAAGTGCAAAGTGTCCAACAAGGCCCTGCCTGCACCAATTGAAAAGACCATC
TCCAAGGCCAAGGGCCAGCCCCGGGAGCCCCAAGTCTACACTCTGCCGCCGTGAG
AGAAGAAATGACCAAGAACCAAGTGTCCCTGACTTGTCTGGTCAAGGGCTTCTATC
CTTCGGACATCGCGGTGGAATGGGAGAGCAACGGCCAGCCGGAGAACAATTACAAG
ACTACGCCACCCGTGCTGGACTCTGACGGCTCCTTTTTCTGTATTCCAAGCTCAC
CGTGGACAAGAGCCGCTGGCAACAGGGAAACGTGTTCAAGCTGCTCCGTGATGCACG
AAGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCTTGTCCCCTGGT (SEQ
ID NO: 91)

FIG. 25C**3-F03_411 and 3-F03_413 light chain DNA sequence**

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

3-F03_413 heavy chain DNA sequence

GAAGTGACAGTTGGTGGAGAGCGGGGGCGGACTGGTGCAGCCGGGGGGCTCGCTGCG
GCTGTCTGCGCCGCGTCCGGTTTCACTTTTTTCGAGCTACGACATGCACTGGGTCC
GCCAAGCACCGGGGAAGGGTCTGGAATGGGTGGCCGTGATGTCGTACGAAGGCTCC
AACAAGTACTACGCCGACTCCGTGAAGGGACGGTTCACCATCTCCCGCGACAACAG
CAAGAACGCCCTTTACCTCCAAATGAACAGCCTGAGGGCCGAGGACACAGCCGTAT
ACTACTGCGCGACCGAGATCGCCGCCAAGGGGGACTACTGGGGTCAAGGCACTCTG
GTCACCGTGTCCTCCGCCTCCACTAAGGGACCCTCAGTGTTCCCCCTTGCCCCGAG
CTCCAAGAGCACTTCGGGCGGAACCGCTGCCCTGGGTGTCCTCGTGAAGGATTACT
TCCCCGAGCCTGTGACCGTGTCCTGGAACCTCCGGGGCCTTGACCAGCGGAGTCCAC
ACCTTCCCGGCCGTGCTGCAATCATCCGGTCTGTACAGTCTGTCTCCGTGGTCAC
GGTGCCCTCGTCCTCACTGGGGACTCAGACTTACATCTGTAACGTGAACCATAAGC
CATCGAACACCAAAGTCGACAAACGGGTGGAACCTAAGTCATGCGACAAGACCCAC
ACGTGCCCACCTTGCCCCGCCCCCGAGCTCCTGGGGGGCCGAGCGTGTTCTCTT
CCCGCCGAAACCGAAGGACACCCTGATGATCTCGAGGACTCCTGAAGTCACTTGCG
TGGTCGTGGACGTGTGCGACGAGGACCCCGAAGTCAAGTTCAATTGGTACGTGGAC
GGAGTCGAAGTGCACAACGCTAAGACCAAACCCCGCGAGGAGCAGTACGCAAGCAC
CTACCGCGTTGTCAGCGTGCTCACCGTGCTGCATCAGGATTGGCTGAATGGAAAGG
AGTACAAGTGCAAAGTGTCCAACAAGGCCCTGCCTGCACCAATTGAAAAGACCATC
TCCAAGGCCAAGGGCCAGCCCCGGGAGCCCCAAGTCTACACTCTGCCGCCGTGAG
AGAAGAAATGACCAAGAACCAAGTGTCCCTGACTTGTCTGGTCAAGGGCTTCTATC
CTTCGACATCGCGGTGGAATGGGAGAGCAACGGCCAGCCGGAGAACAATTACAAG
ACTACGCCACCCGTGCTGGACTCTGACGGCTCCTTTTTCTGTATTCCAAGCTCAC
CGTGGACAAGAGCCGCTGGCAACAGGGAAACGTGTTTCAAGCTGCTCCGTGATGCACG
AAGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCTTGTCCCCTGGT (SEQ
ID NO:93)

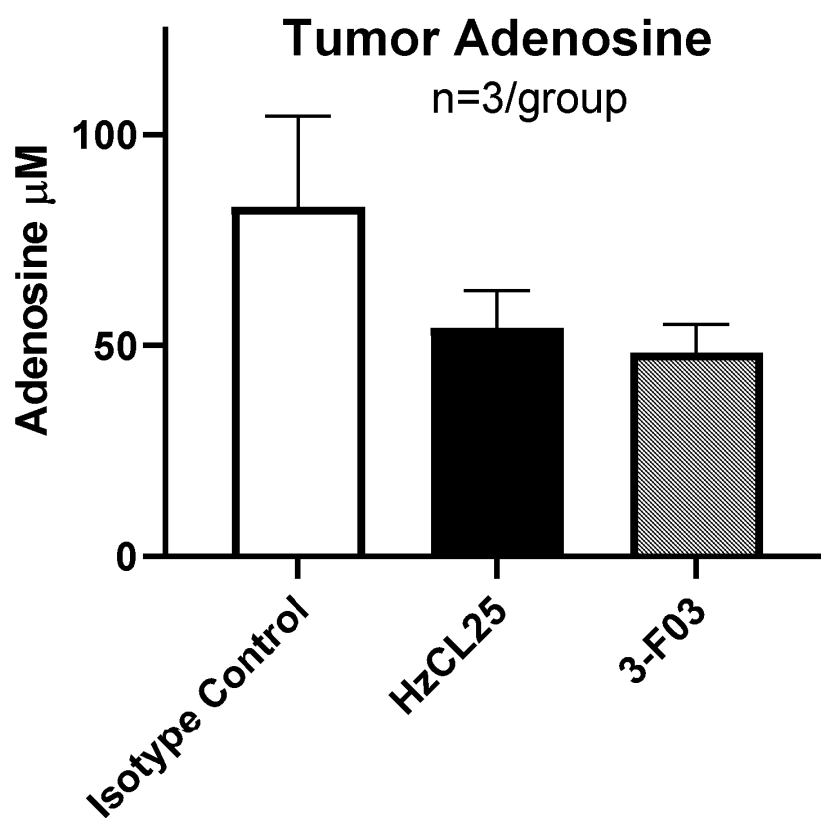
FIG. 26

FIG. 27

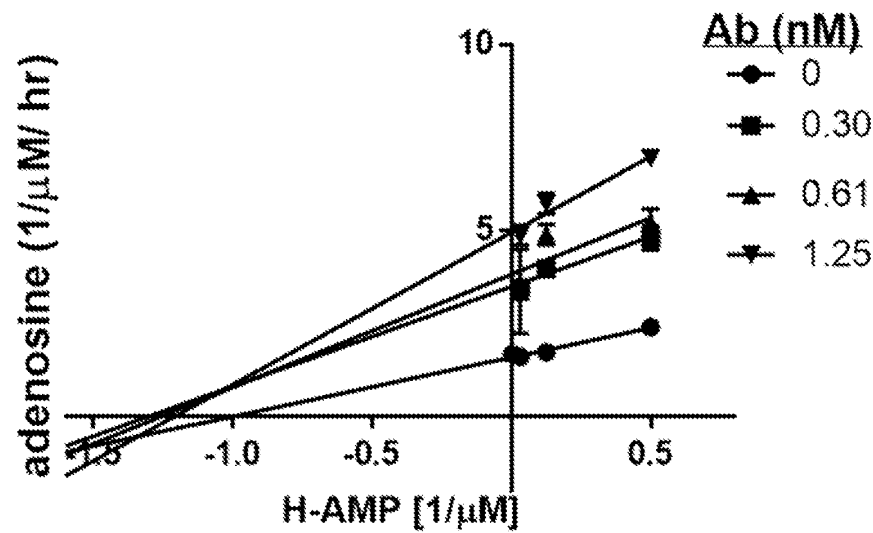


FIG. 28

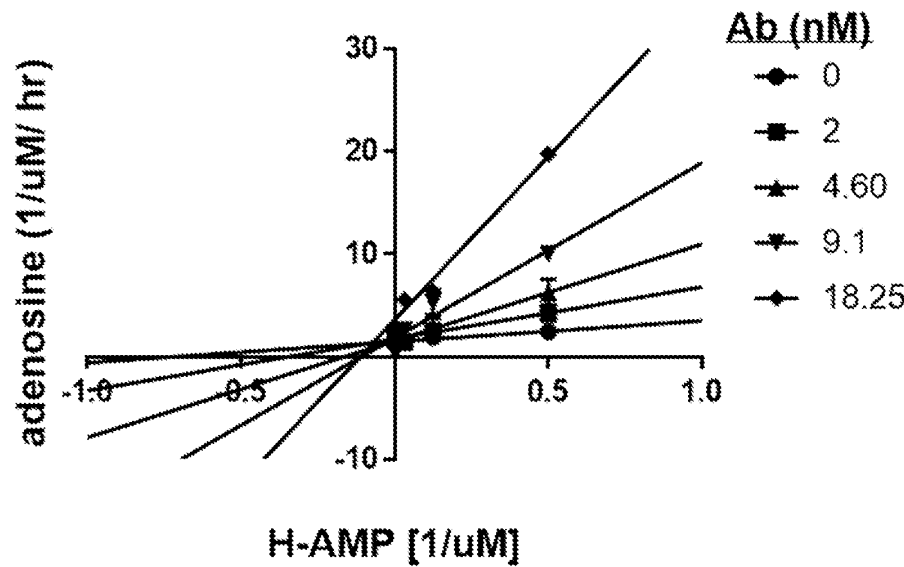


FIG. 29

