SEQUENCE LISTING

<110> Perseus Proteomics Inc.

<120> Anti-CDH3 humanized antibody, its drug condugate, and use thereof

<130> 131977A

<160> 79

<170> PatentIn version 3.5

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1               5                   10                  15

tgc tgg ctg cag tgc gcg gcc tcc gag ccg tgc cgg gcg gtc ttc agg        96
Cys Trp Leu Gln Cys Ala Ala Ser Glu Pro Cys Arg Ala Val Phe Arg
            20                  25                  30

gag gct gaa gtg acc ttg gag gcg gga ggc gcg gag cag gag ccc ggc       144
Glu Ala Glu Val Thr Leu Glu Ala Gly Gly Ala Glu Gln Glu Pro Gly
        35                  40                  45

cag gcg ctg ggg aaa gta ttc atg ggc tgc cct ggg caa gag cca gct       192
Gln Ala Leu Gly Lys Val Phe Met Gly Cys Pro Gly Gln Glu Pro Ala
    50                  55                  60

ctg ttt agc act gat aat gat gac ttc act gtg cgg aat ggc gag aca       240
Leu Phe Ser Thr Asp Asn Asp Asp Phe Thr Val Arg Asn Gly Glu Thr
65                  70                  75                  80

gtc cag gaa aga agg tca ctg aag gaa agg aat cca ttg aag atc ttc       288
Val Gln Glu Arg Arg Ser Leu Lys Glu Arg Asn Pro Leu Lys Ile Phe
                85                  90                  95
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cca tcc aaa cgt atc tta cga aga cac aag aga gat tgg gtg gtt gct        336
Pro Ser Lys Arg Ile Leu Arg Arg His Lys Arg Asp Trp Val Val Ala
            100                 105                 110
cca ata tct gtc cct gaa aat ggc aag ggt ccc ttc ccc cag aga ctg        384
Pro Ile Ser Val Pro Glu Asn Gly Lys Gly Pro Phe Pro Gln Arg Leu
        115                 120                 125
aat cag ctc aag tct aat aaa gat aga gac acc aag att ttc tac agc        432
Asn Gln Leu Lys Ser Asn Lys Asp Arg Asp Thr Lys Ile Phe Tyr Ser
    130                 135                 140
atc acg ggg ccg ggg gca gac agc ccc cct gag ggt gtc ttc gct gta        480
Ile Thr Gly Pro Gly Ala Asp Ser Pro Pro Glu Gly Val Phe Ala Val
145                 150                 155                 160
gag aag gag aca ggc tgg ttg ttg ttg aat aag cca ctg gac cgg gag        528
Glu Lys Glu Thr Gly Trp Leu Leu Leu Asn Lys Pro Leu Asp Arg Glu
                165                 170                 175
gag att gcc aag tat gag ctc ttt ggc cac gct gtg tca gag aat ggt        576
Glu Ile Ala Lys Tyr Glu Leu Phe Gly His Ala Val Ser Glu Asn Gly
            180                 185                 190
gcc tca gtg gag gac ccc atg aac atc tcc atc atc gtg acc gac cag        624
Ala Ser Val Glu Asp Pro Met Asn Ile Ser Ile Ile Val Thr Asp Gln
        195                 200                 205
aat gac cac aag ccc aag ttt acc cag gac acc ttc cga ggg agt gtc        672
Asn Asp His Lys Pro Lys Phe Thr Gln Asp Thr Phe Arg Gly Ser Val
    210                 215                 220
tta gag gga gtc cta cca ggt act tct gtg atg cag gtg aca gcc acg        720
Leu Glu Gly Val Leu Pro Gly Thr Ser Val Met Gln Val Thr Ala Thr
225                 230                 235                 240
gat gag gat gat gcc atc tac acc tac aat ggg gtg gtt gct tac tcc        768
Asp Glu Asp Asp Ala Ile Tyr Thr Tyr Asn Gly Val Val Ala Tyr Ser
                245                 250                 255
atc cat agc caa gaa cca aag gac cca cac gac ctc atg ttc acc att        816
Ile His Ser Gln Glu Pro Lys Asp Pro His Asp Leu Met Phe Thr Ile
            260                 265                 270
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cac cgg agc aca ggc acc atc agc gtc atc tcc agt ggc ctg gac cgg        864
His Arg Ser Thr Gly Thr Ile Ser Val Ile Ser Ser Gly Leu Asp Arg
        275                 280                 285

gaa aaa gtc cct gag tac aca ctg acc atc cag gcc aca gac atg gat        912
Glu Lys Val Pro Glu Tyr Thr Leu Thr Ile Gln Ala Thr Asp Met Asp
    290                 295                 300

ggg gac ggc tcc acc acc acg gca gtg gca gta gtg gag atc ctt gat        960
Gly Asp Gly Ser Thr Thr Thr Ala Val Ala Val Val Glu Ile Leu Asp
305                 310                 315                 320

gcc aat gac aat gct ccc atg ttt gac ccc cag aag tac gag gcc cat       1008
Ala Asn Asp Asn Ala Pro Met Phe Asp Pro Gln Lys Tyr Glu Ala His
                325                 330                 335

gtg cct gag aat gca gtg ggc cat gag gtg cag agg ctg acg gtc act       1056
Val Pro Glu Asn Ala Val Gly His Glu Val Gln Arg Leu Thr Val Thr
            340                 345                 350

gat ctg gac gcc ccc aac tca cca gcg tgg cgt gcc acc tac ctt atc       1104
Asp Leu Asp Ala Pro Asn Ser Pro Ala Trp Arg Ala Thr Tyr Leu Ile
        355                 360                 365

atg ggc ggt gac gac ggg gac cat ttt acc atc acc acc cac cct gag       1152
Met Gly Gly Asp Asp Gly Asp His Phe Thr Ile Thr Thr His Pro Glu
    370                 375                 380

agc aac cag ggc atc ctg aca acc agg aag ggt ttg gat ttt gag gcc       1200
Ser Asn Gln Gly Ile Leu Thr Thr Arg Lys Gly Leu Asp Phe Glu Ala
385                 390                 395                 400

aaa aac cag cac acc ctg tac gtt gaa gtg acc aac gag gcc cct ttt       1248
Lys Asn Gln His Thr Leu Tyr Val Glu Val Thr Asn Glu Ala Pro Phe
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gtg ctg aag ctc cca acc tcc aca gcc acc ata gtg gtc cac gtg gag       1296
Val Leu Lys Leu Pro Thr Ser Thr Ala Thr Ile Val Val His Val Glu
            420                 425                 430

gat gtg aat gag gca cct gtg ttt gtc cca ccc tcc aaa gtc gtt gag       1344
Asp Val Asn Glu Ala Pro Val Phe Val Pro Pro Ser Lys Val Val Glu
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gtc cag gag ggc atc ccc act ggg gag cct gtg tgt gtc tac act gca      1392
Val Gln Glu Gly Ile Pro Thr Gly Glu Pro Val Cys Val Tyr Thr Ala
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gaa gac cct gac aag gag aat caa aag atc agc tac cgc atc ctg aga      1440
Glu Asp Pro Asp Lys Glu Asn Gln Lys Ile Ser Tyr Arg Ile Leu Arg
465                 470                 475                 480
gac cca gca ggg tgg cta gcc atg gac cca gac agt ggg cag gtc aca      1488
Asp Pro Ala Gly Trp Leu Ala Met Asp Pro Asp Ser Gly Gln Val Thr
                485                 490                 495
gct gtg ggc acc ctc gac cgt gag gat gag cag ttt gtg agg aac aac      1536
Ala Val Gly Thr Leu Asp Arg Glu Asp Glu Gln Phe Val Arg Asn Asn
            500                 505                 510
atc tat gaa gtc atg gtc ttg gcc atg gac aat gga agc cct ccc acc      1584
Ile Tyr Glu Val Met Val Leu Ala Met Asp Asn Gly Ser Pro Pro Thr
        515                 520                 525
act ggc acg gga acc ctt ctg cta aca ctg att gat gtc aat gac cat      1632
Thr Gly Thr Gly Thr Leu Leu Leu Thr Leu Ile Asp Val Asn Asp His
    530                 535                 540
ggc cca gtc cct gag ccc cgt cag atc acc atc tgc aac caa agc cct      1680
Gly Pro Val Pro Glu Pro Arg Gln Ile Thr Ile Cys Asn Gln Ser Pro
545                 550                 555                 560
gtg cgc cag gtg ctg aac atc acg gac aag gac ctg tct ccc cac acc      1728
Val Arg Gln Val Leu Asn Ile Thr Asp Lys Asp Leu Ser Pro His Thr
                565                 570                 575
tcc cct ttc cag gcc cag ctc aca gat gac tca gac atc tac tgg acg      1776
Ser Pro Phe Gln Ala Gln Leu Thr Asp Asp Ser Asp Ile Tyr Trp Thr
            580                 585                 590
gca gag gtc aac gag gaa ggt gac aca gtg gtc ttg tcc ctg aag aag      1824
Ala Glu Val Asn Glu Glu Gly Asp Thr Val Val Leu Ser Leu Lys Lys
        595                 600                 605
ttc ctg aag cag gat aca tat gac gtg cac ctt tct ctg tct gac cat      1872
Phe Leu Lys Gln Asp Thr Tyr Asp Val His Leu Ser Leu Ser Asp His
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ggc aac aaa gag cag ctg acg gtg atc agg gcc act gtg tgc gac tgc 1920
Gly Asn Lys Glu Gln Leu Thr Val Ile Arg Ala Thr Val Cys Asp Cys
625 630 635 640

cat ggc cat gtc gaa acc tgc cct gga ccc tgg aag gga ggt ttc atc 1968
His Gly His Val Glu Thr Cys Pro Gly Pro Trp Lys Gly Gly Phe Ile
645 650 655

ctc cct gtg ctg ggg gct gtc ctg gct ctg ctg ttc ctc ctg ctg gtg 2016
Leu Pro Val Leu Gly Ala Val Leu Ala Leu Leu Phe Leu Leu Leu Val
660 665 670

ctg ctt ttg ttg gtg aga aag aag cgg aag atc aag gag ccc ctc cta 2064
Leu Leu Leu Leu Val Arg Lys Lys Arg Lys Ile Lys Glu Pro Leu Leu
675 680 685

ctc cca gaa gat gac acc cgt gac aac gtc ttc tac tat ggc gaa gag 2112
Leu Pro Glu Asp Asp Thr Arg Asp Asn Val Phe Tyr Tyr Gly Glu Glu
690 695 700

ggg ggt ggc gaa gag gac cag gac tat gac atc acc cag ctc cac cga 2160
Gly Gly Gly Glu Glu Asp Gln Asp Tyr Asp Ile Thr Gln Leu His Arg
705 710 715 720

ggt ctg gag gcc agg ccg gag gtg gtt ctc cgc aat gac gtg gca cca 2208
Gly Leu Glu Ala Arg Pro Glu Val Val Leu Arg Asn Asp Val Ala Pro
725 730 735

acc atc atc ccg aca ccc atg tac cgt cct cgg cca gcc aac cca gat 2256
Thr Ile Ile Pro Thr Pro Met Tyr Arg Pro Arg Pro Ala Asn Pro Asp
740 745 750

gaa atc ggc aac ttt ata att gag aac ctg aag gcg gct aac aca gac 2304
Glu Ile Gly Asn Phe Ile Ile Glu Asn Leu Lys Ala Ala Asn Thr Asp
755 760 765

ccc aca gcc ccg ccc tac gac acc ctc ttg gtg ttc gac tat gag ggc 2352
Pro Thr Ala Pro Pro Tyr Asp Thr Leu Leu Val Phe Asp Tyr Glu Gly
770 775 780

agc ggc tcc gac gcc gcg tcc ctg agc tcc ctc acc tcc tcc gcc tcc 2400
Ser Gly Ser Asp Ala Ala Ser Leu Ser Ser Leu Thr Ser Ser Ala Ser
785 790 795 800

gac caa gac caa gat tac gat tat ctg aac gag tgg ggc agc cgc ttc 2448
Asp Gln Asp Gln Asp Tyr Asp Tyr Leu Asn Glu Trp Gly Ser Arg Phe
805 810 815

aag aag ctg gca gac atg tac ggt ggc ggg gag gac gac tag 2490
Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu Asp Asp
820 825

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35 40 45
Gln Ala Leu Gly Lys Val Phe Met Gly Cys Pro Gly Gln Glu Pro Ala
50 55 60
Leu Phe Ser Thr Asp Asn Asp Asp Phe Thr Val Arg Asn Gly Glu Thr
65 70 75 80
Val Gln Glu Arg Arg Ser Leu Lys Glu Arg Asn Pro Leu Lys Ile Phe
85 90 95
Pro Ser Lys Arg Ile Leu Arg Arg His Lys Arg Asp Trp Val Val Ala
100 105 110
Pro Ile Ser Val Pro Glu Asn Gly Lys Gly Pro Phe Pro Gln Arg Leu
115 120 125
Asn Gln Leu Lys Ser Asn Lys Asp Arg Asp Thr Lys Ile Phe Tyr Ser
130 135 140
Ile Thr Gly Pro Gly Ala Asp Ser Pro Pro Glu Gly Val Phe Ala Val
145 150 155 160
Glu Lys Glu Thr Gly Trp Leu Leu Leu Asn Lys Pro Leu Asp Arg Glu
165 170 175

Glu Ile Ala Lys Tyr Glu Leu Phe Gly His Ala Val Ser Glu Asn Gly
180 185 190
Ala Ser Val Glu Asp Pro Met Asn Ile Ser Ile Ile Val Thr Asp Gln
195 200 205
Asn Asp His Lys Pro Lys Phe Thr Gln Asp Thr Phe Arg Gly Ser Val
210 215 220
Leu Glu Gly Val Leu Pro Gly Thr Ser Val Met Gln Val Thr Ala Thr
225 230 235 240
Asp Glu Asp Asp Ala Ile Tyr Thr Tyr Asn Gly Val Val Ala Tyr Ser
245 250 255
Ile His Ser Gln Glu Pro Lys Asp Pro His Asp Leu Met Phe Thr Ile
260 265 270
His Arg Ser Thr Gly Thr Ile Ser Val Ile Ser Ser Gly Leu Asp Arg
275 280 285
Glu Lys Val Pro Glu Tyr Thr Leu Thr Ile Gln Ala Thr Asp Met Asp
290 295 300
Gly Asp Gly Ser Thr Thr Thr Ala Val Ala Val Val Glu Ile Leu Asp
305 310 315 320
Ala Asn Asp Asn Ala Pro Met Phe Asp Pro Gln Lys Tyr Glu Ala His
325 330 335
Val Pro Glu Asn Ala Val Gly His Glu Val Gln Arg Leu Thr Val Thr
340 345 350
Asp Leu Asp Ala Pro Asn Ser Pro Ala Trp Arg Ala Thr Tyr Leu Ile
355 360 365
Met Gly Gly Asp Asp Gly Asp His Phe Thr Ile Thr Thr His Pro Glu
370 375 380
Ser Asn Gln Gly Ile Leu Thr Thr Arg Lys Gly Leu Asp Phe Glu Ala
385 390 395 400
Lys Asn Gln His Thr Leu Tyr Val Glu Val Thr Asn Glu Ala Pro Phe
405 410 415
Val Leu Lys Leu Pro Thr Ser Thr Ala Thr Ile Val Val His Val Glu
420 425 430
Asp Val Asn Glu Ala Pro Val Phe Val Pro Pro Ser Lys Val Val Glu

435 440 445

Val Gln Glu Gly Ile Pro Thr Gly Glu Pro Val Cys Val Tyr Thr Ala

450 455 460

Glu Asp Pro Asp Lys Glu Asn Gln Lys Ile Ser Tyr Arg Ile Leu Arg

465 470 475 480

Asp Pro Ala Gly Trp Leu Ala Met Asp Pro Asp Ser Gly Gln Val Thr

485 490 495

Ala Val Gly Thr Leu Asp Arg Glu Asp Glu Gln Phe Val Arg Asn Asn

500 505 510

Ile Tyr Glu Val Met Val Leu Ala Met Asp Asn Gly Ser Pro Pro Thr

515 520 525

Thr Gly Thr Gly Thr Leu Leu Leu Thr Leu Ile Asp Val Asn Asp His

530 535 540

Gly Pro Val Pro Glu Pro Arg Gln Ile Thr Ile Cys Asn Gln Ser Pro

545 550 555 560

Val Arg Gln Val Leu Asn Ile Thr Asp Lys Asp Leu Ser Pro His Thr

565 570 575

Ser Pro Phe Gln Ala Gln Leu Thr Asp Asp Ser Asp Ile Tyr Trp Thr

580 585 590

Ala Glu Val Asn Glu Glu Gly Asp Thr Val Val Leu Ser Leu Lys Lys

595 600 605

Phe Leu Lys Gln Asp Thr Tyr Asp Val His Leu Ser Leu Ser Asp His

610 615 620

Gly Asn Lys Glu Gln Leu Thr Val Ile Arg Ala Thr Val Cys Asp Cys

625 630 635 640

His Gly His Val Glu Thr Cys Pro Gly Pro Trp Lys Gly Gly Phe Ile

645 650 655

Leu Pro Val Leu Gly Ala Val Leu Ala Leu Leu Phe Leu Leu Leu Val

660 665 670

Leu Leu Leu Leu Val Arg Lys Lys Arg Lys Ile Lys Glu Pro Leu Leu

675 680 685

Leu Pro Glu Asp Asp Thr Arg Asp Asn Val Phe Tyr Tyr Gly Glu Glu

690 695 700

Gly Gly Gly Glu Glu Asp Gln Asp Tyr Asp Ile Thr Gln Leu His Arg
705 710 715 720
Gly Leu Glu Ala Arg Pro Glu Val Val Leu Arg Asn Asp Val Ala Pro
725 730 735
Thr Ile Ile Pro Thr Pro Met Tyr Arg Pro Arg Pro Ala Asn Pro Asp
740 745 750
Glu Ile Gly Asn Phe Ile Ile Glu Asn Leu Lys Ala Ala Asn Thr Asp
755 760 765
Pro Thr Ala Pro Pro Tyr Asp Thr Leu Leu Val Phe Asp Tyr Glu Gly
770 775 780
Ser Gly Ser Asp Ala Ala Ser Leu Ser Ser Leu Thr Ser Ser Ala Ser
785 790 795 800
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Lys Lys Leu Ala Asp Met Tyr Gly Gly Gly Glu Asp Asp
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Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

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

Arg Asn Ser Asn Asn Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser

115

<210> 49

<211> 107

<212> PRT

<213> mouse/human

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Phe Tyr Asp Thr Pro Trp
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
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Thr Val Ser Ser
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35 40 45
Tyr Ala Ala Lys Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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20 25 30

Gly Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35 40 45

Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val Lys

50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu

65 70 75 80

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

85 90 95

Arg Asn Ser Asn Asn Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val

100 105 110

Thr Val Ser Ser

115

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<213> mouse/human

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Tyr Ser Asn

20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val

35 40 45

Tyr Ala Ala Lys Asn Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

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

Gly Val Ile Trp Ser Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Lys Asp Asn Ser Lys Asn Thr Val Tyr Leu
65 70 75 80

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

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100 105 110

Thr Val Ser Ser
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20 25 30

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

Tyr Ala Ala Lys Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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Gln His Phe Tyr Asp Thr Pro Trp Thr

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Tyr Tyr Cys
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1 5 10
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1 5 10

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20 25 30

Ala Val Tyr Tyr Cys
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ttc cct cag cga ctg aac cag ctg aag agt aac aag gac cgt gat act 96
Phe Pro Gln Arg Leu Asn Gln Leu Lys Ser Asn Lys Asp Arg Asp Thr
20 25 30

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Lys Ile Phe Tyr Ser Ile Thr Gly Pro Gly Ala Asp Ser Pro Pro Glu
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Gly Val Phe Ala Val Glu Lys Glu Thr Gly Trp Leu Leu Leu Asn Lys
    50                  55                  60
cct ctg gac cga gag gaa atc gcc aag tat gag ctg ttt ggg cac gct        240
Pro Leu Asp Arg Glu Glu Ile Ala Lys Tyr Glu Leu Phe Gly His Ala
65                  70                  75                  80
gtc agc gaa aac ggt gca tct gtg gag gat ccc atg aat att agc atc        288
Val Ser Glu Asn Gly Ala Ser Val Glu Asp Pro Met Asn Ile Ser Ile
                85                  90                  95
att gtg acc gat cag aac gac cat aag cct aaa ttc aca cag gac act        336
Ile Val Thr Asp Gln Asn Asp His Lys Pro Lys Phe Thr Gln Asp Thr
            100                 105                 110
ttt cgg ggc agt gtc ctg gaa ggc gtg ctg cca gga act tca gtc atg        384
Phe Arg Gly Ser Val Leu Glu Gly Val Leu Pro Gly Thr Ser Val Met
        115                 120                 125
cag gtg acc gcc aca gat gag gac gat gct atc tac acc tat aac ggc        432
Gln Val Thr Ala Thr Asp Glu Asp Asp Ala Ile Tyr Thr Tyr Asn Gly
    130                 135                 140
gtg gtc gct tac tct att cac agt cag gag ccc aag gat cct cac gac        480
Val Val Ala Tyr Ser Ile His Ser Gln Glu Pro Lys Asp Pro His Asp
145                 150                 155                 160
ctg atg ttc aca atc cat aga agt act ggc acc atc tca gtg att tcc        528
Leu Met Phe Thr Ile His Arg Ser Thr Gly Thr Ile Ser Val Ile Ser
                165                 170                 175
agc gga ctg gac cgc gaa aag gtg ccc gag tat aca ctg act att cag        576
Ser Gly Leu Asp Arg Glu Lys Val Pro Glu Tyr Thr Leu Thr Ile Gln
            180                 185                 190
gca act gac atg gat ggg gac ggt agc acc aca act gcc gtg gct gtg        624
Ala Thr Asp Met Asp Gly Asp Gly Ser Thr Thr Thr Ala Val Ala Val
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cct acc att aag cca agc cca ccc tgc aaa tgt cca gct ccc aat ctg        720
Pro Thr Ile Lys Pro Ser Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu
225                 230                 235                 240
ctg ggc gga ccc tct gtg ttc atc ttt cct cca aag atc aag gat gtg        768
Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val
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ctg atg atc tct ctg agt cct att gtc aca tgc gtg gtc gtg gat gtg        816
Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val
            260                 265                 270
agc gag gac gat cca gac gtc cag atc tct tgg ttc gtg aac aat gtc        864
Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val
        275                 280                 285
gaa gtg cac acc gcc cag acc cag aca cat agg gag gac tac aac tct        912
Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser
    290                 295                 300
aca ctg cgg gtc gtg agt gct ctg cca atc cag cat cag gat tgg atg        960
Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met
305                 310                 315                 320
tct ggg aaa gag ttc aag tgc aaa gtg aac aat aag gac ctg cct gct       1008
Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala
                325                 330                 335
cca atc gag agg aca att tcc aag cca aaa gga agc gtg cgg gca cca       1056
Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro
            340                 345                 350
cag gtc tat gtg ctg cca cct cca gag gaa gag atg aca aag aaa cag       1104
Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln
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gtc act ctg acc tgt atg gtg act gat ttc atg cct gaa gac atc tac       1152
Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr
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Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr
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Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu
405 410 415
aga gtc gaa aag aaa aac tgg gtg gag cgc aat tca tac tcc tgt agc 1296
Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser
420 425 430
gtc gtg cac gag ggt ctg cac aac cac cac aca aca aag agt ttc tca 1344
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35 40 45
Gly Val Phe Ala Val Glu Lys Glu Thr Gly Trp Leu Leu Leu Asn Lys
50 55 60
Pro Leu Asp Arg Glu Glu Ile Ala Lys Tyr Glu Leu Phe Gly His Ala
65 70 75 80
Val Ser Glu Asn Gly Ala Ser Val Glu Asp Pro Met Asn Ile Ser Ile
85 90 95
Ile Val Thr Asp Gln Asn Asp His Lys Pro Lys Phe Thr Gln Asp Thr

100 105 110

Phe Arg Gly Ser Val Leu Glu Gly Val Leu Pro Gly Thr Ser Val Met
115 120 125

Gln Val Thr Ala Thr Asp Glu Asp Asp Ala Ile Tyr Thr Tyr Asn Gly
130 135 140

Val Val Ala Tyr Ser Ile His Ser Gln Glu Pro Lys Asp Pro His Asp
145 150 155 160

Leu Met Phe Thr Ile His Arg Ser Thr Gly Thr Ile Ser Val Ile Ser
165 170 175

Ser Gly Leu Asp Arg Glu Lys Val Pro Glu Tyr Thr Leu Thr Ile Gln
180 185 190

Ala Thr Asp Met Asp Gly Asp Gly Ser Thr Thr Thr Ala Val Ala Val
195 200 205

Val Glu Ile Leu Asp Ala Asn Asp Asn Ala Pro Met Phe Pro Arg Gly
210 215 220

Pro Thr Ile Lys Pro Ser Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu
225 230 235 240

Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val
245 250 255

Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val
260 265 270

Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val
275 280 285

Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser
290 295 300

Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met
305 310 315 320

Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala
325 330 335

Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro
340 345 350

Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln
355 360 365

Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr
370 375 380
Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr
385 390 395 400
Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu
405 410 415
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Arg Ser Leu Gly Lys
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Tyr Tyr Cys
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1 5 10

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Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
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20 25 30

Ala Val Tyr Tyr Cys
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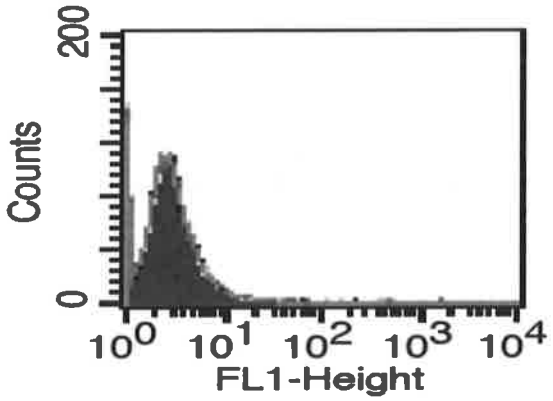
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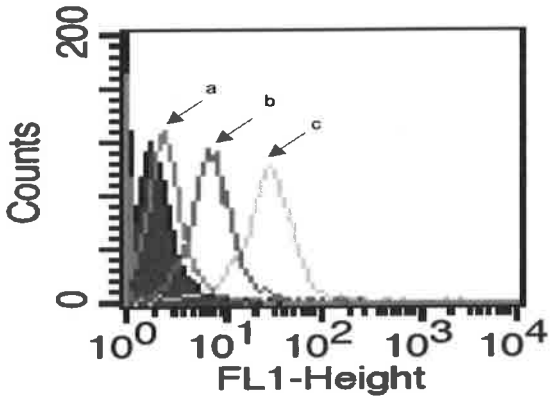
[Figure 1]

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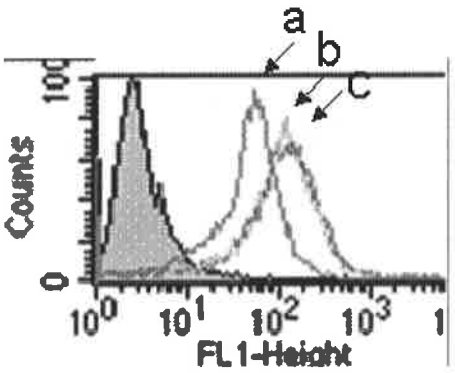
CHO

B:



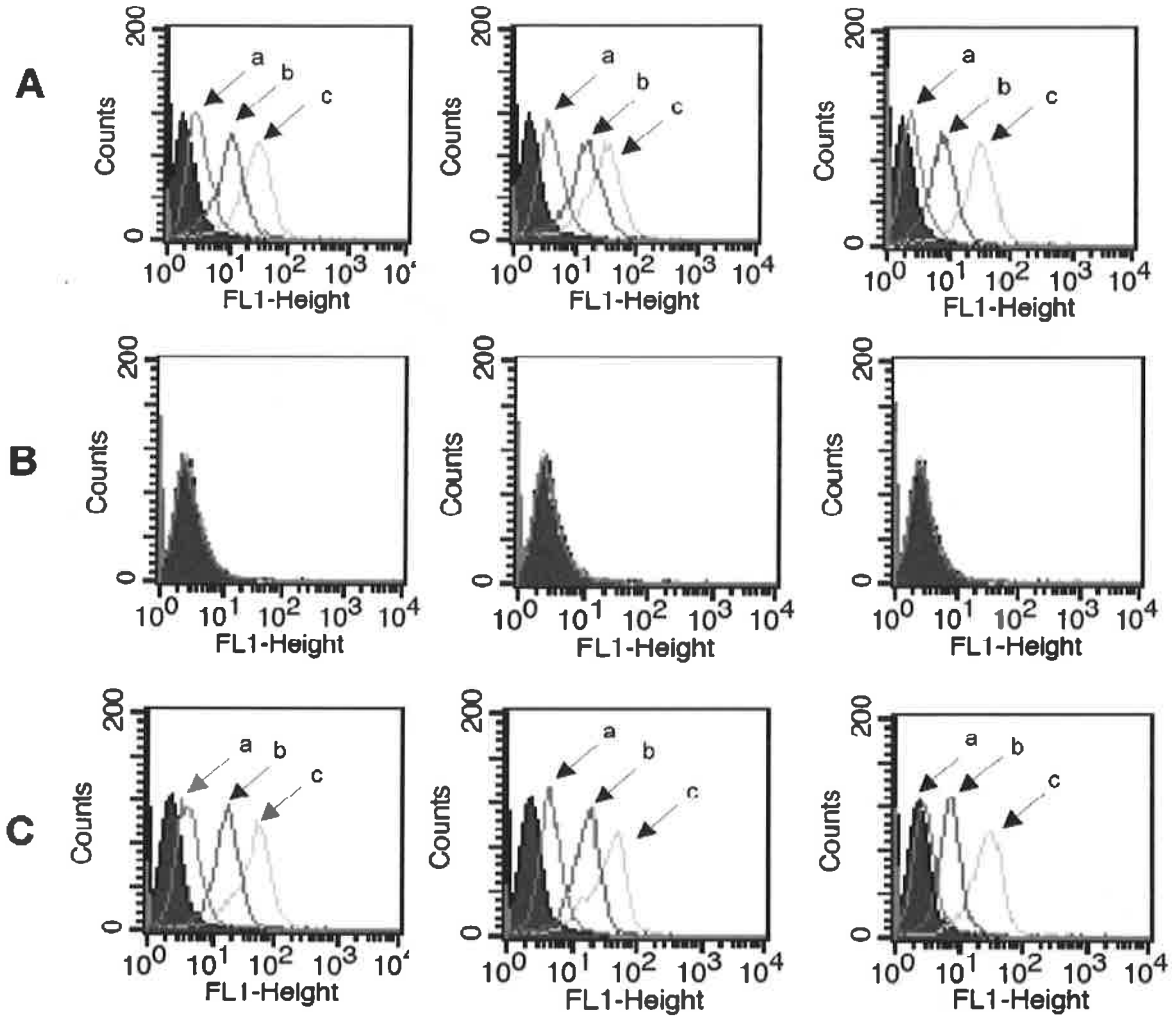
CHO that forcibly expresses CDH3

C:



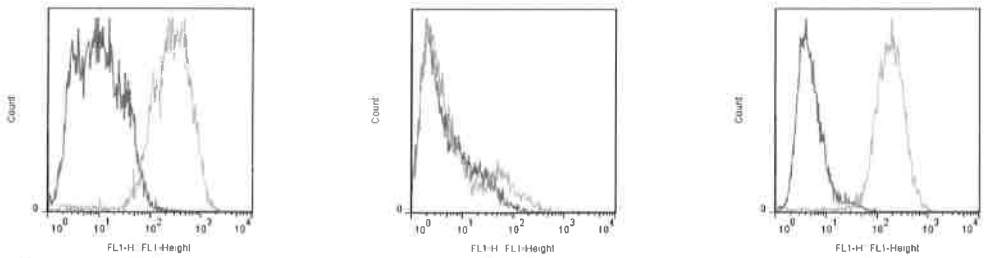
NCI-H358

[Figure 2]



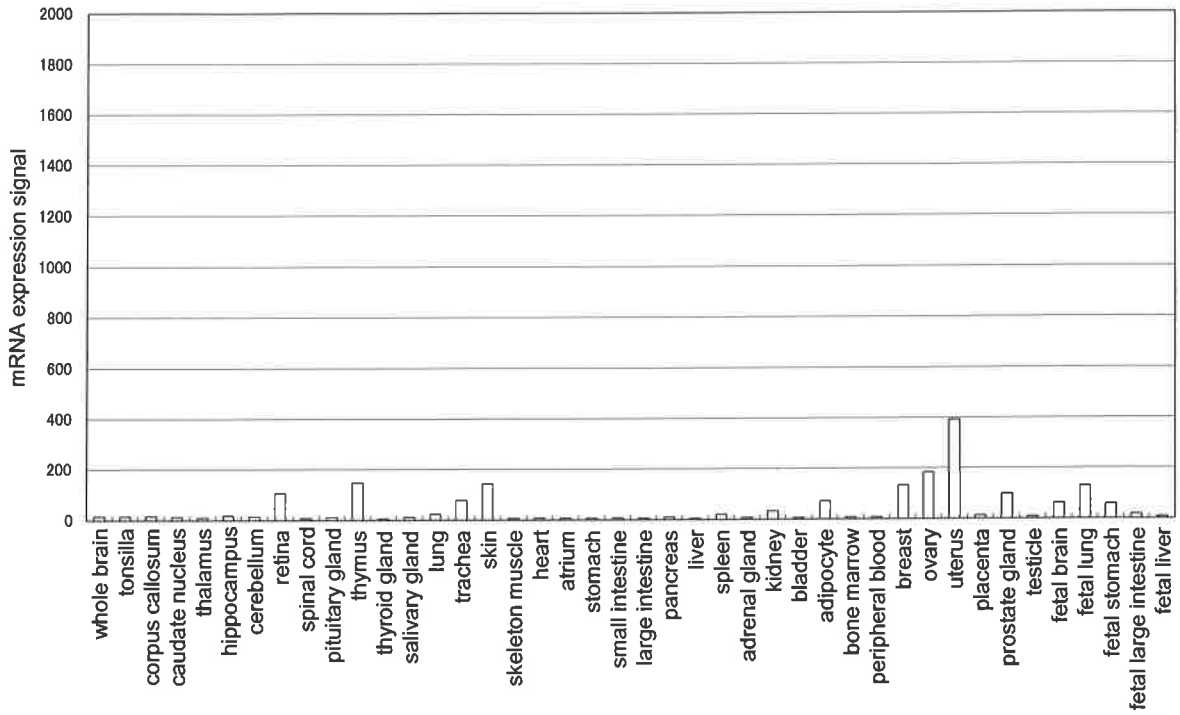
D: Mouse antibody (PPAT-076-44M) derived from Accession No. NITE BP-1536

CHO that forcibly expresses DH3 CHO NCI-H358

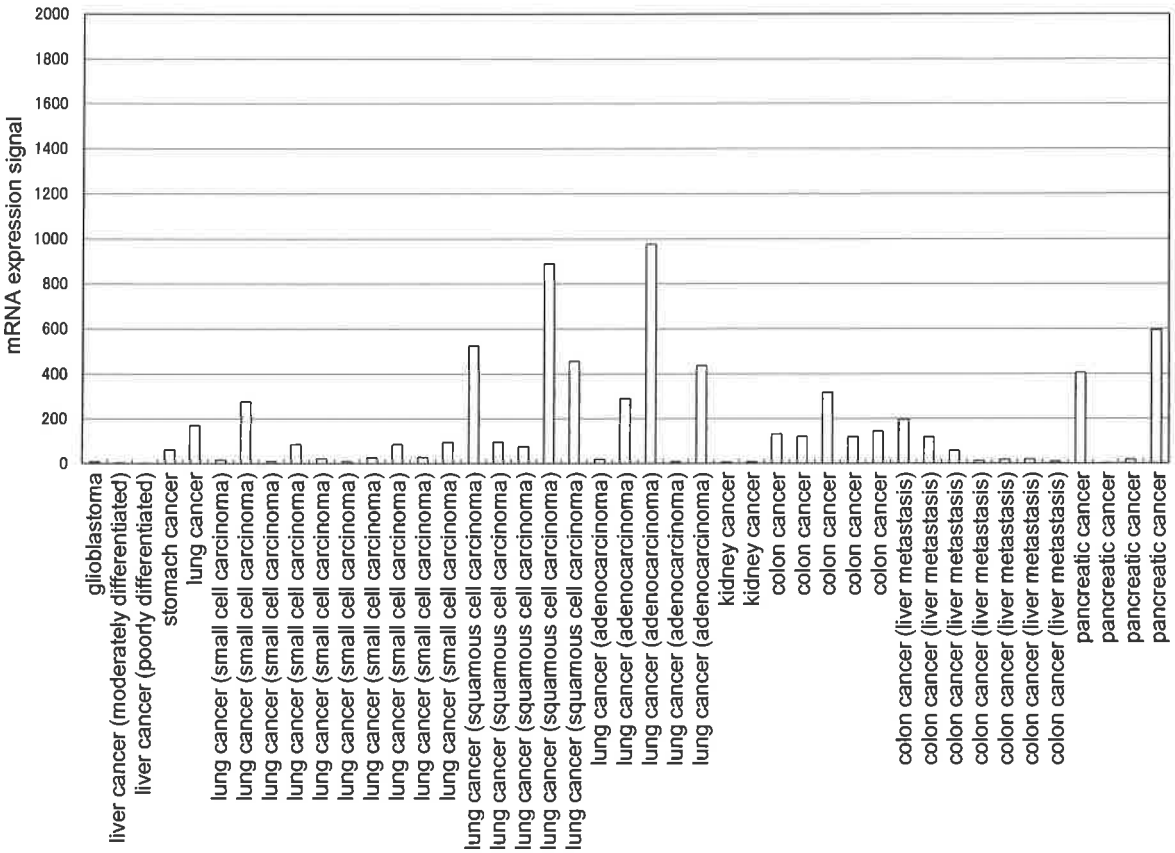


[Figure 3]

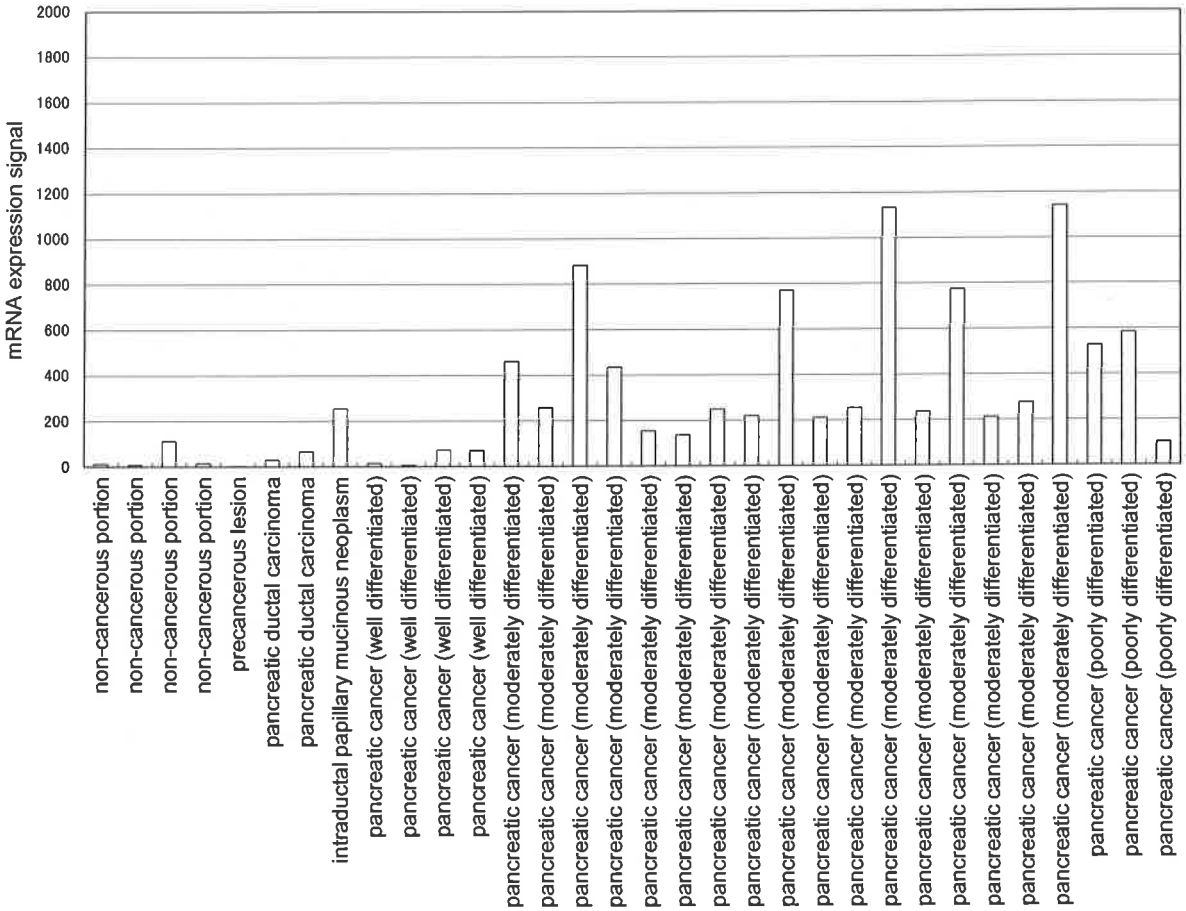
A


mRNA expression signal
2000
1800
1600
1400
1200
1000
800
600
400
200
0
whole brain
tonsilla
corpus callosum
caudate nucleus
thalamus
hippocampus
cerebellum
retina
spinal cord
pituitary gland
thymus
thyroid gland
salivary gland
lung
trachea
skin
skeleton muscle
heart
atrium
stomach
small intestine
large intestine
pancreas
liver
spleen
adrenal gland
kidney
bladder
adipocyte
bone marrow
peripheral blood
breast
ovary
uterus
placenta
prostate gland
testicle
fetal brain
fetal lung
fetal stomach
fetal large intestine
fetal liver

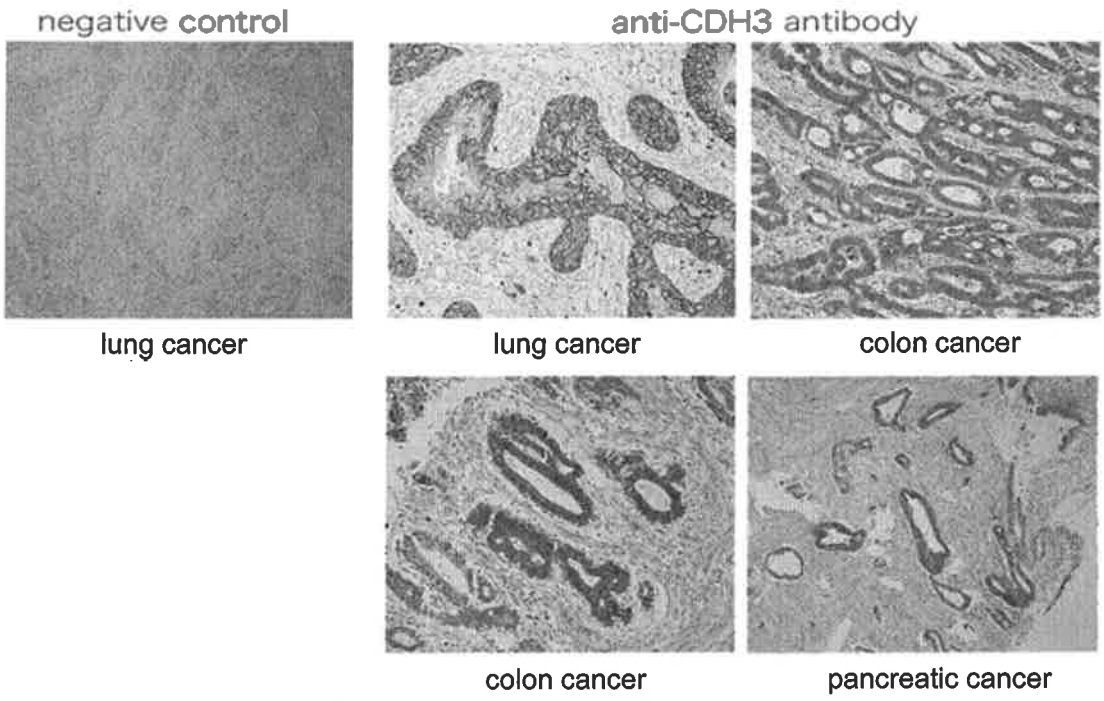
B


mRNA expression signal
2000
1800
1600
1400
1200
1000
800
600
400
200
0
glioblastoma
liver cancer (moderately differentiated)
liver cancer (poorly differentiated)
stomach cancer
lung cancer
lung cancer (small cell carcinoma)
lung cancer (small cell carcinoma)
lung cancer (small cell carcinoma)
lung cancer (small cell carcinoma)
lung cancer (small cell carcinoma)
lung cancer (small cell carcinoma)
lung cancer (small cell carcinoma)
lung cancer (small cell carcinoma)
lung cancer (small cell carcinoma)
lung cancer (squamous cell carcinoma)
lung cancer (squamous cell carcinoma)
lung cancer (squamous cell carcinoma)
lung cancer (squamous cell carcinoma)
lung cancer (squamous cell carcinoma)
lung cancer (adenocarcinoma)
lung cancer (adenocarcinoma)
lung cancer (adenocarcinoma)
lung cancer (adenocarcinoma)
lung cancer (adenocarcinoma)
kidney cancer
kidney cancer
colon cancer
colon cancer
colon cancer
colon cancer
colon cancer
colon cancer (liver metastasis)
colon cancer (liver metastasis)
colon cancer (liver metastasis)
colon cancer (liver metastasis)
colon cancer (liver metastasis)
colon cancer (liver metastasis)
colon cancer (liver metastasis)
pancreatic cancer
pancreatic cancer
pancreatic cancer
pancreatic cancer

C


mRNA expression signal
2000
1800
1600
1400
1200
1000
800
600
400
200
0
non-cancerous portion
non-cancerous portion
non-cancerous portion
non-cancerous portion
precancerous lesion
pancreatic ductal carcinoma
pancreatic ductal carcinoma
intraductal papillary mucinous neoplasm
pancreatic cancer (well differentiated)
pancreatic cancer (well differentiated)
pancreatic cancer (well differentiated)
pancreatic cancer (well differentiated)
pancreatic cancer (moderately differentiated)
pancreatic cancer (moderately differentiated)
pancreatic cancer (moderately differentiated)
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pancreatic cancer (moderately differentiated)
pancreatic cancer (moderately differentiated)
pancreatic cancer (moderately differentiated)
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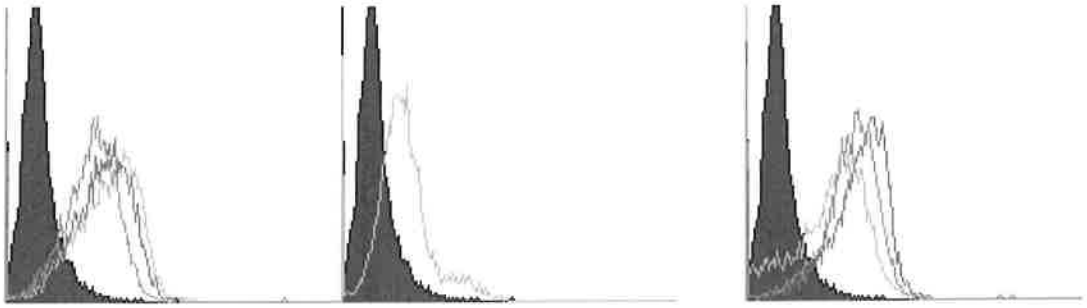
[Figure 4]


negative control
anti-CDH3 antibody
lung cancer
lung cancer
colon cancer
colon cancer
pancreatic cancer

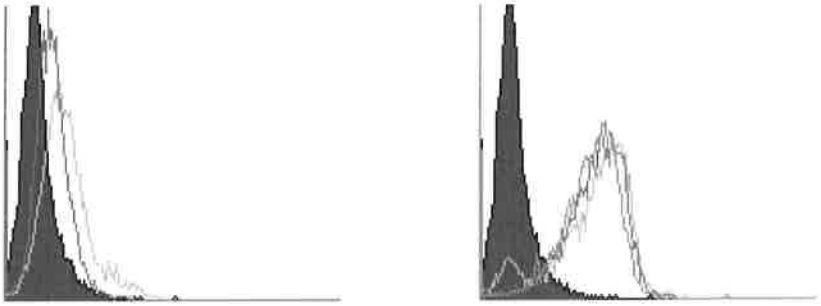
[Figure 5]

A: NCI-H358

PPAT-076-44C PPAT-076-44Ha PPAT-076-44Hb

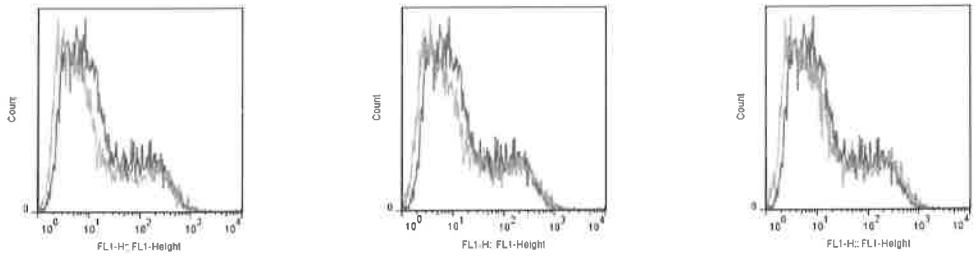


PPAT-076-44Hc PPAT-076-44Hd



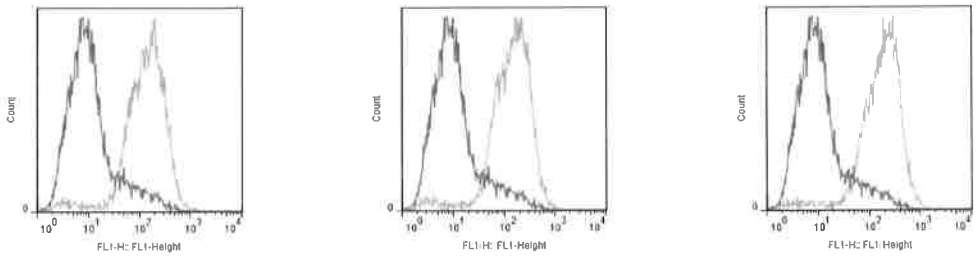
B: CHO cells

PPAT-076-44C PPAT-076-44Hb PPAT-076-44Hd

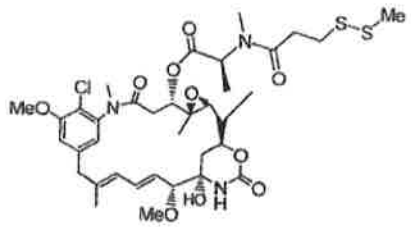


C: Cells that forcibly express CDH3

PPAT-076-44C PPAT-076-44Hb PPAT-076-44Hd

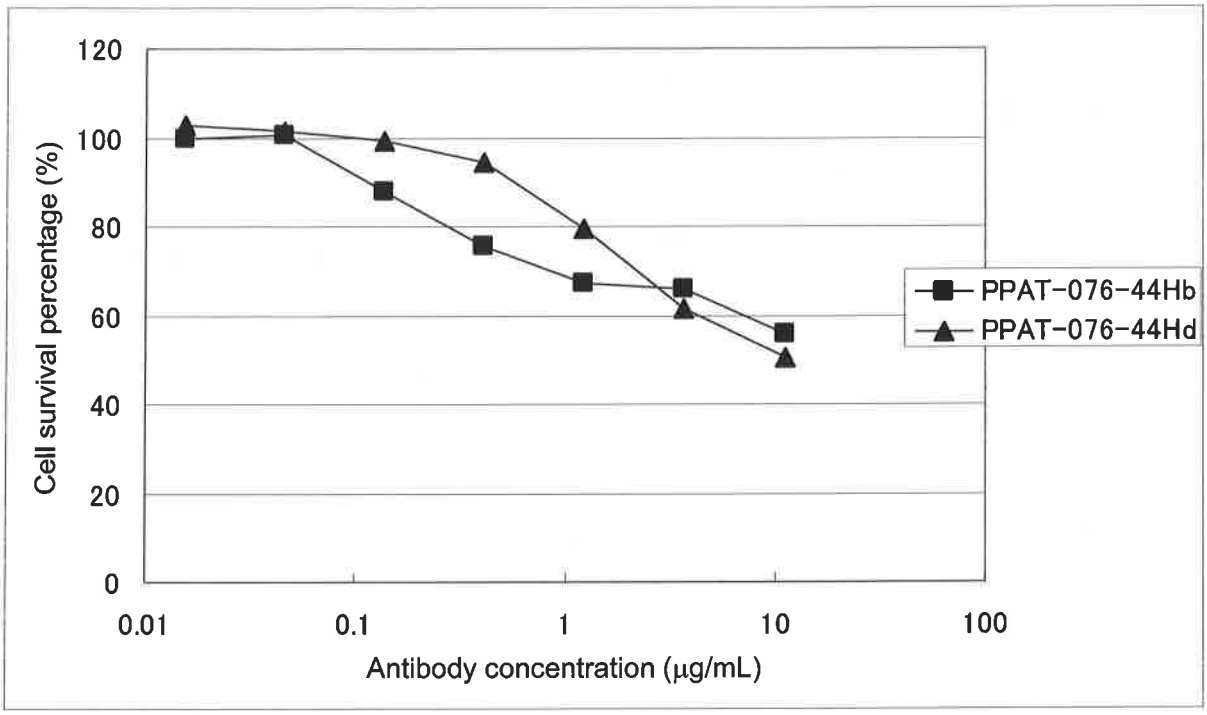


[Figure 6]

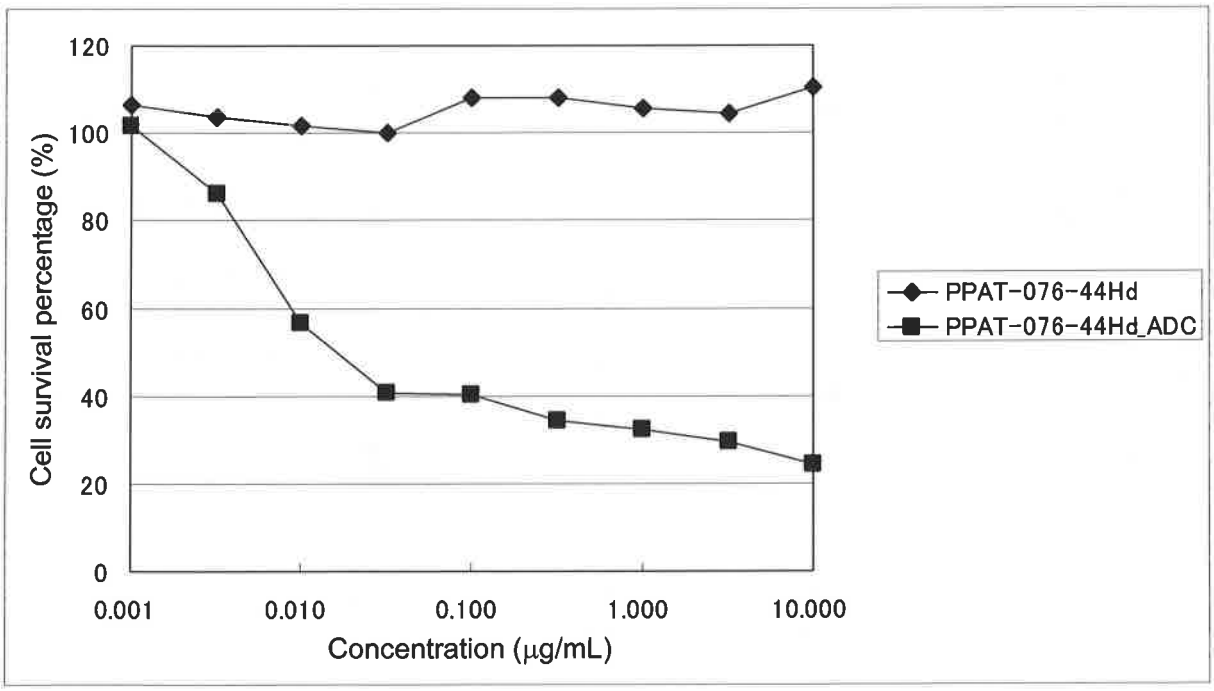


[Figure 7]

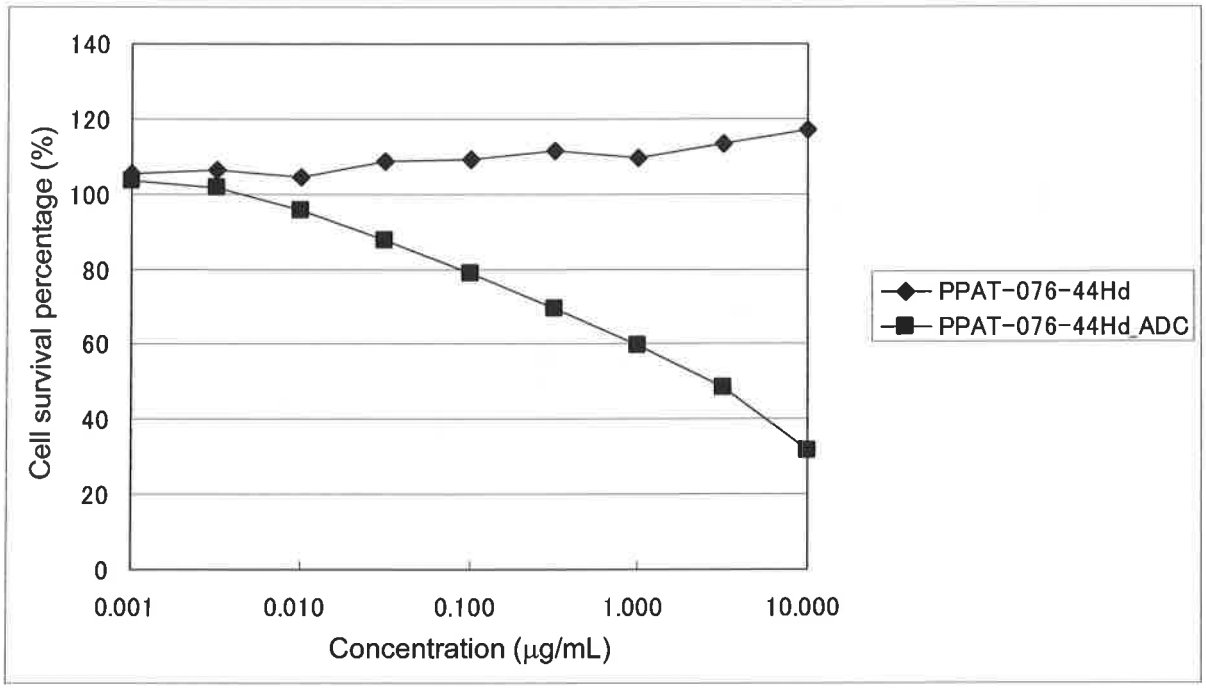
A: NCI-H358



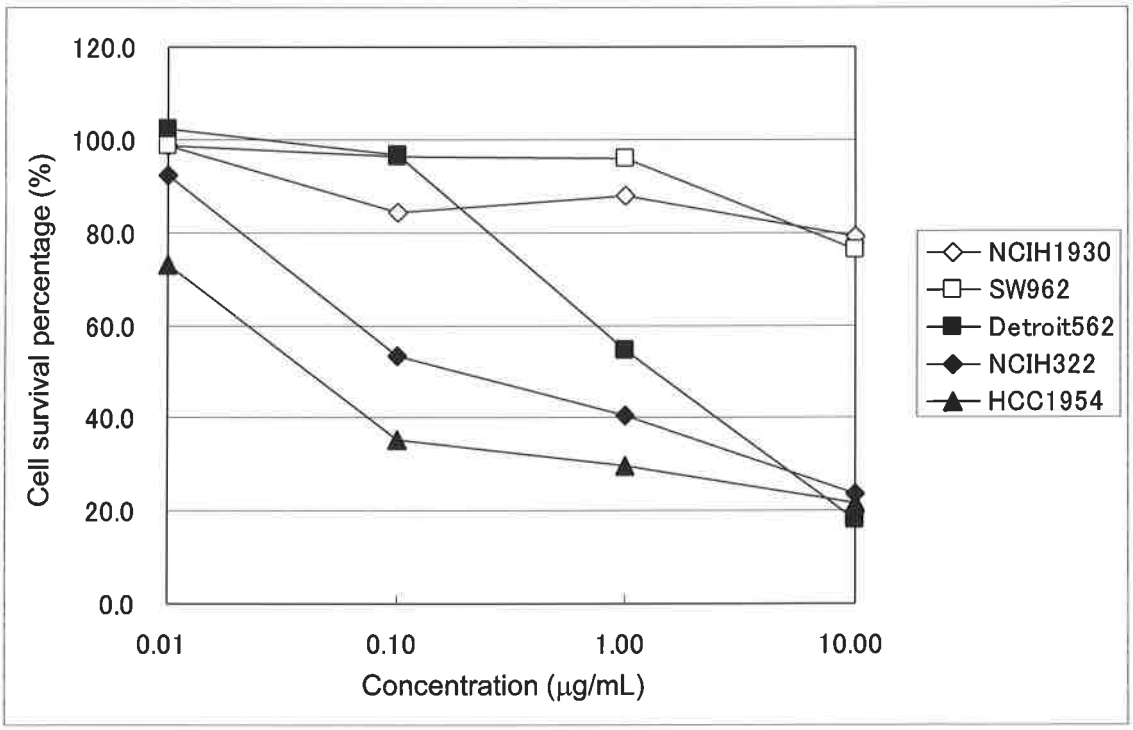
B: HCC-1954



C: HCC70

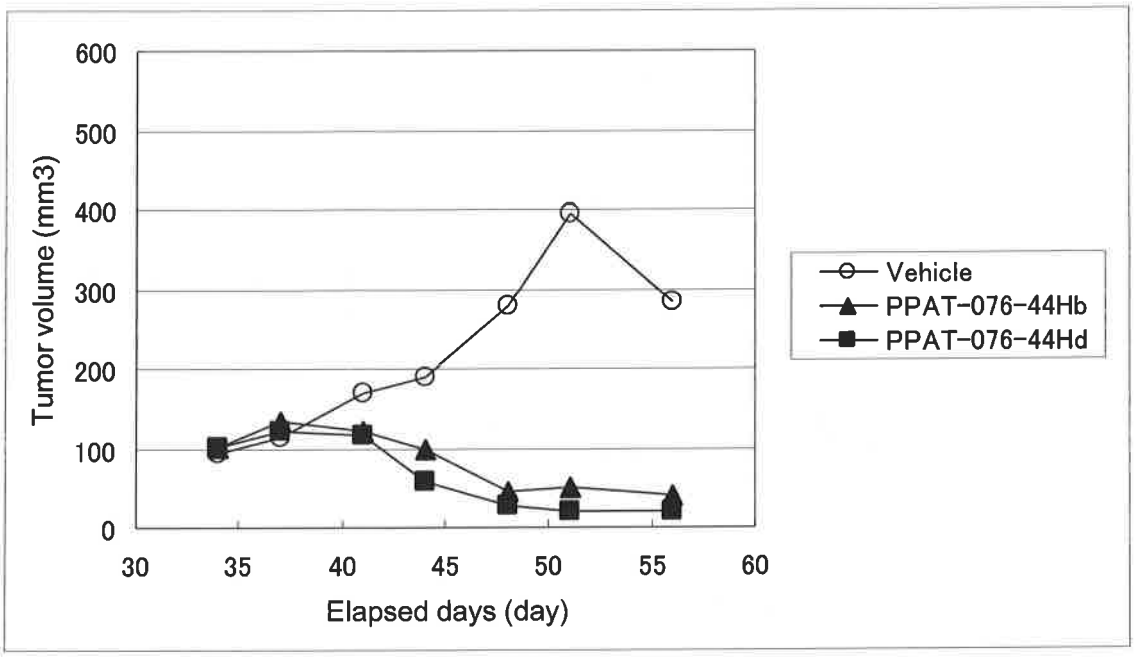


D: Individual cancer cell lines



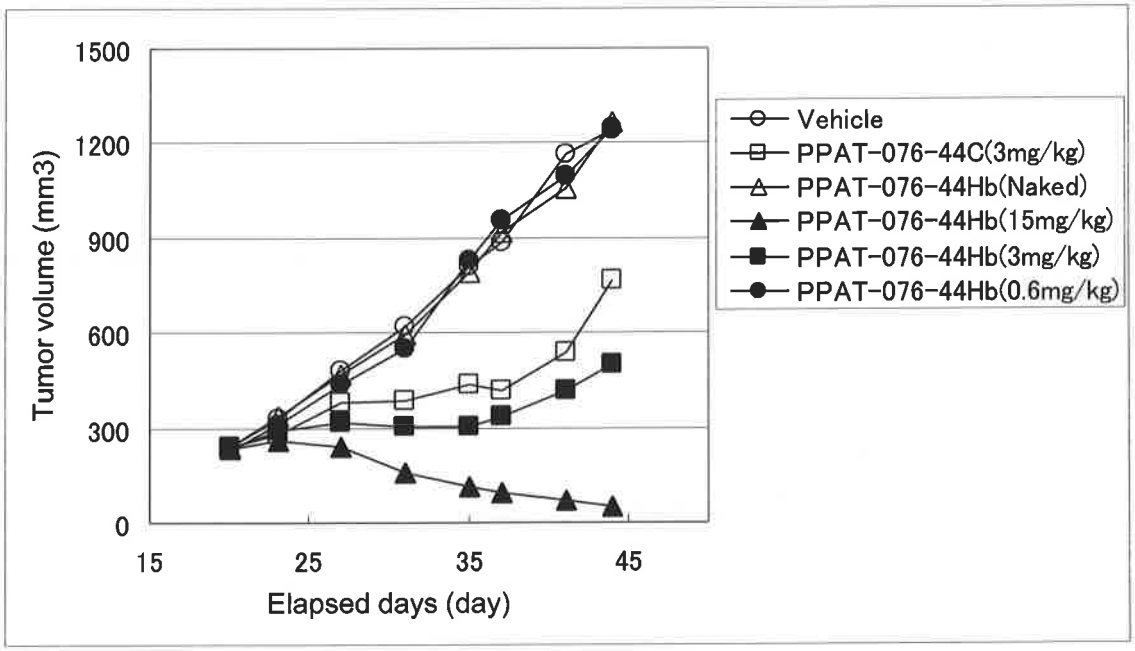
[Figure 8]

HCC1954



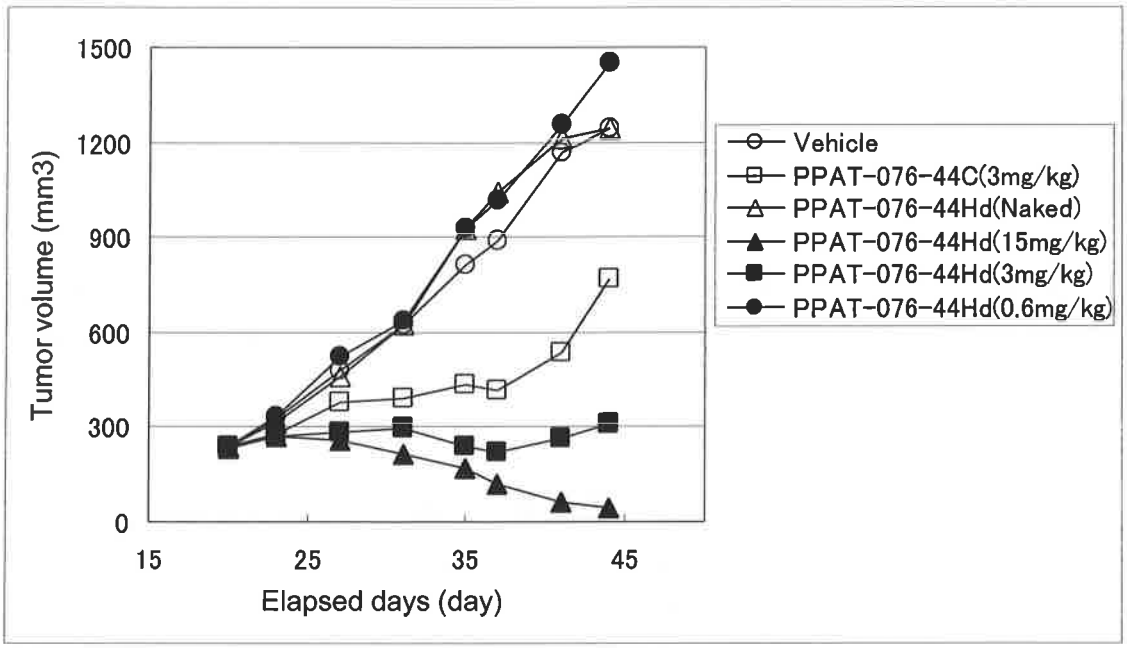
[Figure 9]

HCC70



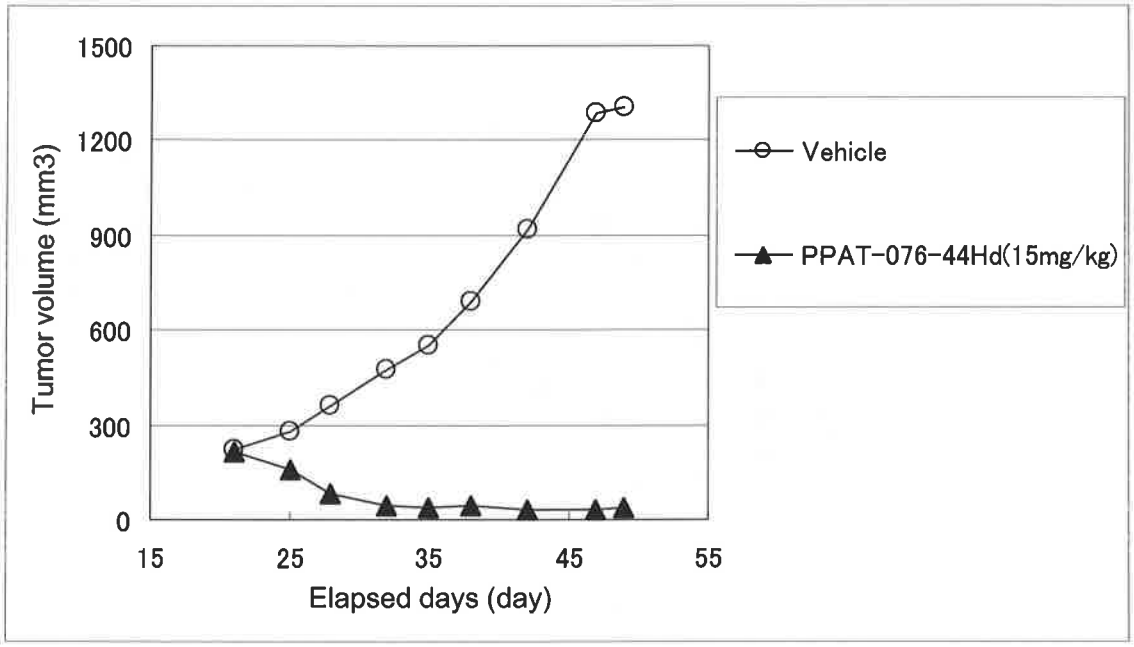
[Figure 10]

HCC70



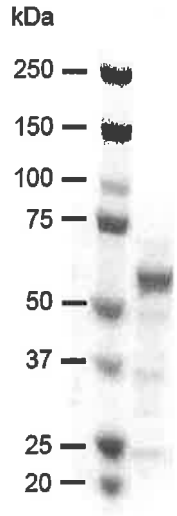
[Figure 11]

Oka-C-1

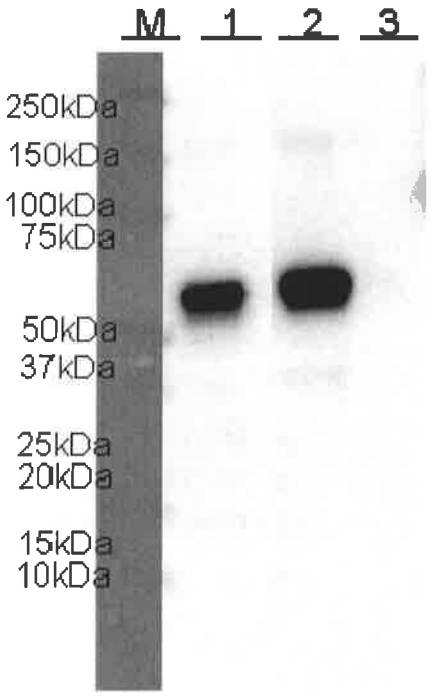


[Figure 12]

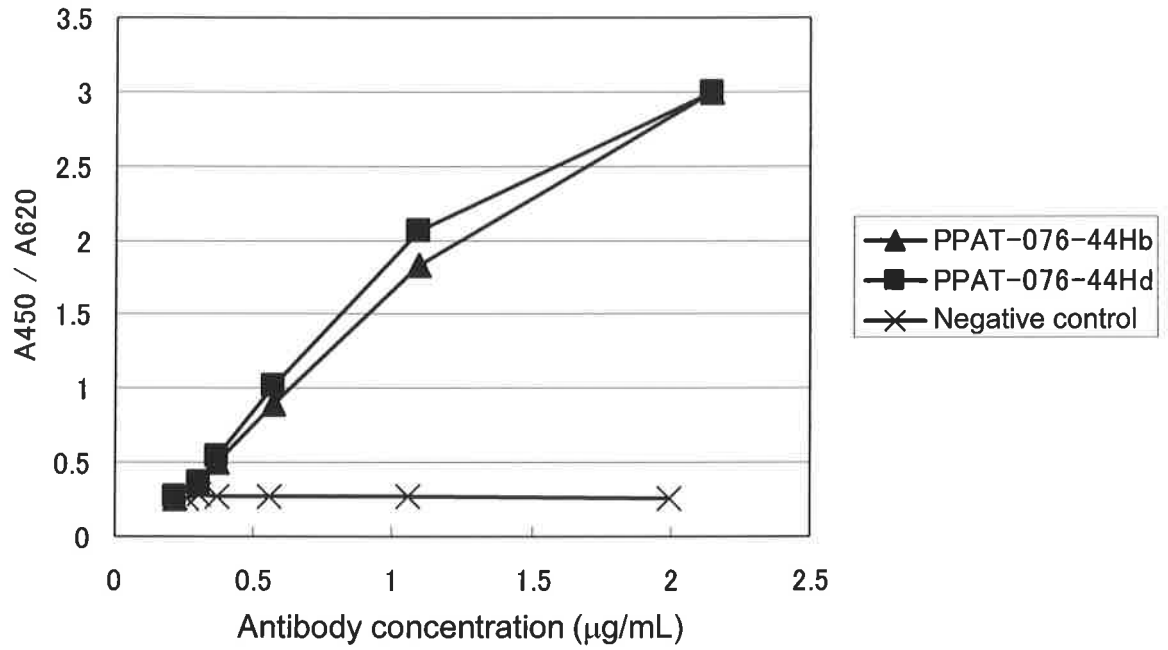
A: CBB-stained image



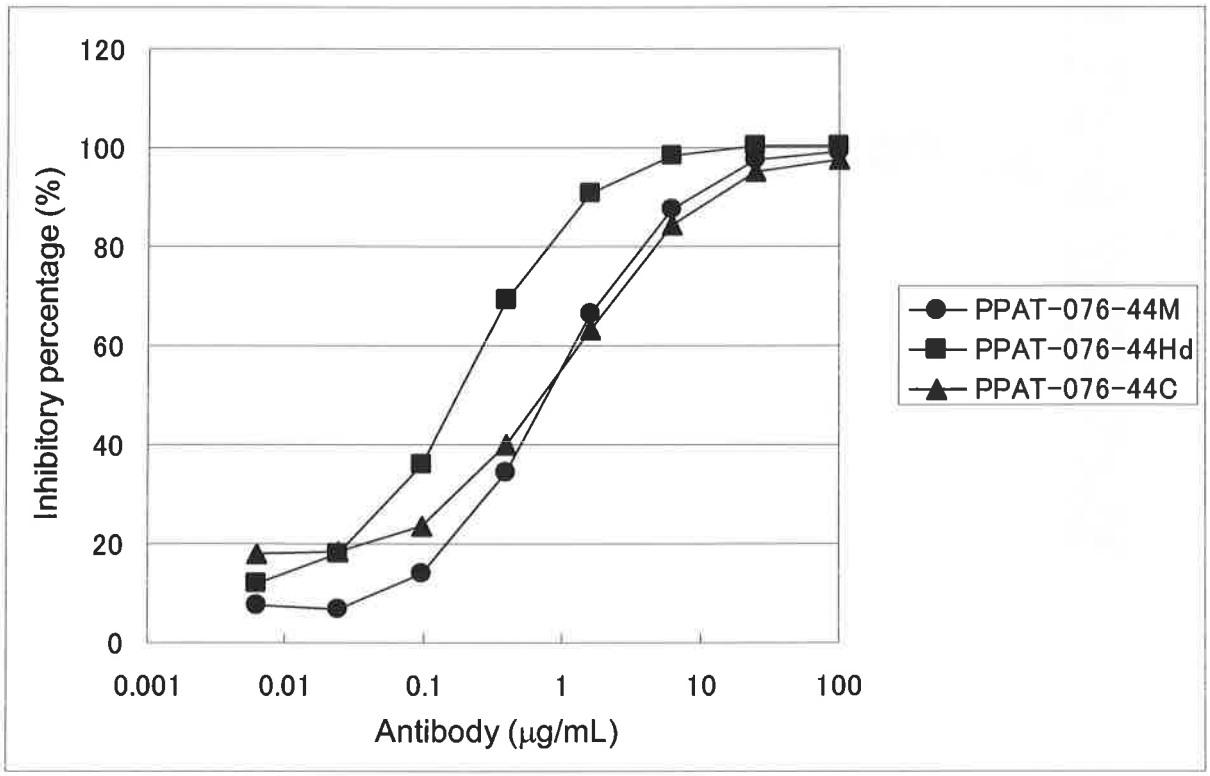
B: Western blotting



[Figure 13]

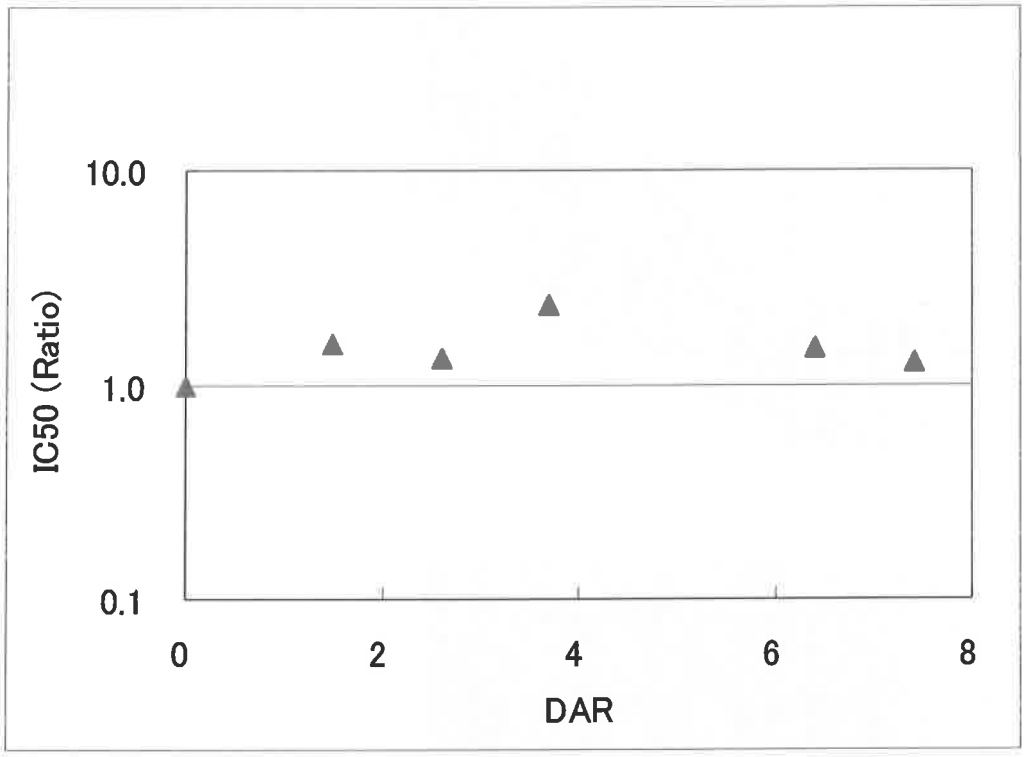


[Figure 14]

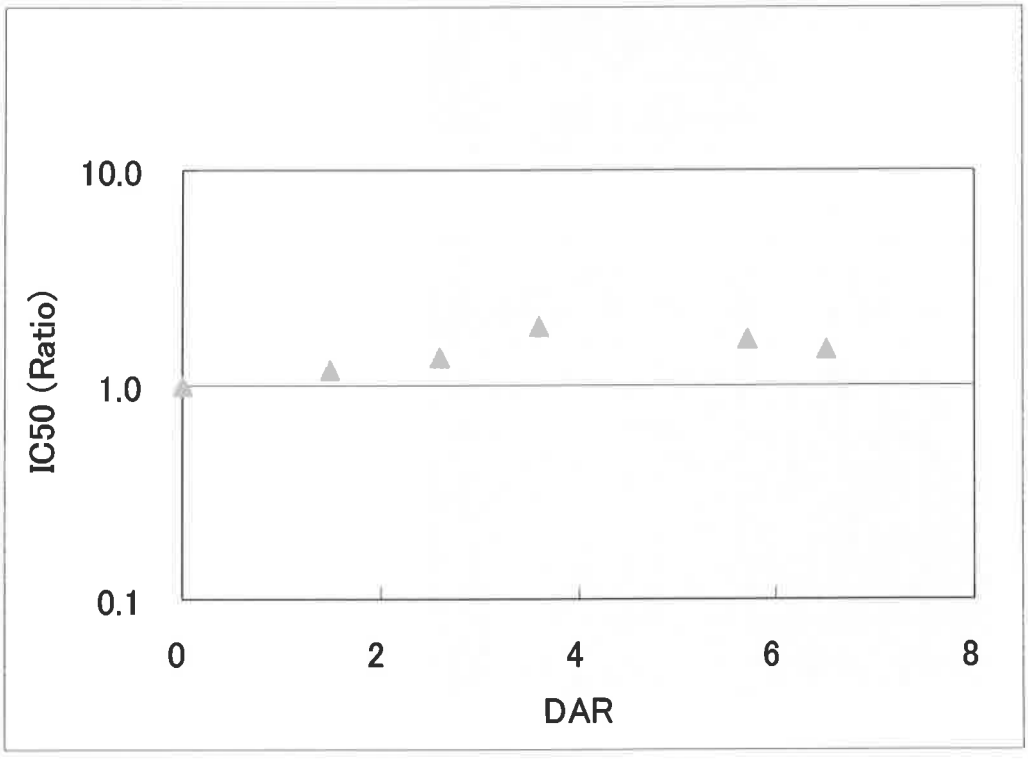


[Figure 15]

A: PPAT-076-44Hb

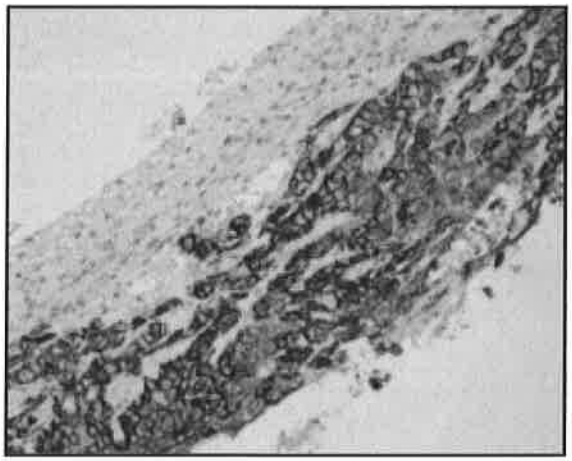


B: PPAT-076-44Hd

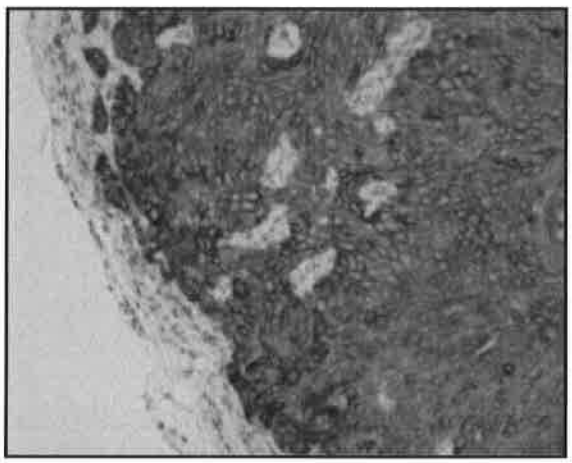


[Figure 16]

A: HCC1954



B: HCC70



C: Oka-C-1

