Fig. 1A

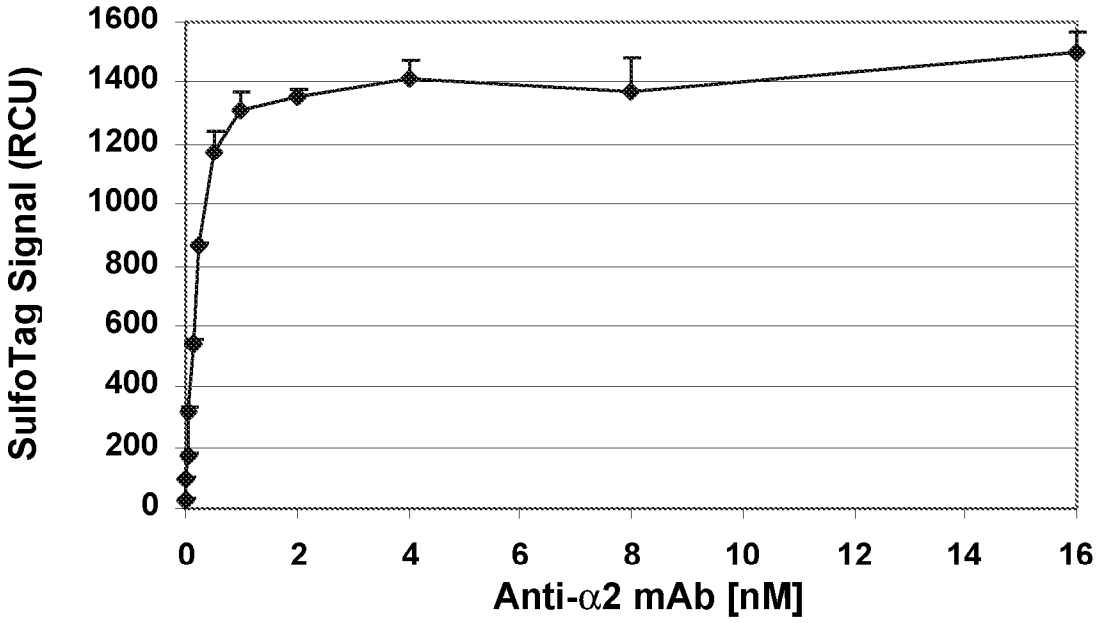
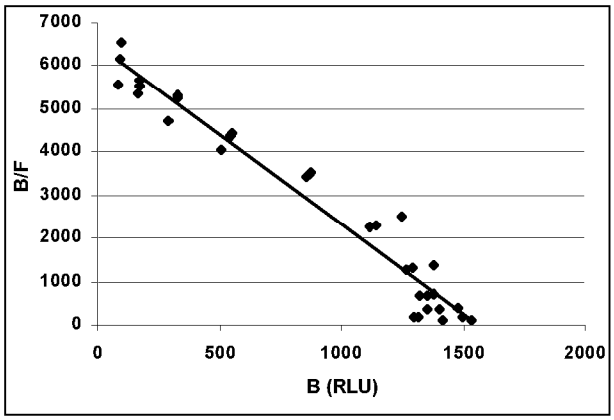


Fig. 1B



Parameter+	Estimate	SD	CV(%)	95%CI
KD (nM)	0.2146	0.01291	6.0	[0.1899 ; 0.2425]

Fig. 2

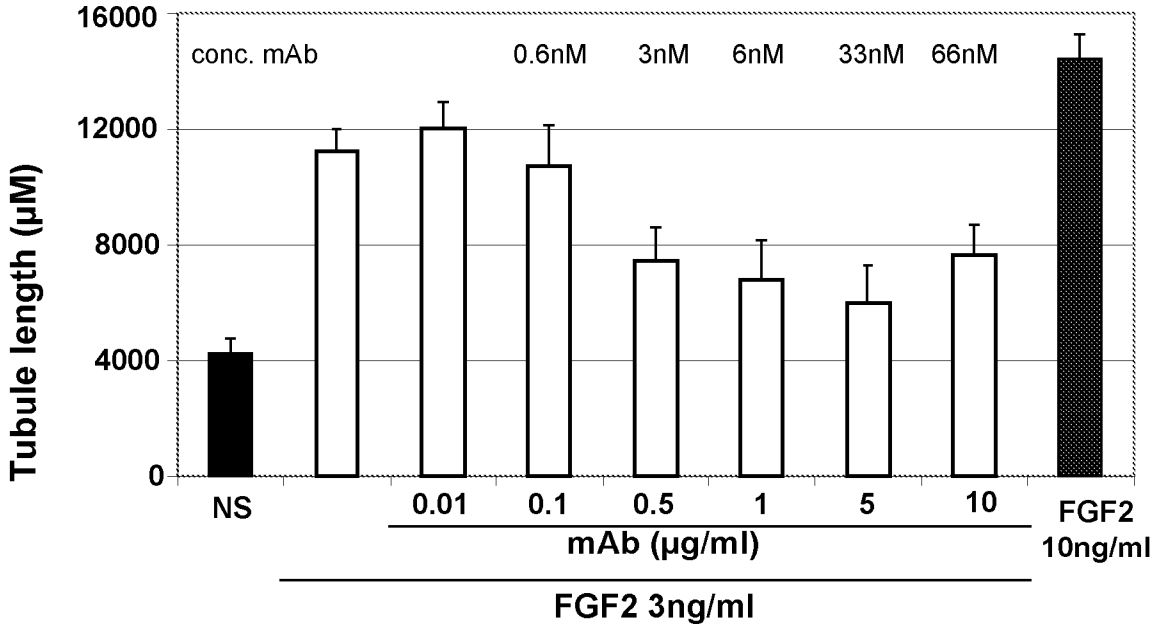

16000
12000
8000
4000
0
Tubule length (μM)
conc. mAb
0.6nM
3nM
6nM
33nM
66nM
NS
0.01
0.1
0.5
1
5
10
FGF2
10ng/ml
mAb (μg/ml)
FGF2 3ng/ml

Fig.3

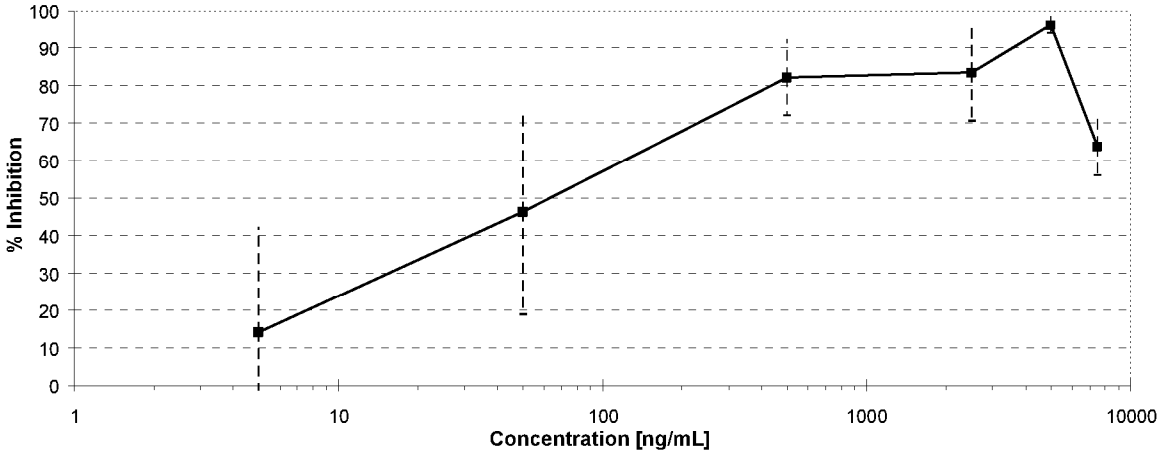

100
90
80
70
60
50
40
30
20
10
0
% Inhibition
1
10
100
1000
10000
Concentration [ng/mL]

Fig.4

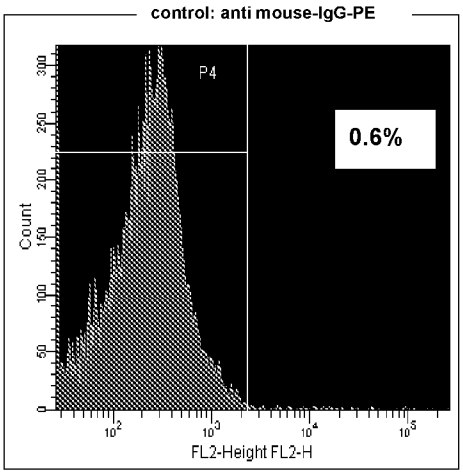


Figure 4a

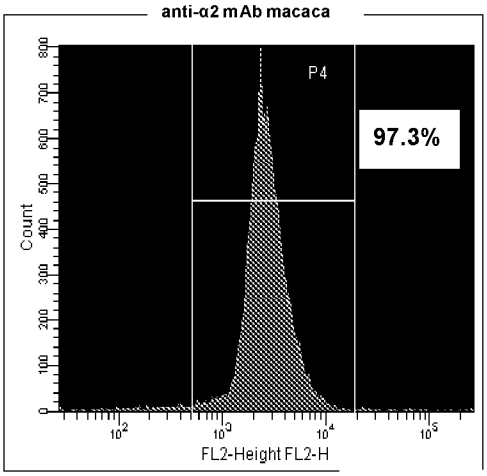


Figure 4b

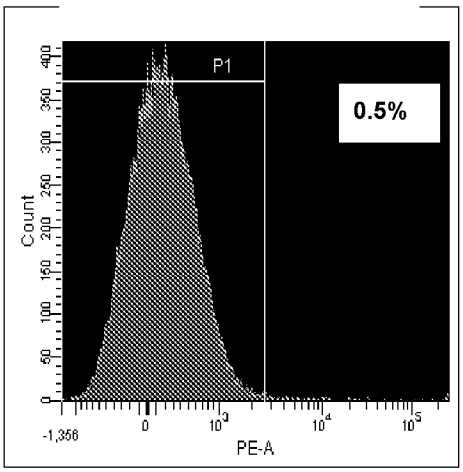


Figure 4c

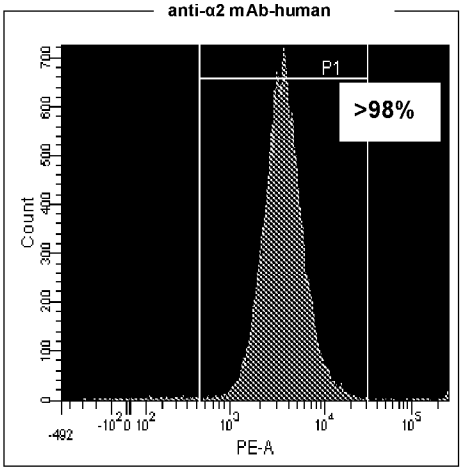


Figure 4d

Fig.5

Fig. 5a) Light chain variable domain of the anti-α2-integrin mAb

NIVLTQSPAS LAVSLGQRAT ISCRASESVE SYGNSFIYWY QQKPGQAPKL LIYLASNLAS GVPARFSGSG
SRTDFTLTID PVEADDAATY YCQQNNEDPY TFGGGTKLEI K

(SEQ ID NO:1)

AACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATATCCTGCAGAGCCAG
TGAAAGTGTTGAGAGTTATGGCAACAGTTTTATTTACTGGTACCAGCAGAAACCAGGACAGGCACCCAAACTCCTCA
TCTATCTTGCATCCAACCTAGCATCTGGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACCCTC
ACCATTGATCCTGTGGAGGCTGATGATGCTGCAACCTATTACTGTCAGCAAAATAATGAGGATCCGTACACGTTCGG
AGGGGGGACCAAGCTGGAAATAAAA

(SEQ ID NO:12)

Fig. 5b) Heavy chain variable domain the anti-α2-integrin mAb

QVQLEQPGAE LVKPGAPVKL SCKASGYTFT SYWMNWVKQR PGRGLEWIGR IDPSDSETHY NQKFKDKATL
TVDKSSSTAY IQLSSLTSED SAVYYCAKVG RGYFDYWGQG TTLTVSS

(SEQ ID NO:2)

CAGGTCCAACTGCATCAGCCTGGGGCTGAACTTGTGAAGCCTGGGGCTCCAGTGAAGCTGTCCTGCAAGGCTTCTGG
CTACACCTTCACCAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACGAGGCCTCGAGTGGATTGGCAGGATTG
ATCCTTCCGATAGTGAAACTCACTACAATCAAAAGTTCAAGGACAAGGCCACACTGACTGTAGACAAATCCTCCAGC
ACAGCCTACATCCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAAGGTGGGACGGGGGTA
CTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA

(SEQ ID NO:13)

Fig.6

Fig. 6a: CDRs of the heavy chain variable domain

HCDR1

GYTFTSYWMN

(SEQ ID NO:3)

HCDR2

RIDPSDSETHYNQKFK

(SEQ ID NO:4)

HCDR3

VGRGYFDY

(SEQ ID NO:5)

Figure 6b: CDRs of the light chain variable domain

LCDR1:

RASESVESYGNSFIY

(SEQ ID NO: 6)

LCDR2:

LASNLAS

(SEQ ID NO: 7)

LCDR3:

QQNNEDPYT

(SEQ ID NO: 8)

Fig.7

Fig. 7a: chimeric (anti alpha 2VL-IGKC CL) Light Chain

NIVLTQSPASLAVSLGQRATISCRASESVESYGNSFIYWYQQKPGQAPKLLIYLASNLASGVPA
RFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPYTFGGGTKLEIKRTVAAPSVFIFPPSDEQ
LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEK
HKVYACEVTHQGLSSPVTKSFNRGEC

(Amino Acid Sequence: SEQ ID NO:9)

AACATTGTGCTGACCCAATCTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGAGGGCCACCATATCCTGCAGAGCCAG
TGAAAGTGTTGAGAGTTATGGCAACAGTTTTATTTACTGGTACCAGCAGAAACCAGGACAGGCACCCAAACTCCTCA
TCTATCTTGCATCCAACCTAGCATCTGGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTAGGACAGACTTCACCCTC
ACCATTGATCCTGTGGAGGCTGATGATGCTGCAACCTATTACTGTCAGCAAAATAATGAGGATCCGTACACGTTCGG
AGGGGGGACCAAGCTGGAAATAAAACGTACGGTGGCCGCTCCTTCCGTGTTCATCTTCCCTCCCTCCGACGAGCAGC
TGAAGTCCGGCACCGCCTCCGTGGTGTGTCTGCTGAACAACTTCTACCCTCGGGAGGCCAAGGTGCAGTGGAAGGTG
GACAACGCCCTGCAGTCCGGCAACTCCCAGGAGTCCGTCACCGAGCAGGACTCCAAGGACAGCACCTACTCCCTGTC
CTCCACCCTGACCCTGTCCAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGTGAGGTGACCCACCAGGGCCTGT
CCAGCCCTGTGACCAAGTCCTTCAACCGGGGCGAGTGC

(coding Sequence: SEQ ID NO:14)

Fig.7b: Chimeric (anti α2 VH-IGHG4 CH1) mAb

QVQLHQPGAELVKPGAPVKLSCKASGYTFTSYWMNWVKQRPGRGLEWIGRIDPSDSETHYNQKF
KDKATLTVDKSSSTAYIQLSSLTSEDSAVYYCAKVGRGYFDYWGQGTTLTVSSASTKGPSVFPL
APCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV
SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG

(Amino Acid Sequence: SEQ ID NO:10)

CAGGTCCAACTGCATCAGCCTGGGGCTGAACTTGTGAAGCCTGGGGCTCCAGTGAAGCTGTCCTGCAAGGCTTCTGG
CTACACCTTCACCAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACGAGGCCTCGAGTGGATTGGCAGGATTG

ATCCTTCCGATAGTGAAACTCACTACAATCAAAAGTTCAAGGACAAGGCCACACTGACTGTAGACAAATCCTCCAGC
ACAGCCTACATCCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAAGGTGGGACGGGGGTA
CTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAGCACCAAGGGCCCTTCCGTGTTCCCTCTGG
CCCCTTGCTCCCGGTCCACCTCCGAGTCCACCGCCGCTCTGGGCTGCCTGGTGAAGGACTACTTCCCTGAGCCTGTG
ACCGTGTCCTGGAACTCTGGCGCCCTGACCTCCGGCGTGCACACCTTCCCTGCCGTGCTGCAGTCCTCCGGCCTGTA
CTCCCTGTCCTCCGTGGTGACCGTGCCTTCCTCCTCCCTGGGCACCAAGACCTACACCTGTAACGTGGACCACAAGC
CTTCCAACACCAAGGTGGACAAGCGGGTGGAGTCCAAGTACGGCCCTCCTTGCCCTCCCTGCCCTGCCCCTGAGTTC
GAGGGCGGACCTAGCGTGTTCCTGTTCCCTCCTAAGCCTAAGGACACCCTGATGATCTCCCGGACCCCTGAGGTGAC
CTGTGTGGTGGTGGACGTGTCCCAGGAGGACCCTGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACA
ACGCCAAGACCAAGCCTCGGGAGGAGCAGTTCAATTCCACCTACCGGGTGGTGTCTGTGCTGACCGTGCTGCACCAG
GACTGGCTGAACGGCAAAGAATACAAGTGTAAGGTCTCCAACAAGGGCCTGCCCTCCTCCATCGAGAAAACCATCTC
CAAGGCCAAGGGCCAGCCTAGGGAGCCTCAGGTGTACACCCTGCCTCCTAGCCAGGAAGAGATGACCAAGAACCAGG
TGTCCCTGACCTGTCTGGTGAAGGGCTTCTACCCTTCCGACATCGCCGTGGAGTGGGAGTCCAACGGCCAGCCTGAG
AACAACTACAAGACCACCCCTCCTGTGCTGGACTCCGACGGCTCCTTCTTCCTGTACTCCAGGCTGACCGTGGACAA
GTCCCGGTGGCAGGAGGGCAACGTCTTTTCCTGCTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGT
CCCTGTCCCTGTCTCTGGGC

(coding Sequence: SEQ ID NO:15)

Fig. 7c: Chimeric (anti α2 VH-IGHG1 CH1) heavy chain Fab fragment

QVQLHQPGAELVKPGAPVKLSCKASGYTFTSYWMNWVKQRPGRGLEWIGRIDPSDSETHYNQKF
KDKATLTVDKSSSTAYIQLSSLTSEDSAVYYCAKVGRGYFDYWGQGTTLTVSSASTKGPSVFPL
APSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
LGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT*HHHHHH*

(Amino Acid Sequence: SEQ ID NO:11)

CAGGTCCAACTGCATCAGCCTGGGGCTGAACTTGTGAAGCCTGGGGCTCCAGTGAAGCTGTCCTGCAAGGCTTCTGG
CTACACCTTCACCAGCTACTGGATGAACTGGGTGAAGCAGAGGCCTGGACGAGGCCTCGAGTGGATTGGCAGGATTG
ATCCTTCCGATAGTGAAACTCACTACAATCAAAAGTTCAAGGACAAGGCCACACTGACTGTAGACAAATCCTCCAGC
ACAGCCTACATCCAACTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAAGGTGGGACGGGGGTA
CTTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCAGCCAGCACCAAGGGCCCATCCGTGTTCCCTCTGG
CCCCTTCCTCCAAGTCCACCTCCGGCGGCACCGCCGCTCTGGGCTGCCTGGTGAAGGACTACTTCCCTGAGCCTGTG
ACCGTGTCCTGGAACTCTGGCGCCCTGACCAGCGGCGTGCACACCTTCCCTGCCGTGCTGCAGTCCTCCGGCCTGTA
CTCCCTGTCCTCCGTGGTGACCGTGCCTTCCTCCTCCCTGGGCACCCAGACCTACATCTGTAACGTGAACCACAAGC
CCTCCAACACCAAGGTGGACAAGAAGGTGGAGCCTAAGTCCTGTGACAAGACCCACACCCATCACCATCACCATCAC

(coding Sequence: SEQ ID NO:16)

Fig.8

Human constant regions for generation of chimeric antibody constructs

Swiss-Prot: Q502W4

>gi|74740177|sp|Q502W4|Q502W4_HUMAN IGKC protein

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA

DYEKHKVYACEVTHQGLSSPVTKSFNRGEC

(Amino Acid Sequence: SEQ ID NO:17)

Swiss-Prot: P01861.1 (S108P, L115E)

>gi|121047|sp|P01861.1|IGHG4_HUMAN RecName: Full=Ig gamma-4 chain C region

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG

TKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ

FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL

PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVM

HEALHNHYTQKSLSLSLGK

(Amino Acid Sequence: SEQ ID NO:18)

Swiss-Prot: Q569F4

>gi|74735951|sp|Q569F4|Q569F4_HUMAN IGHG1 protein

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG

TQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP

EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV

YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC

SVMHEALHNHYTQKSLSLSPGK

(Amino Acid Sequence: SEQ ID NO:19)

Fig.9

Human α2 and β1 integrin sequences

α2 integrin precursor according to accession No: NP_002194.2:

```
   1 mgpertgaap lplllvlals qgilncclay nvglpeakif sgpsseqfgy avqqfinpkg
  61 nwllvgspws gfpenrmgdv ykcpvdlsta tceklnlqts tsipnvtemk tnmslglilt
 121 rnmgtggflt cgplwaqqcg nqyyttgvcs dispdfqlsa sfspatqpcp slidvvvvcd
 181 esnsiypwda vknflekfvq gldigptktq vgliqyannp rvvfnlntyk tkeemivats
 241 qtsqyggdlt ntfgaiqyar kyaysaasgg rrsatkvmvv vtdgeshdgs mlkavidqcn
 301 hdnilrfgia vlgylnrnal dtknlikeik aiasiptery ffnvsdeaal lekagtlgeq
 361 ifsiegtvqg gdnfqmemsq vgfsadyssq ndilmlgavg afgwsgtivq ktshghlifp
 421 kqafdqilqd rnhssylgys vaaistgest hfvagapran ytgqivlysv nengnitviq
 481 ahrgdqigsy fgsvlcsvdv dkdtitdvll vgapmymsdl kkeegrvylf tikegilgqh
 541 qflegpegie ntrfgsaiaa lsdinmdgfn dvivgsplen qnsgavyiyn ghqgtirtky
 601 sqkilgsdga frshlqyfgr sldgygdlng dsitdvsiga fgqvvqlwsq siadvaieas
 661 ftpekitlvn knaqiilklc fsakfrptkq nnqvaivyni tldadgfssr vtsrglfken
 721 nerclqknmv vnqaqscpeh iiyiqepsdv vnsldlrvdi slenpgtspa leaysetakv
 781 fsipfhkdcg edglcisdlv ldvrqipaaq eqpfivsnqn krltfsvtlk nkresayntg
 841 ivvdfsenlf fasfslpvdg tevtcqvaas qksvacdvgy palkreqqvt ftinfdfnlq
 901 nlqnqaslsf qalsesqeen kadnlvnlki pllydaeihl trstninfye issdgnvpsi
 961 vhsfedvgpk fifslkvttg svpvsmatvi ihipqytkek nplmyltgvq tdkagdiscn
1021 adinplkigq tsssvsfkse nfrhtkelnc rtascsnvtc wlkdvhmkge yfvnvttriw
1081 ngtfasstfq tvqltaaaei ntynpeiyvi edntvtiplm imkpdekaev ptgviigsii
1141 agillllalv ailwklgffk rkyekmtknp deidettels s
```

(SEQ ID NO:20)

α2 integrin coding sequence (hs) according to NCBI accession No: NM_002203.3:

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   1 atggggccag aacggacagg ggccgcgccg ctgccgctgc tgctggtgtt agcgctcagt
  61 caaggcattt taaattgttg tttggcctac aatgttggtc tcccagaagc aaaaatattt
 121 tccggtcctt caagtgaaca gtttggctat gcagtgcagc agtttataaa tccaaaaggc
 181 aactggttac tggttggttc accctggagt ggctttcctg agaaccgaat gggagatgtg
 241 tataaatgtc ctgttgacct atccactgcc acatgtgaaa aactaaattt gcaaacttca
 301 acaagcattc caaatgttac tgagatgaaa accaacatga gcctcggctt gatcctcacc
 361 aggaacatgg gaactggagg ttttctcaca tgtggtcctc tgtgggcaca gcaatgtggg
 421 aatcagtatt acacaacggg tgtgtgttct gacatcagtc ctgattttca gctctcagcc
 481 agcttctcac ctgcaactca gccctgccct tccctcatag atgttgtggt tgtgtgtgat
 541 gaatcaaata gtatttatcc ttgggatgca gtaaagaatt ttttggaaaa atttgtacaa
 601 ggcctggata taggccccac aaagacacag gtggggttaa ttcagtatgc caataatcca
 661 agagttgtgt ttaacttgaa cacatataaa accaaagaag aaatgattgt agcaacatcc
 721 cagacatccc aatatggtgg ggacctcaca aacacattcg gagcaattca atatgcaaga
 781 aaatatgctt attcagcagc ttctggtggg cgacgaagtg ctacgaaagt aatggtagtt
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1021 tttttcaatg tgtctgatga agcagctcta ctagaaaagg ctgggacatt aggagaacaa
1081 attttcagca ttgaaggtac tgttcaagga ggagacaact ttcagatgga aatgtcacaa
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1441 gctcaccgag gtgaccagat tggctcctat tttggtagtg tgctgtgttc agttgatgtg
1501 gataaagaca ccattacaga cgtgctcttg gtaggtgcac caatgtacat gagtgaccta
1561 aagaaagagg aaggaagagt ctacctgttt actatcaaag agggcatttt gggtcagcac
1621 caatttcttg aaggccccga gggcattgaa aacactcgat ttggttcagc aattgcagct
1681 ctttcagaca tcaacatgga tggctttaat gatgtgattg ttggttcacc actagaaaat
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1741 cagaattctg gagctgtata catttacaat ggtcatcagg gcactatccg cacaaagtat

1801 tcccagaaaa tcttgggatc cgatggagcc tttaggagcc atctccagta ctttgggagg

1861 tccttggatg gctatggaga tttaaatggg gattccatca ccgatgtgtc tattggtgcc

1921 tttggacaag tggttcaact ctggtcacaa agtattgctg atgtagctat agaagcttca

1981 ttcacaccag aaaaaatcac tttggtcaac aagaatgctc agataattct caaactctgc

2041 ttcagtgcaa agttcagacc tactaagcaa aacaatcaag tggccattgt atataacatc

2101 acacttgatg cagatggatt ttcatccaga gtaacctcca gggggttatt taaagaaaac

2161 aatgaaaggt gcctgcagaa gaatatggta gtaaatcaag cacagagttg ccccgagcac

2221 atcatttata tacaggagcc ctctgatgtt gtcaactctt tggatttgcg tgtggacatc

2281 agtctggaaa accctggcac tagccctgcc cttgaagcct attctgagac tgccaaggtc

2341 ttcagtattc ctttccacaa agactgtggt gaggacggac tttgcatttc tgatctagtc

2401 ctagatgtcc gacaaatacc agctgctcaa gaacaaccct ttattgtcag caaccaaaac

2461 aaaaggttaa cattttcagt aacgctgaaa aataaaaggg aaagtgcata caacactgga

2521 attgttgttg atttttcaga aaacttgttt tttgcatcat tctccctgcc ggttgatggg

2581 acagaagtaa catgccaggt ggctgcatct cagaagtctg ttgcctgcga tgtaggctac

2641 cctgctttaa agagagaaca acaggtgact tttactatta actttgactt caatcttcaa

2701 aaccttcaga atcaggcgtc tctcagtttc caagccttaa gtgaaagcca agaagaaaac

2761 aaggctgata atttggtcaa cctcaaaatt cctctcctgt atgatgctga aattcactta

2821 acaagatcta ccaacataaa tttttatgaa atctcttcgg atgggaatgt tccttcaatc

2881 gtgcacagtt ttgaagatgt tggtccaaaa ttcatcttct ccctgaaggt aacaacagga

2941 agtgttccag taagcatggc aactgtaatc atccacatcc ctcagtatac caaagaaaag

3001 aacccactga tgtacctaac tggggtgcaa acagacaagg ctggtgacat cagttgtaat

3061 gcagatatca atccactgaa aataggacaa acatcttctt ctgtatcttt caaaagtgaa

3121 aatttcaggc acaccaaaga attgaactgc agaactgctt cctgtagtaa tgttacctgc

3181 tggttgaaag acgttcacat gaaaggagaa tactttgtta atgtgactac cagaatttgg

3241 aacgggactt tcgcatcatc aacgttccag acagtacagc taacggcagc tgcagaaatc

3301 aacacctata accctgagat atatgtgatt gaagataaca ctgttacgat tcccctgatg

3361 ataatgaaac ctgatgagaa agccgaagta ccaacaggag ttataatagg aagtataatt

3421 gctggaatcc ttttgctgtt agctctggtt gcaattttat ggaagctcgg cttcttcaaa

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3481 agaaaatatg aaaagatgac caaaaatcca gatgagattg atgagaccac agagctcagt
3541 agctga
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(SEQ ID NO: 21)

β1 integrin isoform 1A precursor (hs) according to NCBI accession No. NP_002202.2:

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   1 mnlqpifwig lissvccvfa qtdenrclka nakscgeciq agpncgwctn stflqegmpt
  61 sarcddleal kkkgcppddi enprgskdik knknvtnrsk gtaeklkped itqiqpqqlv
 121 lrlrsgepqt ftlkfkraed ypidlyylmd lsysmkddle nvkslgtdlm nemrritsdf
 181 rigfgsfvek tvmpyisttp aklrnpctse qnctspfsyk nvlsltnkge vfnelvgkqr
 241 isgnldspeg gfdaimqvav cgsligwrnv trllvfstda gfhfagdgkl ggivlpndgq
 301 chlennmytm shyydypsia hlvqklsenn iqtifavtee fqpvykelkn lipksavgtl
 361 sanssnviql iidaynslss evilengkls egvtisyksy ckngvngtge ngrkcsnisi
 421 gdevqfeisi tsnkcpkkds dsfkirplgf teevevilqy icececqseg ipespkcheg
 481 ngtfecgacr cnegrvgrhc ecstdevnse dmdaycrken sseicsnnge cvcgqcvcrk
 541 rdntneiysg kfcecdnfnc drsnglicgg ngvckcrvce cnpnytgsac dcsldtstce
 601 asngqicngr gicecgvckc tdpkfqgqtc emcqtclgvc aehkecvqcr afnkgekkdt
 661 ctqecsyfni tkvesrdklp qpvqpdpvsh ckekdvddcw fyftysvngn nevmvhvven
 721 pecptgpdii pivagvvagi vliglallli wkllmiihdr refakfekek mnakwdtgen
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(SEQ ID NO:22)

β1 integrin coding sequence (hs) isoform 1A according to NCBI accession No. NM_002211.3:

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  61 cgccgagtcc cctcctcccg cccctgagga ggaggagccg ccgccacccg ccgcgcccga
 121 cacccgggag gccccgccag cccgcgggag aggcccagcg ggagtcgcgg aacagcaggc
 181 ccgagcccac cgcgccgggc cccggacgcc gcgcggaaaa gatgaattta caaccaattt
 241 tctggattgg actgatcagt tcagtttgct gtgtgtttgc tcaaacagat gaaaatagat
```

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 301 gtttaaaagc aaatgccaaa tcatgtggag aatgtataca agcagggcca aattgtgggt
 361 ggtgcacaaa ttcaacattt ttacaggaag gaatgcctac ttctgcacga tgtgatgatt
 421 tagaagcctt aaaaaagaag ggttgccctc cagatgacat agaaaatccc agaggctcca
 481 aagatataaa gaaaaataaa aatgtaacca accgtagcaa aggaacagca gagaagctca
 541 agccagagga tattactcag atccaaccac agcagttggt tttgcgatta agatcagggg
 601 agccacagac atttacatta aaattcaaga gagctgaaga ctatcccatt gacctctact
 661 accttatgga cctgtcttac tcaatgaaag acgatttgga gaatgtaaaa agtcttggaa
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 961 ctccagaagg tggtttcgat gccatcatgc aagttgcagt ttgtggatca ctgattggct
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1861 tttattctgg caaattctgc gagtgtgata atttcaactg tgatagatcc aatggcttaa
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2161 ttcagtgcag agccttcaat aaaggagaaa agaaagacac atgcacacag gaatgttcct

2221 attttaacat taccaaggta gaaagtcggg acaaattacc ccagccggtc caacctgatc

2281 ctgtgtccca ttgtaaggag aaggatgttg acgactgttg gttctatttt acgtattcag

2341 tgaatgggaa caacgaggtc atggttcatg ttgtggagaa tccagagtgt cccactggtc

2401 cagacatcat tccaattgta gctggtgtgg ttgctggaat tgttcttatt ggccttgcat

2461 tactgctgat atggaagctt ttaatgataa ttcatgacag aagggagttt gctaaatttg

2521 aaaaggagaa aatgaatgcc aaatgggaca cgggtgaaaa tcctatttat aagagtgccg

2581 taacaactgt ggtcaatccg aagtatgagg gaaaatgagt actgcccgtg caaatcccac

2641 aacactgaat gcaaagtagc aatttccata gtcacagtta ggtagcttta gggcaatatt

2701 gccatggttt tactcatgtg caggttttga aaatgtacaa tatgtataat ttttaaaatg

2761 ttttattatt ttgaaaataa tgttgtaatt catgccaggg actgacaaaa gacttgagac

2821 aggatggtta ctcttgtcag ctaaggtcac attgtgcctt tttgaccttt tcttcctgga

2881 ctattgaaat caagcttatt ggattaagtg atatttctat agcgattgaa agggcaatag

2941 ttaaagtaat gagcatgatg agagtttctg ttaatcatgt attaaaactg atttttagct

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3121 ctgaaagaca agtatgttga gagttgctgg tgtaaaatac gtttgaaata gttgatctac

3181 aaaggccatg ggaaaaattc agagagttag gaaggaaaaa ccaatagctt taaaacctgt

3241 gtgccatttt aagagttact taatgtttgg taacttttat gccttcactt tacaaattca

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3601 ctcacctacg cgagtcttac tttgagttag tgccataaca gaccactgta tgtttacttc

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3841 tttatagatt aaagaagttg aggaaaagca aaaaaaaaa

(SEQ ID NO:23)

Fig.10

Fig. 10a: cDNA encoding LC of anti-α2 integrin mAB

```
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```

(SEQ ID NO:45)

Fig. 10b: cDNA encoding HC anti-α2 integrin mAB

```
atgggatggagctgtatcatcctcttcttggtagcaacagccacaggtgtccactcccaggtccaactgcatcagcc
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actcccgggaagtga
```

(SEQ ID NO:46)

Fig. 10c: Amino acid sequence of secreted LC of anti-α2 integrin mAB

```
nivltqspaslavslgqratiscrasesvesygnsfiywyqqkpgqapklliylasnlasgvparfsgsgsrtdftl
tidpveaddaatyycqqnnedpytfgggtkleikradaaptvsifppsseqltsggasvvcflnnfypkdinvkwki
dgserqngvlnswtdqdskdstysmsstltltkdeyerhnsytceathktstspivksfnrnec
```

(SEQ ID NO:47)

Fig. 10d: Amino acid sequence of secreted HC of anti-α2 integrin mAB

qvqlhqpgaelvkpgapvklsckasgytftsywmnwvkqrpgrglewigridpsdsethynqkfkdkatltvdksss
tayiqlssltsedsavyycakvgrgyfdywgqgttltvssakttapsvyplapvcgdttgssvtlgclvkgyfpepv
tltwnsgslssgvhtfpavlqsdlytlsssvtvtsstwpsqsitcnvahpasstkvdkkieprgptikpcppckcpa
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ktelnykntepvldsdgsyfmysklrvekknwvernsyscsvvheglhnhhttksfsrtpgk

(SEQ ID NO:48)

Fig. 10e: Amino acid sequence of comparator antibody

Amino acid sequence of LC of comparator

DFVMTQSPAFLSVTPGEKVTITCSAQSSVNYIHWYQQKPDQAPKKLIYDTSKLASGVPSR
FSGSGSGTDYTFTISSLEAEDAATYYCQQWTTNPLTFGQGTKVEIKRTVAAPSVFIFPPS
DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL
SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

(SEQ ID NO.53)

Fig. 10f: Amino acid sequence of HC of comparator

QVQLQESGPGLVKPSETLSLTCTVSGFSLTNYGIHWIRQPPGKGLEWLGVIWARGFTN
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VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPE
FEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP
REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVY
TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG

(SEQ ID NO:54)

Fig.11

Fig. 11: Equilibrium dissociation constants K_D for the humanized variants and the comparator as determined by Biacore

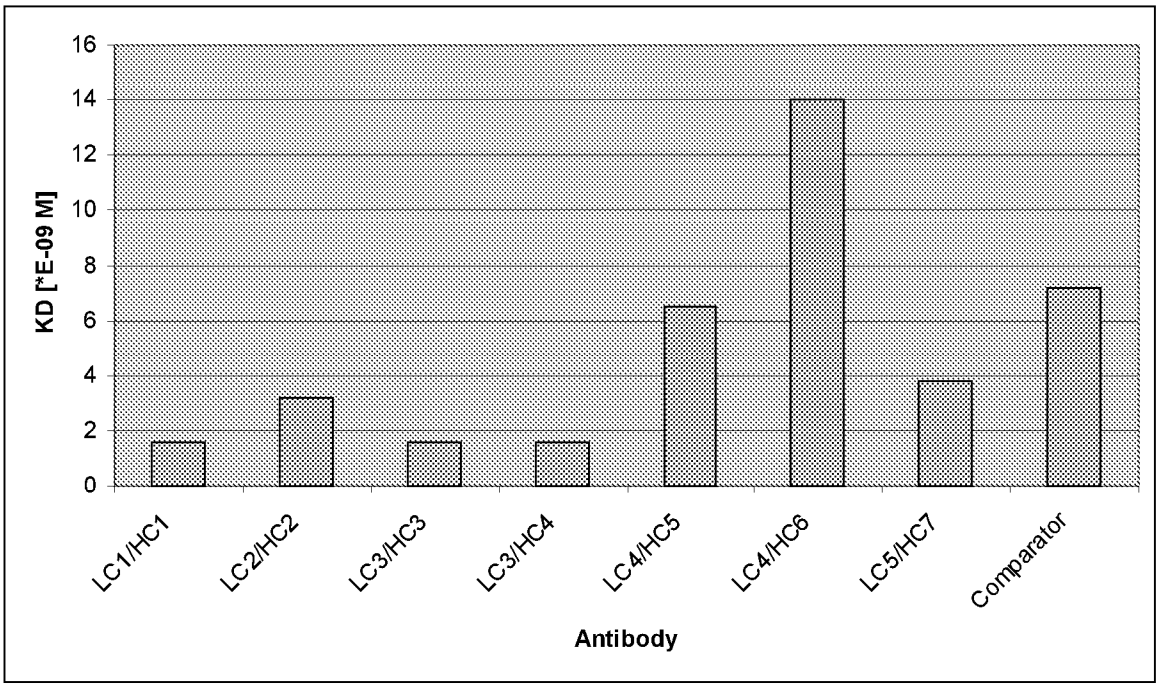


Fig.12

Fig. 12: Binding of comparator mAb TMC2206 to integrin α_2 I domain pre-bound by non-humanized Fab measured using Biacore

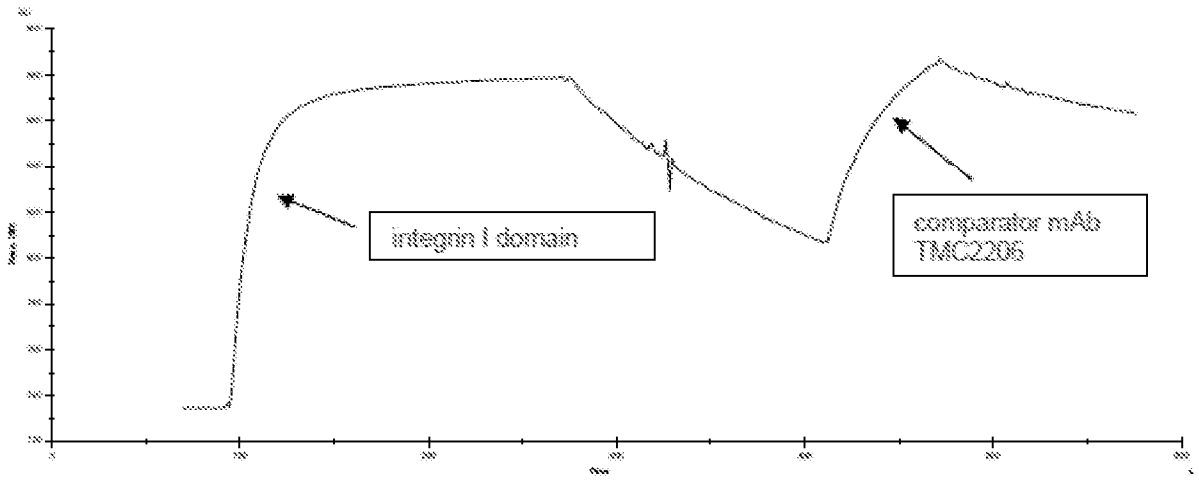


Fig.13

Fig. 13: Binding of non-humanized Fab to integrin α_2 I domain pre-bound by comparator mAb TMC2206

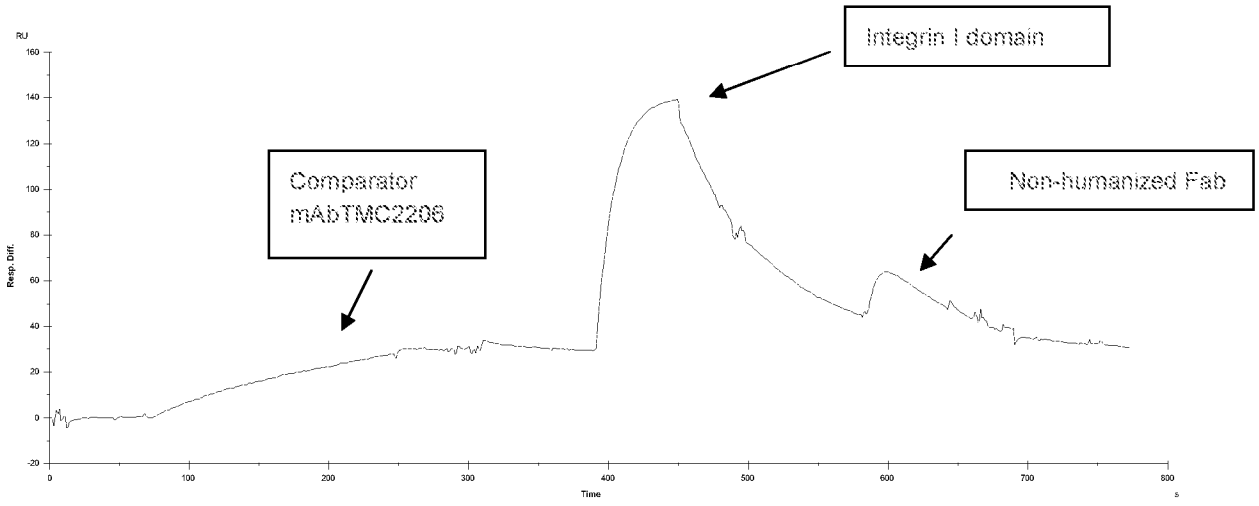


Fig.14

Figure 14: Inhibiton of platelet adhesion to collagen under static conditions using washed platelets

