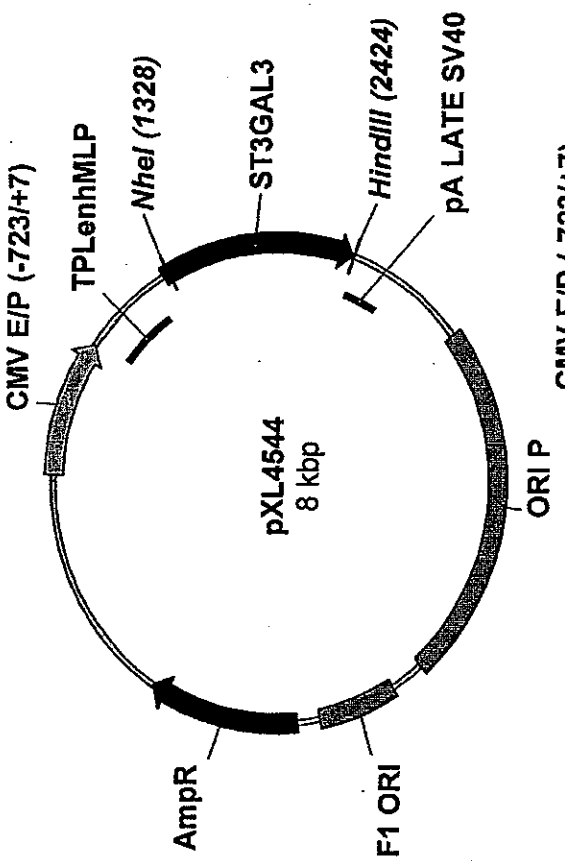

CMV E/P (-723/+7)
TPLenhMLP
NheI (1328)
ST3GAL3
HindIII (2424)
pA LATE SV40
pXL4544
8 kbp
ORI P
AmpR
F1 ORI

Fig. 1A

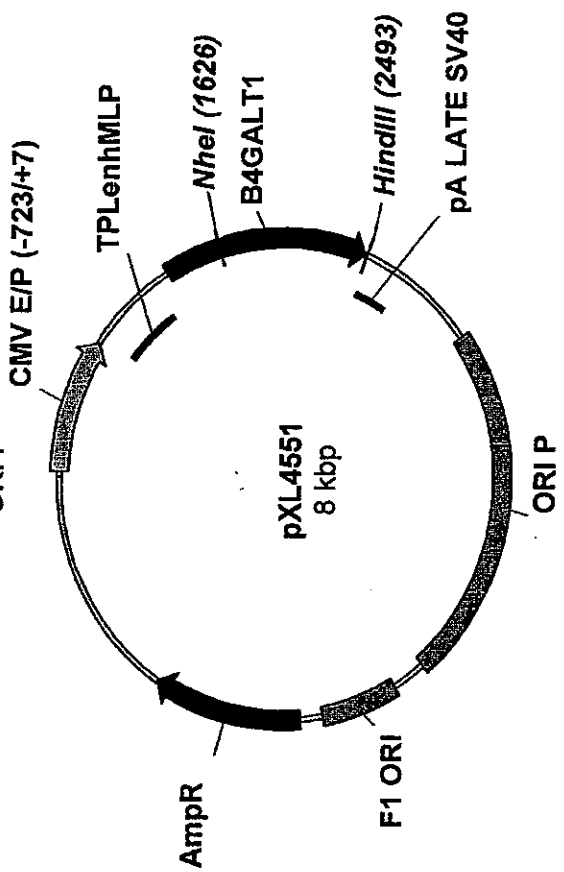

CMV E/P (-723/+7)
TPLenhMLP
NheI (1626)
B4GALT1
HindIII (2493)
pA LATE SV40
pXL4551
8 kbp
ORI P
AmpR
F1 ORI

Fig. 1B

Fig. 2A


1281
ATGAGG CTTCGGGAGC CGCTCCTGAG CGGCAGCGCC GCGATGCCAG GCGCGTCCCT ACAGCGGGCC
TACTCC GAAGCCCTCG GCGAGGACTC GCCGTCGCGG CGCTACGGTC CGCGCAGGGA TGTCGCCCGG
1361
TGCCGCCTGC TCGTGGCCGT CTGCGCTCTG CACCTTGGCG TCACCCTCGT TTACTACCTG GCTGGCCGCG ACCTGAGCCG
ACGGCGGACG AGCACCGGCA GACGCGAGAC GTGGAACCGC AGTGGGAGCA AATGATGGAC CGACCGGCGC TGGACTCGGC
1441
CCTGCCCCAA CTGGTCGGAG TCTCCACACC GCTGCAGGGC GGCTCGAACA GTGCCGCCGC CATCGGGCAG TCCTCCGGGG
GGACGGGGTT GACCAGCCTC AGAGGTGTGG CGACGTCCCG CCGAGCTTGT CACGGCGGCG GTAGCCCGTC AGGAGGCCCC
1521
AGCTCCGGAC CGGAGGGGCC CGGCCGCCGC CTCCTCTAGG CGCCTCCTCC CAGCCGCGCC CGGGTGGCGA CTCCAGCCCA
TCGAGGCCTG GCCTCCCCGG GCCGGCGGCG GAGGAGATCC GCGGAGGAGG GTCGGCGCGG GCCCACCGCT GAGGTCGGGT
1601
GTCGTGGATT CTGGCCCTGG CCCCGCTAGC AACTTGACCT CGGTCCCAGT GCCCCACACC ACCGCACTGT CGCTGCCCGC
CAGCACCTAA GACCGGGACC GGGGCGATCG TTGAACTGGA GCCAGGGTCA CGGGGTGTGG TGGCGTGACA GCGACGGGCG
1681
CTGCCCTGAG GAGTCCCCGC TGCTTGTGGG CCCCATGCTG ATTGAGTTTA ACATGCCTGT GGACCTGGAG CTCGTGGCAA
GACGGGACTC CTCAGGGGCG ACGAACACCC GGGGTACGAC TAACTCAAAT TGTACGGACA CCTGGACCTC GAGCACCGTT
1761
AGCAGAACCC AAATGTGAAG ATGGGCGGCC GCTATGCCCC CAGGGACTGC GTCTCTCCTC ACAAGGTGGC CATCATCATT
TCGTCTTGGG TTTACACTTC TACCCGCCGG CGATACGGGG GTCCCTGACG CAGAGAGGAG TGTTCCACCG GTAGTAGTAA
1841
CCATTCCGCA ACCGGCAGGA GCACCTCAAG TACTGGCTAT ATTATTTGCA YCCAGTCCTG CAGCGCCAGC AGCTGGACTA
GGTAAGGCGT TGGCCGTCCT CGTGGAGTTC ATGACCGATA TAATAAACGT RGGTCAGGAC GTCGCGGTCG TCGACCTGAT
1921
TGGCATCTAT GTTATCAACC AGGCGGGAGA CACTATATTC AATCGTGCTA AGCTCCTCAA TGTTGGCTTT CAAGAAGCCT
ACCGTAGATA CAATAGTTGG TCCGCCCTCT GTGATATAAG TTAGCACGAT TCGAGGAGTT ACAACCGAAA GTTCTTCGGA
2001
TGAAGGACTA TGACTACACC TGCTTTGTGT TTAGTGACGT GGACCTCATT CCAATGAATG ACCATAATGC GTACAGGTGT
ACTTCCTGAT ACTGATGTGG ACGAAACACA AATCACTGCA CCTGGAGTAA GGTTACTTAC TGGTATTACG CATGTCCACA
2081
TTTTCACAGC CACGGCACAT TTCCGTTGCA ATGGATAAGT TTGGATTCAG CCTACCTTAT GTTCAGTATT TTGGAGGTGT
AAAAGTGTCG GTGCCGTGTA AAGGCAACGT TACCTATTCA AACCTAAGTC GGATGGAATA CAAGTCATAA AACCTCCACA
2161
CTCTGCTCTA AGTAAACAAC AGTTTCTAAC CATCAATGGA TTTCCTAATA ATTATTGGGG CTGGGGAGGA GAAGATGATG
GAGACGAGAT TCATTTGTTG TCAAAGATTG GTAGTTACCT AAAGGATTAT TAATAACCCC GACCCCTCCT CTTCTACTAC
2241
ACATTTTTAA CAGATTAGTT TTTAGAGGCA TGTCTATATC TCGCCCAAAT GCTGTGGTCG GGAGGTGTCG CATGATCCGC
TGTAAAAATT GTCTAATCAA AAATCTCCGT ACAGATATAG AGCGGGTTTA CGACACCAGC CCTCCACAGC GTACTAGGCG
2321
CACTCAAGAG ACAAGAAAAA TGAACCCAAT CCTCAGAGGT TTGACCGAAT TGCACACACA AAGGAGACAA TGCTCTCTGA
GTGAGTTCTC TGTTCTTTTT ACTTGGGTTA GGAGTCTCCA AACTGGCTTA ACGTGTGTGT TTCCTCTGTT ACGAGAGACT
2401
TGGTTTGAAC TCACTCACCT ACCAGGTGCT GGATGTACAG AGATACCCAT TGTATACCCA AATCACAGTG GACATCGGGA
ACCAAACTTG AGTGAGTGGA TGGTCCACGA CCTACATGTC TCTATGGGTA ACATATGGGT TTAGTGTCAC CTGTAGCCCT
2481
CACCGAGCTA G
GTGGCTCGAT C

Fig. 2B

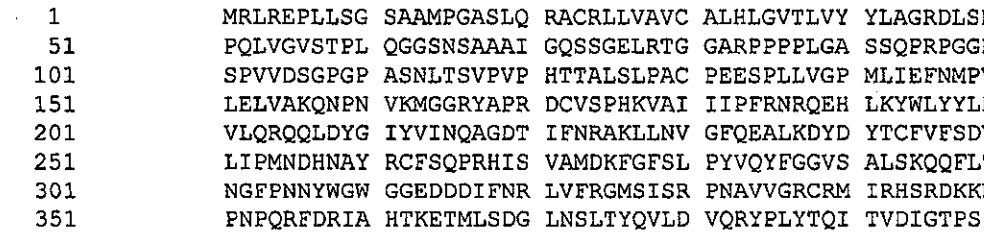

1
MRLREPLLSG SAAMPGASLQ RACRLLVAVC ALHLGVTLVY YLAGRDLSRL
51
PQLVGVSTPL QGGSNSAAAI GQSSGELRTG GARPPPPLGA SSQPRPGGDS
101
SPVVDSGPGP ASNLTSVPVP HTTALSLPAC PEESPLLVGP MLIEFNMPVD
151
LELVAKQNPN VKMGGRYAPR DCVSPHKVAI IIPFRNRQEH LKYWLYYLHP
201
VLQRQQLDYG IYVINQAGDT IFNRAKLLNV GFQEALKDYD YTCFVFSDVD
251
LIPMNDHNAY RCFSQPRHIS VAMDKFGFSL PYVQYFGGVS ALSKQQFLTI
301
NGFPNNYWGW GGEDDDIFNR LVFRGMSISR PNAVVGRCRM IRHSRDKKNE
351
PNPQRFDRIA HTKETMLSDG LNSLTYQVLD VQRYPLYTQI TVDIGTPS

Fig. 3A

```
1281                ATGGGA CTCTTGGTAT TTGTGCGCAA TCTGCTGCTA GCCCTCTGCC TCTTTCTGGT ACTGGGATTT
                    TACCCT GAGAACCATA AACACGCGTT AGACGACGAT CGGGAGACGG AGAAAGACCA TGACCCTAAA
1361        TTGTATTATT CTGCGTGGAA GCTACACTTA CTCCAGTGGG AGGAGGACTC CAATTCAGTG GTTCTTTCCT TTGACTCCGC
            AACATAATAA GACGCACCTT CGATGTGAAT GAGGTCACCC TCCTCCTGAG GTTAAGTCAC CAAGAAAGGA AACTGAGGCG
1441        TGGACAAACA CTAGGCTCAG AGTATGATCG GTTGGGCTTC CTCCTGAATC TGGACTCTAA ACTGCCTGCT GAATTAGCCA
            ACCTGTTTGT GATCCGAGTC TCATACTAGC CAACCCGAAG GAGGACTTAG ACCTGAGATT TGACGGACGA CTTAATCGGT
1521        CCAAGTACGC AAACTTTTCA GAGGGAGCTT GCAAGCCTGG CTATGCTTCA GCCTTGATGA CGGCCATCTT CCCCCGGTTC
            GGTTCATGCG TTTGAAAAGT CTCCCTCGAA CGTTCGGACC GATACGAAGT CGGAACTACT GCCGGTAGAA GGGGGCCAAG
1601        TCCAAGCCAG CACCCATGTT CCTGGATGAC TCCTTTCGCA AGTGGGCTAG AATCCGGGAG TTCGTGCCGC CTTTTGGGAT
            AGGTTCGGTC GTGGGTACAA GGACCTACTG AGGAAAGCGT TCACCCGATC TTAGGCCCTC AAGCACGGCG GAAAACCCTA
1681        CAAAGGTCAA GACAATCTGA TCAAAGCCAT CTTGTCAGTC ACCAAAGAGT ACCGCCTGAC CCCTGCCTTG GACAGCCTCC
            GTTTCCAGTT CTGTTAGACT AGTTTCGGTA GAACAGTCAG TGGTTTCTCA TGGCGGACTG GGGACGGAAC CTGTCGGAGG
1761        GCTGCCGCCG CTGCATCATC GTGGGCAATG GAGGCGTTCT TGCCAACAAG TCTCTGGGGT CACGAATTGA CGACTATGAC
            CGACGGCGGC GACGTAGTAG CACCCGTTAC CTCCGCAAGA ACGGTTGTTC AGAGACCCCA GTGCTTAACT GCTGATACTG
1841        ATTGTGGTGA GACTGAATTC AGCACCAGTG AAAGGCTTTG AGAAGGACGT GGGCAGCAAA ACGACACTGC GCATCACCTA
            TAACACCACT CTGACTTAAG TCGTGGTCAC TTTCCGAAAC TCTTCCTGCA CCCGTCGTTT TGCTGTGACG CGTAGTGGAT
1921        CCCCGAGGGC GCCATGCAGC GGCCTGAGCA GTACGAGCGC GATTCTCTCT TTGTCCTCGC CGGCTTCAAG TGGCAGGACT
            GGGGCTCCCG CGGTACGTCG CCGGACTCGT CATGCTCGCG CTAAGAGAGA AACAGGAGCG GCCGAAGTTC ACCGTCCTGA
2001        TTAAGTGGTT GAAATACATC GTCTACAAGG AGAGAGTGAG TGCATCGGAT GGCTTCTGGA AATCTGTGGC CACTCGAGTG
            AATTCACCAA CTTTATGTAG CAGATGTTCC TCTCTCACTC ACGTAGCCTA CCGAAGACCT TTAGACACCG GTGAGCTCAC
2081        CCCAAGGAGC CCCCTGAGAT TCGAATCCTC AACCCATATT TCATCCAGGA GGCCGCCTTC ACCCTCATTG GCCTGCCCTT
            GGGTTCCTCG GGGGACTCTA AGCTTAGGAG TTGGGTATAA AGTAGGTCCT CCGGCGGAAG TGGGAGTAAC CGGACGGGAA
2161        CAACAATGGC CTCATGGGCC GGGGGAACAT CCCTACCCTT GGCAGTGTGG CAGTGACCAT GGCACTACAC GGCTGTGACG
            GTTGTTACCG GAGTACCCGG CCCCCTTGTA GGGATGGGAA CCGTCACACC GTCACTGGTA CCGTGATGTG CCGACACTGC
2241        AGGTGGCAGT CGCAGGATTT GGCTATGACA TGAGCACACC CAACGCACCC CTGCACTACT ATGAGACCGT TCGCATGGCA
            TCCACCGTCA GCGTCCTAAA CCGATACTGT ACTCGTGTGG GTTGCGTGGG GACGTGATGA TACTCTGGCA AGCGTACCGT
2321        GCCATCAAAG AGTCCTGGAC GCACAATATC CAGCGAGAGA AAGAGTTTCT GCGGAAGCTG GTGAAAGCTC GCGTCATCAC
            CGGTAGTTTC TCAGGACCTG CGTGTTATAG GTCGCTCTCT TTCTCAAAGA CGCCTTCGAC CACTTTCGAG CGCAGTAGTG
2401        TGATCTAAGC AGTGGCATCT GA
            ACTAGATTCG TCACCGTAGA CT
```

Fig. 3B

```
  1         MGLLVFVRNL LLALCLFLVL GFLYYSAWKL HLLQWEEDSN SVVLSFDSAG
 51         QTLGSEYDRL GFLLNLDSKL PAELATKYAN FSEGACKPGY ASALMTAIFP
101         RFSKPAPMFL DDSFRKWARI REFVPPFGIK GQDNLIKAIL SVTKEYRLTP
151         ALDSLRCRRC IIVGNGGVLA NKSLGSRIDD YDIVVRLNSA PVKGFEKDVG
201         SKTTLRITYP EGAMQRPEQY ERDSLFVLAG FKWQDFKWLK YIVYKERVSA
251         SDGFWKSVAT RVPKEPPEIR ILNPYFIQEA AFTLIGLPFN NGLMGRGNIP
301         TLGSVAVTMA LHGCDEVAVA GFGYDMSTPN APLHYYETVR MAAIKESWTH
351         NIQREKEFLR KLVKARVITD LSSGI
```

Fig. 4A

```
6241                                                ATGTACA GGATGCAACT CCTGTCTTGC ATTGCACTAA GTCTTGCACT
                                                    TACATGT CCTACGTTGA GGACAGAACG TAACGTGATT CAGAACGTGA
6321    TGTCACGAAT TCATTAGTTG AGGATACCAC ATTAGAGCCA GAAGAGCCAC CAACTAAATA CCAAATCTCT CAACCAGAAG
        ACAGTGCTTA AGTAATCAAC TCCTATGGTG TAATCTCGGT CTTCTCGGTG GTTGATTTAT GGTTTAGAGA GTTGGTCTTC
6401    TGTACGTGGC TGCACCAGGG GAGTCGCTAG AGGTGCGCTG CCTGTTGAAA GATGCCGCCG TGATCAGTTG GACTAAGGAT
        ACATGCACCG ACGTGGTCCC CTCAGCGATC TCCACGCGAC GGACAACTTT CTACGGCGGC ACTAGTCAAC CTGATTCCTA
6481    GGGGTGCACT TGGGGCCCAA CAATAGGACA GTGCTTATTG GGGAGTACTT GCAGATAAAG GGCGCCACGC CTAGAGACTC
        CCCCACGTGA ACCCCGGGTT GTTATCCTGT CACGAATAAC CCCTCATGAA CGTCTATTTC CCGCGGTGCG GATCTCTGAG
6561    CGGCCTCTAT GCTTGTACTG CCAGTAGGAC TGTAGACAGT GAAACTTGGT ACTTCATGGT GAATGTCACA GATGCCATCT
        GCCGGAGATA CGAACATGAC GGTCATCCTG ACATCTGTCA CTTTGAACCA TGAAGTACCA CTTACAGTGT CTACGGTAGA
6641    CATCCGGAGA TGATGAGGAT GACACCGATG GTGCGGAAGA TTTTGTCAGT GAGAACAGTA ACAACAAGAG AGCACCATAC
        GTAGGCCTCT ACTACTCCTA CTGTGGCTAC CACGCCTTCT AAAACAGTCA CTCTTGTCAT TGTTGTTCTC TCGTGGTATG
6721    TGGACCAACA CAGAAAAGAT GGAAAAGCGG CTCCATGCTG TGCCTGCGGC CAACACTGTC AAGTTTCGCT GCCCAGCCGG
        ACCTGGTTGT GTCTTTTCTA CCTTTTCGCC GAGGTACGAC ACGGACGCCG GTTGTGACAG TTCAAAGCGA CGGGTCGGCC
6801    GGGGAACCCA ATGCCAACCA TGCGGTGGCT GAAAAACGGG AAGGAGTTTA AGCAGGAGCA TCGCATTGGA GGCTACAAGG
        CCCCTTGGGT TACGGTTGGT ACGCCACCGA CTTTTTGCCC TTCCTCAAAT TCGTCCTCGT AGCGTAACCT CCGATGTTCC
6881    TACGAAACCA GCACTGGAGC CTCATTATGG AAAGTGTGGT CCCATCTGAC AAGGGAAATT ATACCTGTGT GGTGGAGAAT
        ATGCTTTGGT CGTGACCTCG GAGTAATACC TTTCACACCA GGGTAGACTG TTCCCTTTAA TATGGACACA CCACCTCTTA
6961    GAATACGGGT CCATCAATCA CACGTACCAC CTGGATGTTG TGGAGCGATC GCCTCACCGG CCCATCCTCC AAGCCGGACT
        CTTATGCCCA GGTAGTTAGT GTGCATGGTG GACCTACAAC ACCTCGCTAG CGGAGTGGCC GGGTAGGAGG TTCGGCCTGA
7041    GCCGGCAAAT GCCTCCACAG TGGTCGGAGG AGACGTAGAG TTTGTCTGCA AGGTTTACAG TGATGCCCAG CCCCACATCC
        CGGCCGTTTA CGGAGGTGTC ACCAGCCTCC TCTGCATCTC AAACAGACGT TCCAAATGTC ACTACGGGTC GGGGTGTAGG
7121    AGTGGATCAA GCACGTGGAA AAGAACGGCA GTAAATACGG GCCCGACGGG CTGCCCTACC TCAAGGTTCT CAAGGCCGCC
        TCACCTAGTT CGTGCACCTT TTCTTGCCGT CATTTATGCC CGGGCTGCCC GACGGGATGG AGTTCCAAGA GTTCCGGCGG
7201    GGTGTTAACA CCACGGACAA AGAGATTGAG GTTCTCTATA TTCGGAATGT AACTTTTGAG GACGCTGGGG AATATACGTG
        CCACAATTGT GGTGCCTGTT TCTCTAACTC CAAGAGATAT AAGCCTTACA TTGAAAACTC CTGCGACCCC TTATATGCAC
7281    CTTGGCGGGT AATTCTATTG GGATATCCTT TCACTCTGCA TGGTTGACAG TTCTGCCAGC GCCTGGAAGA GAAAAGGAGA
        GAACCGCCCA TTAAGATAAC CCTATAGGAA AGTGAGACGT ACCAACTGTC AAGACGGTCG CGGACCTTCT CTTTTCCTCT
7361    TTACAGCTTC CCCAGACTAC CTGTCAGCGC TAGAGCCCAA ATCTTGTGAC AAAACTCACA CATGCCCACC GTGCCCAGCA
        AATGTCGAAG GGGTCTGATG GACAGTCGCG ATCTCGGGTT TAGAACACTG TTTTGAGTGT GTACGGGTGG CACGGGTCGT
7441    CCTGAACTCC TGGGGGGACC GTCAGTCTTC CTCTTCCCCC CAAAACCCAA GGACACCCTC ATGATCTCCC GGACCCCTGA
        GGACTTGAGG ACCCCCCTGG CAGTCAGAAG GAGAAGGGGG GTTTTGGGTT CCTGTGGGAG TACTAGAGGG CCTGGGGACT
7521    GGTCACATGC GTGGTGGTGG ACGTGAGCCA CGAAGACCCT GAGGTCAAGT TCAACTGGTA CGTGGACGGC GTGGAGGTGC
        CCAGTGTACG CACCACCACC TGCACTCGGT GCTTCTGGGA CTCCAGTTCA AGTTGACCAT GCACCTGCCG CACCTCCACG
7601    ATAATGCCAA GACAAAGCCG CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCGT CCTGCACCAG
        TATTACGGTT CTGTTTCGGC GCCCTCCTCG TCATGTTGTC GTGCATGGCA CACCAGTCGC AGGAGTGGCA GGACGTGGTC
7681    GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA ACAAAGCCCT CCCAGCCCCC ATCGAGAAAA CCATCTCCAA
        CTGACCGACT TACCGTTCGT CATGTTCACG TTCCAGAGGT TGTTTCGGGA GGGTCGGGGG TAGCTCTTTT GGTAGAGGTT
7761    AGCCAAAGGG CAGCCCCGAG AACCACAGGT GTACACCCTG CCCCCATCCC GGGATGAGCT GACCAAGAAC CAGGTCAGCC
        TCGGTTTCCC GTCGGGGCTC TTGGTGTCCA CATGTGGGAC GGGGGTAGGG CCCTACTCGA CTGGTTCTTG GTCCAGTCGG
7841    TGACCTGCCT GGTCAAAGGC TTCTATCCCA GCGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACTAC
        ACTGGACGGA CCAGTTTCCG AAGATAGGGT CGCTGTAGCG GCACCTCACC CTCTCGTTAC CCGTCGGCCT CTTGTTGATG
7921    AAGACCACGC CTCCCGTGCT GGACTCCGAC GGCTCCTTCT TCCTCTACAG CAAGCTCACC GTGGACAAGA GCAGGTGGCA
        TTCTGGTGCG GAGGGCACGA CCTGAGGCTG CCGAGGAAGA AGGAGATGTC GTTCGAGTGG CACCTGTTCT CGTCCACCGT
8001    GCAGGGGAAC GTCTTCTCAT GCTCCGTGAT GCATGAGGCT CTGCACAACC ACTACACGCA GAAGAGCCTC TCCCTGTCTC
        CGTCCCCTTG CAGAAGAGTA CGAGGCACTA CGTACTCCGA GACGTGTTGG TGATGTGCGT CTTCTCGGAG AGGGACAGAG
8081    CGGGTTGA
        GCCCAACT
```

Fig. 4B

```
  1          LVEDTTLEPE EPPTKYQISQ PEVYVAAPGE SLEVRCLLKD AAVISWTKDG
 51          VHLGPNNRTV LIGEYLQIKG ATPRDSGLYA CTASRTVDSE TWYFMVNVTD
101          AISSGDDEDD TDGAEDFVSE NSNNKRAPYW TNTEKMEKRL HAVPAANTVK
151          FRCPAGGNPM PTMRWLKNGK EFKQEHRIGG YKVRNQHWSL IMESVVPSDK
201          GNYTCVVENE YGSINHTYHL DVVERSPHRP ILQAGLPANA STVVGGDVEF
251          VCKVYSDAQP HIQWIKHVEK NGSKYGPDGL PYLKVLKAAG VNTTDKEIEV
301          LYIRNVTFED AGEYTCLAGN SIGISFHSAW LTVLPAPGRE KEITASPDYL
351          SALEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM ISRTPEVTCV
401          VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD
451          WLNGKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTLP PSRDELTKNQ
501          VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV
551          DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPG
```

Fig. 4C

```
  1          LVEDTTLEPE EPPTKYQISQ PEVYVAAPGE SLEVRCLLKD AAVISWTKDG
 51          VHLGPNNRTV LIGEYLQIKG ATPRDSGLYA CTASRTVDSE TWYFMVNVTD
101          AISSGDDEDD TDGAEDFVSE NSNNKRAPYW TNTEKMEKRL HAVPAANTVK
151          FRCPAGGNPM PTMRWLKNGK EFKQEHRIGG YKVRNQHWSL IMESVVPSDK
201          GNYTCVVENE YGSINHTYHL DVVERSPHRP ILQAGLPANA STVVGGDVEF
251          VCKVYSDAQP HIQWIKHVEK NGSKYGPDGL PYLKVLKAAG VNTTDKEIEV
301          LYIRNVTFED AGEYTCLAGN SIGISFHSAW LTVLPAPGRE KEITASPDYL
```

Fig. 4D

```
  1          EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD
 51          VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN
101          GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR DELTKNQVSL
151          TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS
201          RWQQGNVFSC SVMHEALHNH YTQKSLSLSP G
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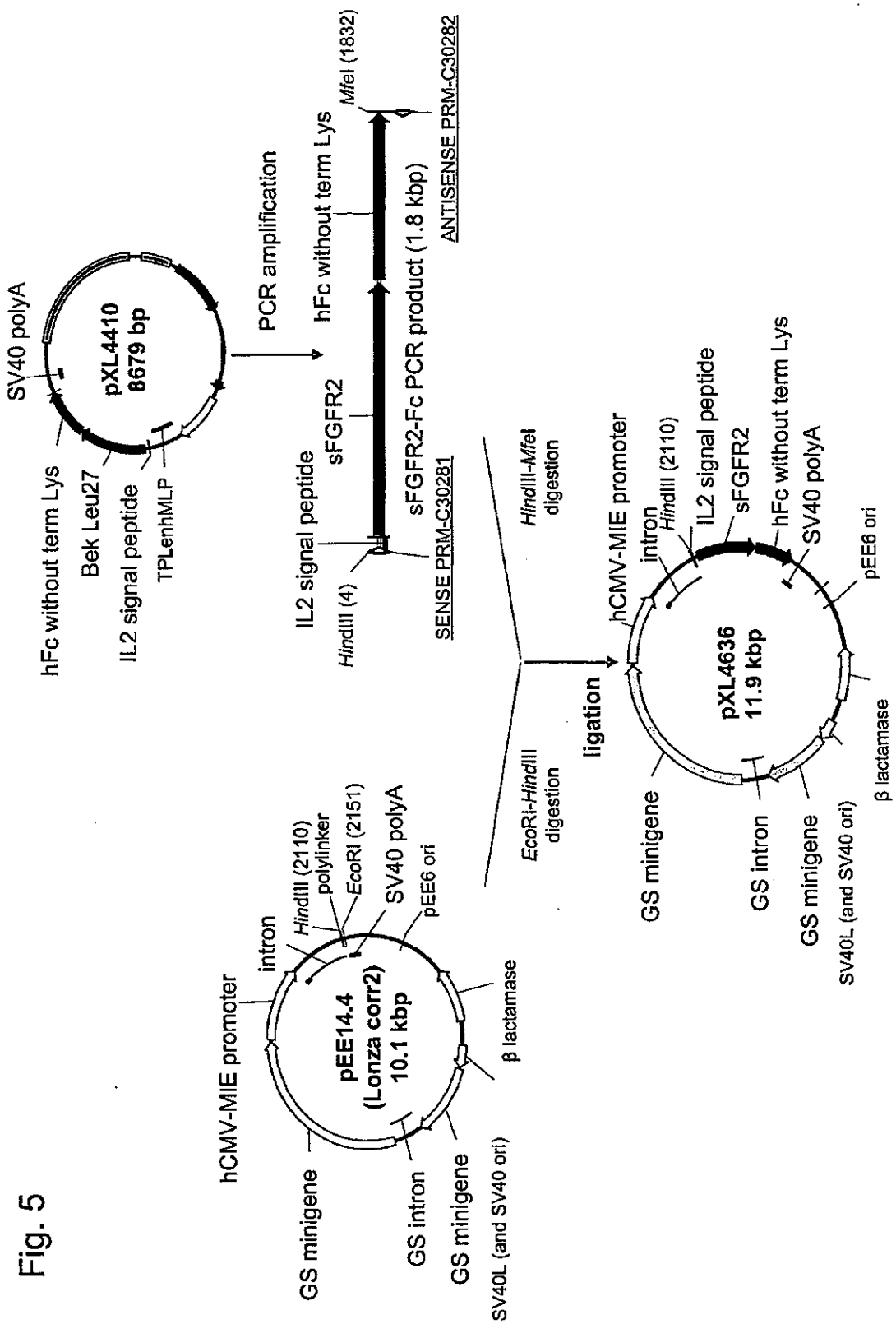
Fig. 4E

```
1    SAL
```

Fig. 4F

```
1    MYRMQLLSCI ALSLALVTNS
```

Fig. 5


SV40 polyA
pXL4410
8679 bp
hFc without term Lys
Bek Leu27
IL2 signal peptide
TPLenhMLP
PCR amplification
hFc without term Lys
MfeI (1832)
IL2 signal peptide
sFGFR2
HindIII (4)
sFGFR2-Fc PCR product (1.8 kbp)
ANTISENSE PRM-C30282
SENSE PRM-C30281
HindIII-MfeI digestion
EcoRI-HindIII digestion
ligation
hCMV-MIE promoter
intron
HindIII (2110)
polylinker
EcoRI (2151)
SV40 polyA
pEE6 ori
β lactamase
GS minigene
GS intron
GS minigene
SV40L (and SV40 ori)
pEE14.4
(Lonza corr2)
10.1 kbp
hCMV-MIE promoter
intron
HindIII (2110)
IL2 signal peptide
sFGFR2
hFc without term Lys
SV40 polyA
pEE6 ori
β lactamase
GS minigene
GS intron
GS minigene
SV40L (and SV40 ori)
pXL4636
11.9 kbp

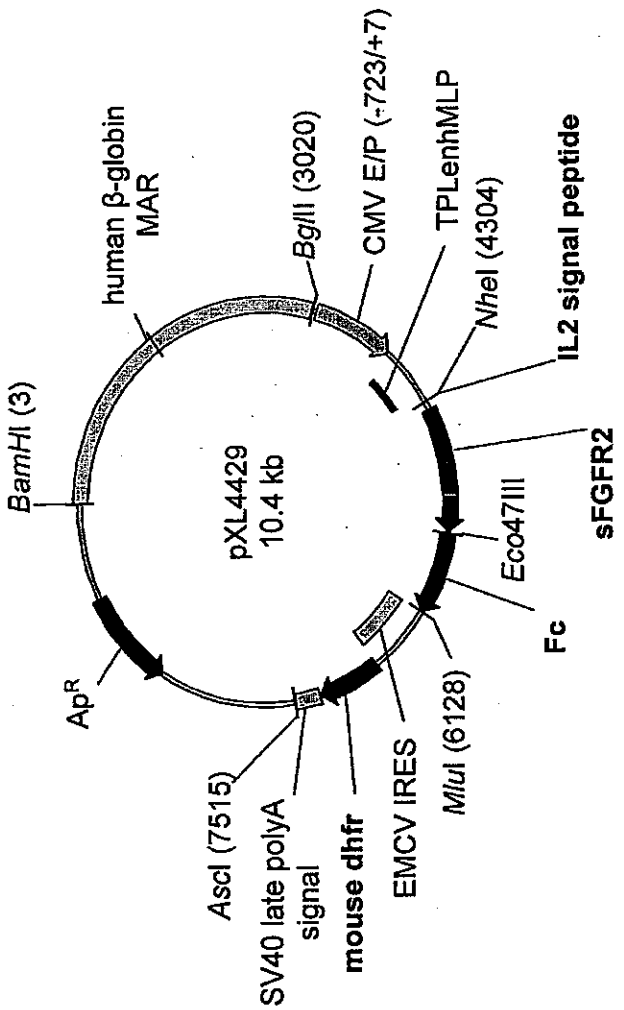

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human β-globin MAR
BglII (3020)
CMV E/P (-723/+7)
TPLenhMLP
NheI (4304)
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sFGFR2
Fc
Eco47III
MluI (6128)
EMCV IRES
mouse dhfr
SV40 late polyA signal
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ApR
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Fig. 6A

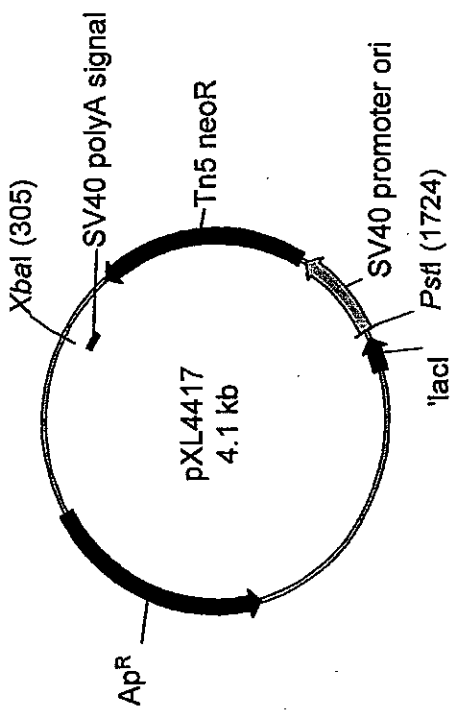
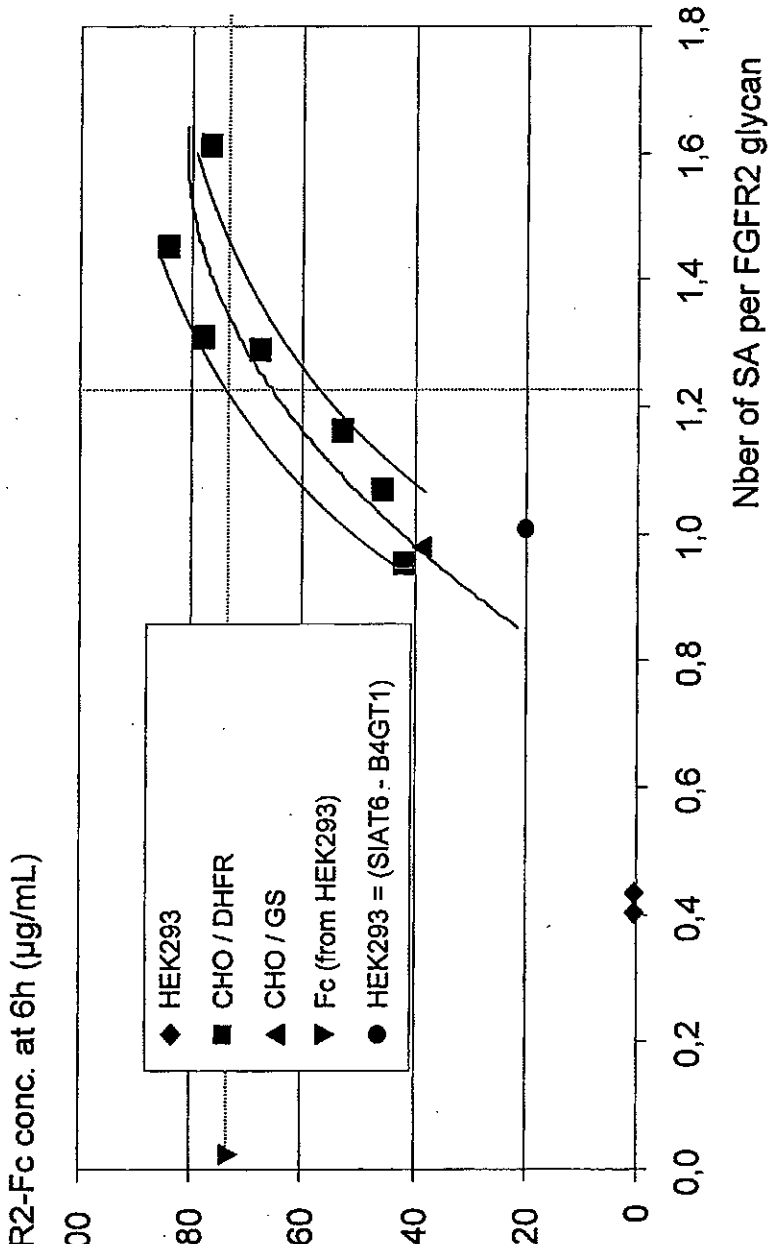

XbaI (305)
SV40 polyA signal
Tn5 neoR
SV40 promoter ori
PstI (1724)
'lacI
ApR
pXL4417
4.1 kb

Fig. 6B

Fig. 7


FGFR2-Fc conc. at 6h (µg/mL)
100
80
60
40
20
0
0,0
0,2
0,4
0,6
0,8
1,0
1,2
1,4
1,6
1,8
Nber of SA per FGFR2 glycan
HEK293
CHO / DHFR
CHO / GS
Fc (from HEK293)
HEK293 = (SIAT6 - B4GT1)

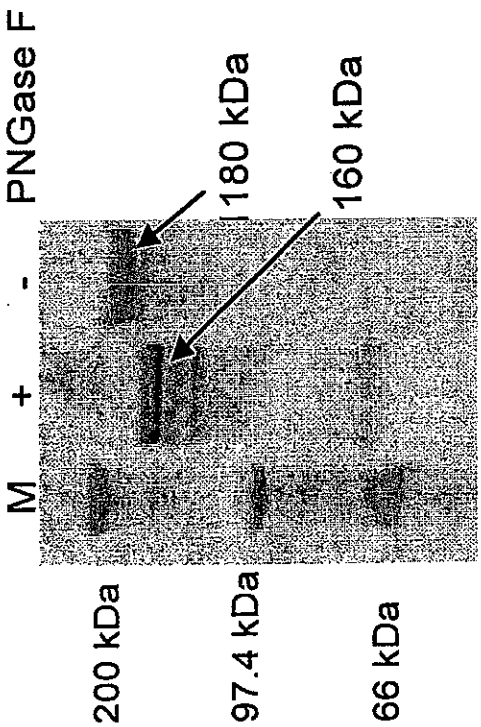
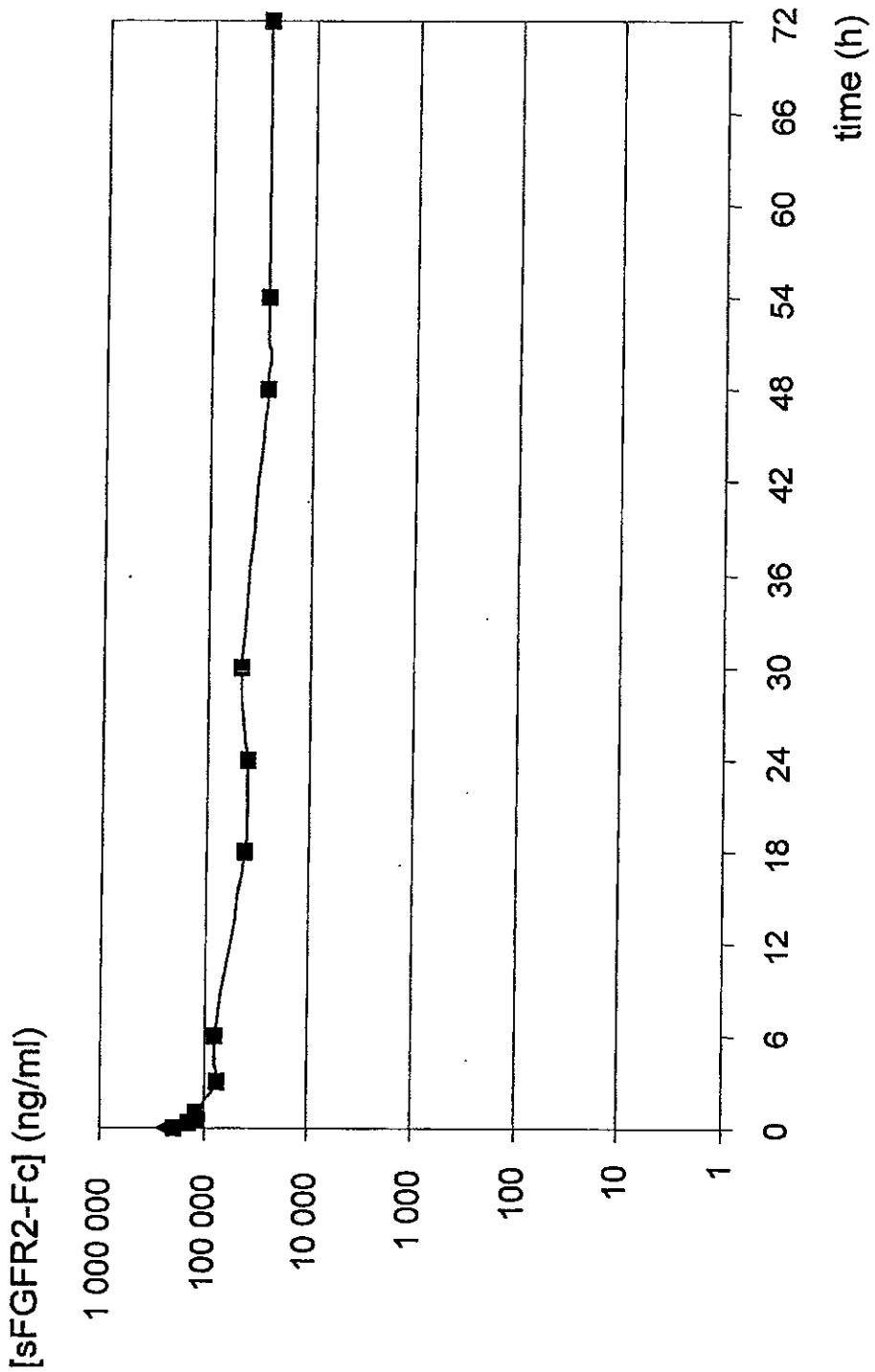


Fig. 8


Potential N-glycosylation sites
N1
N2
N3
N4
N5
N6
N7
N8
N 297
N
N
Ig-like 1
Ig-like 2
Ig-like 3
C_H2
C_H3

Fig. 9

Fig. 10


[sFGFR2-Fc] (ng/ml)
1 000 000
100 000
10 000
1 000
100
10
1
0
6
12
18
24
30
36
42
48
54
60
66
72
time (h)

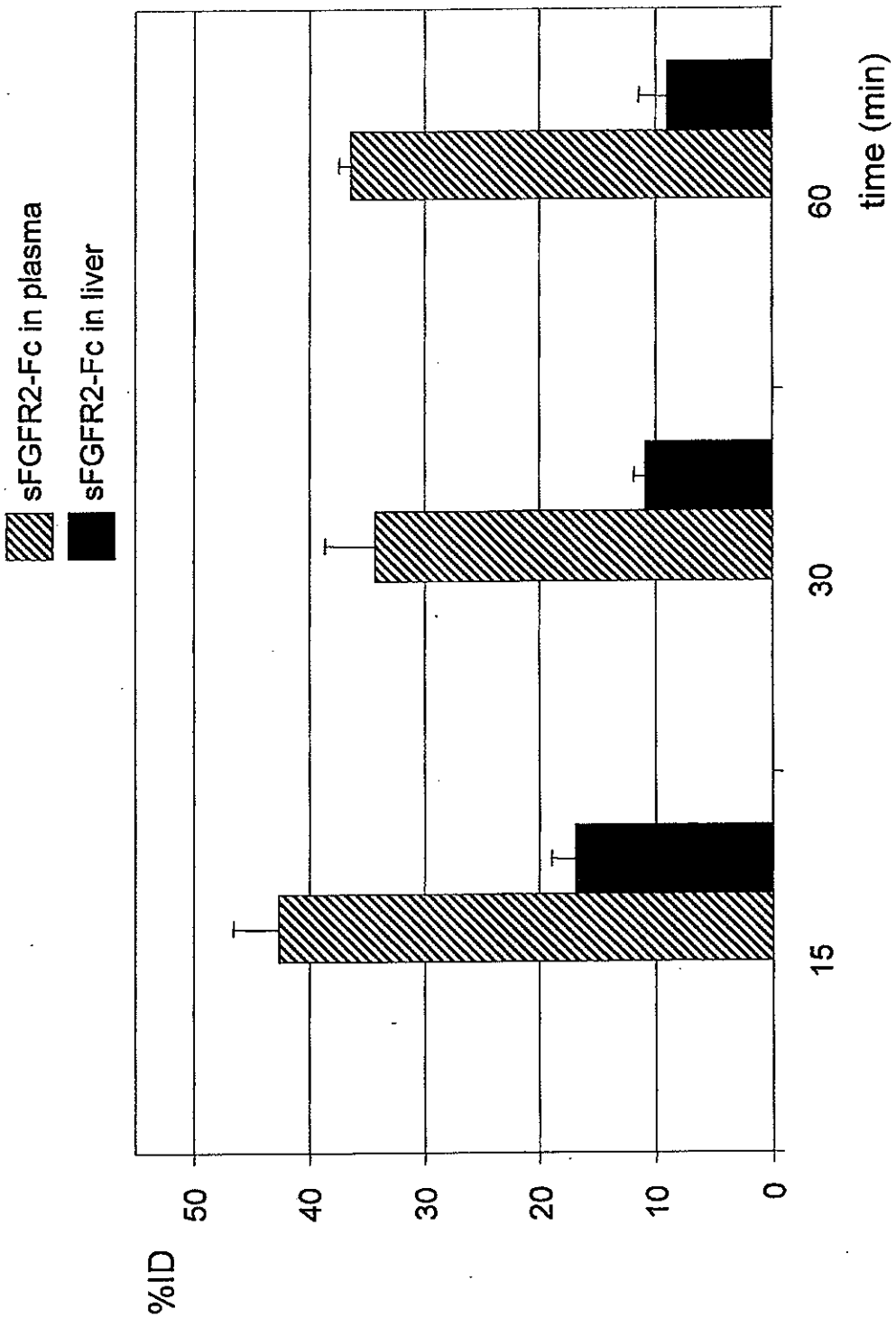

sFGFR2-Fc in plasma
sFGFR2-Fc in liver
%ID
50
40
30
20
10
0
15
30
60
time (min)

Fig. 11

Fig. 12

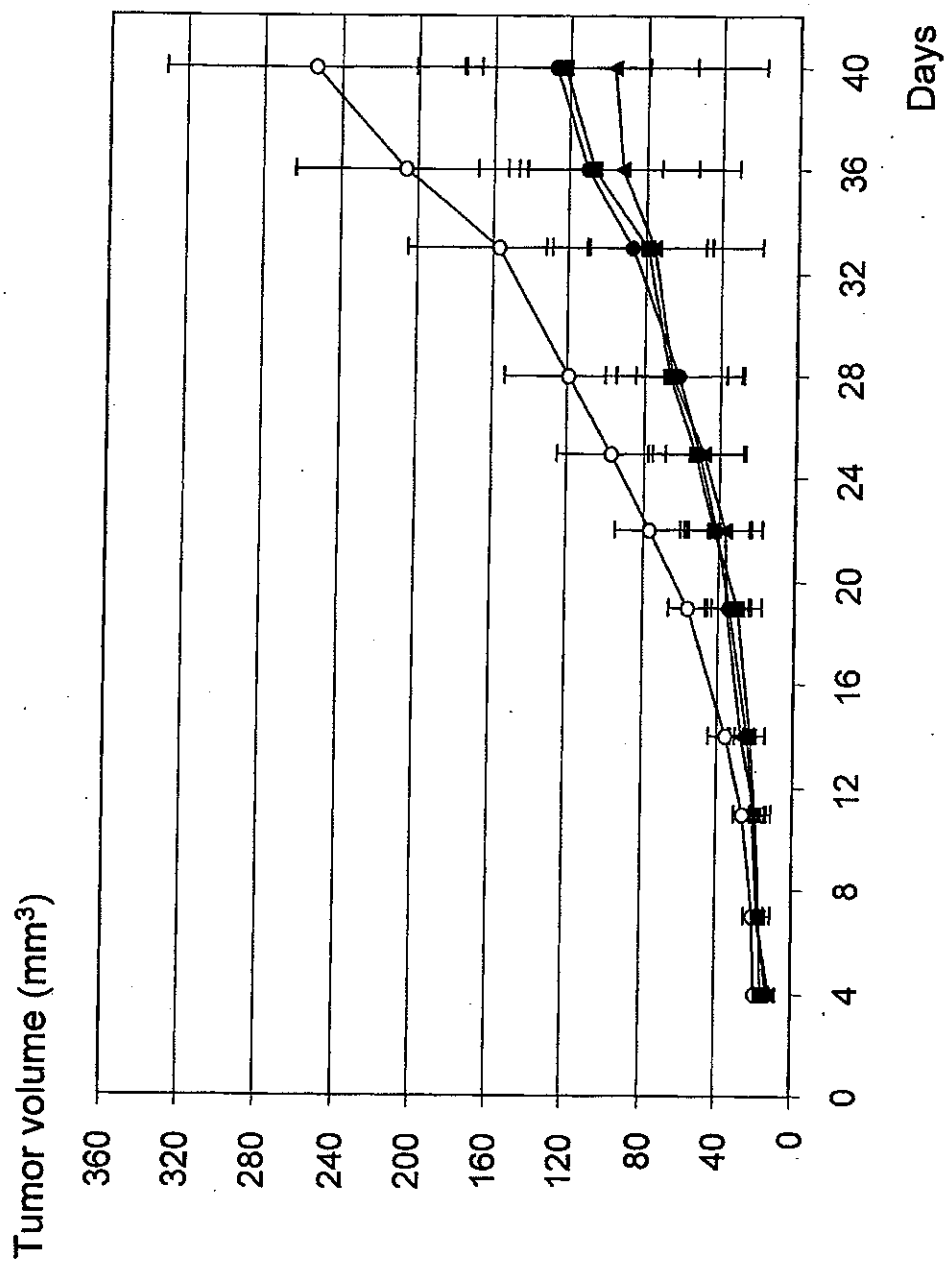

Tumor volume (mm³)
360
320
280
240
200
160
120
80
40
0
0
4
8
12
16
20
24
28
32
36
40
Days

Fig. 13

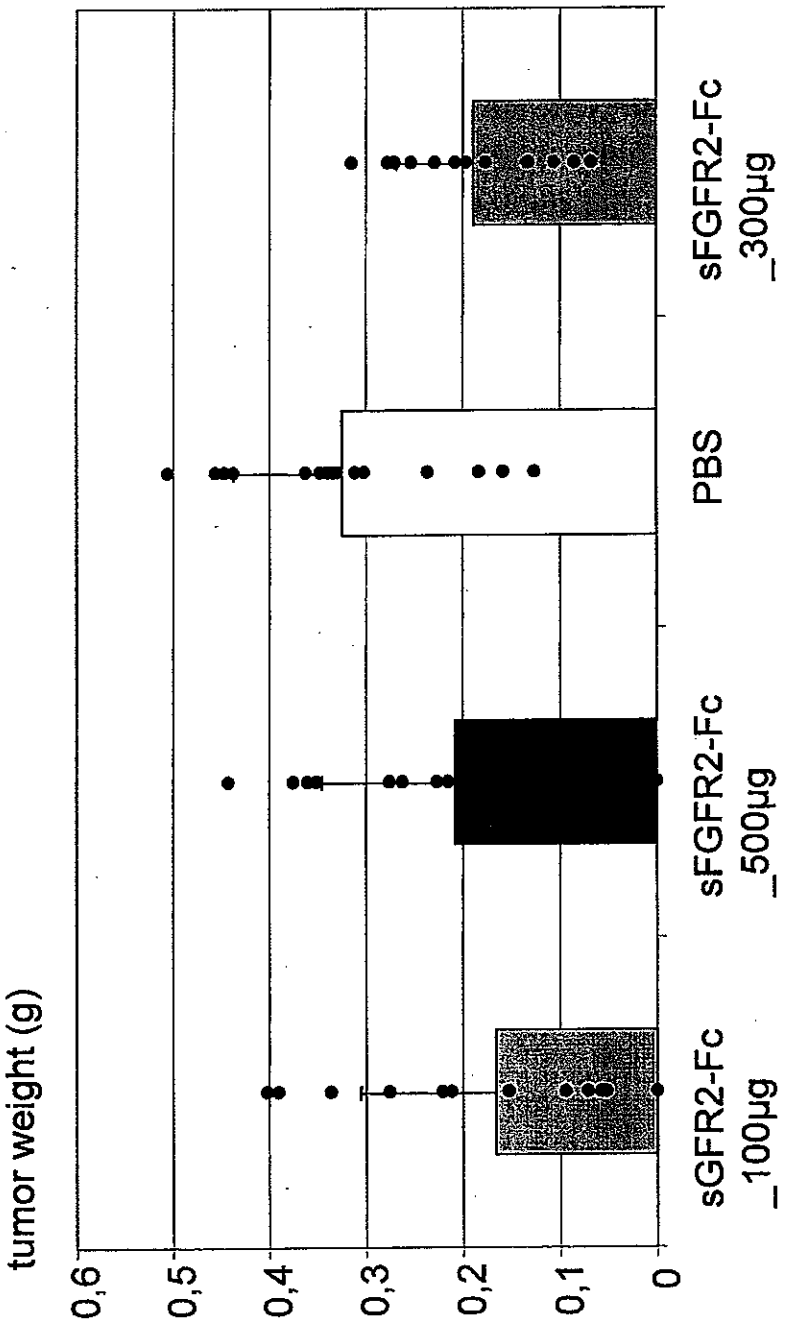

tumor weight (g)
0,6
0,5
0,4
0,3
0,2
0,1
0
sGFR2-Fc _100µg
sFGFR2-Fc _500µg
PBS
sFGFR2-Fc _300µg

Fig. 14

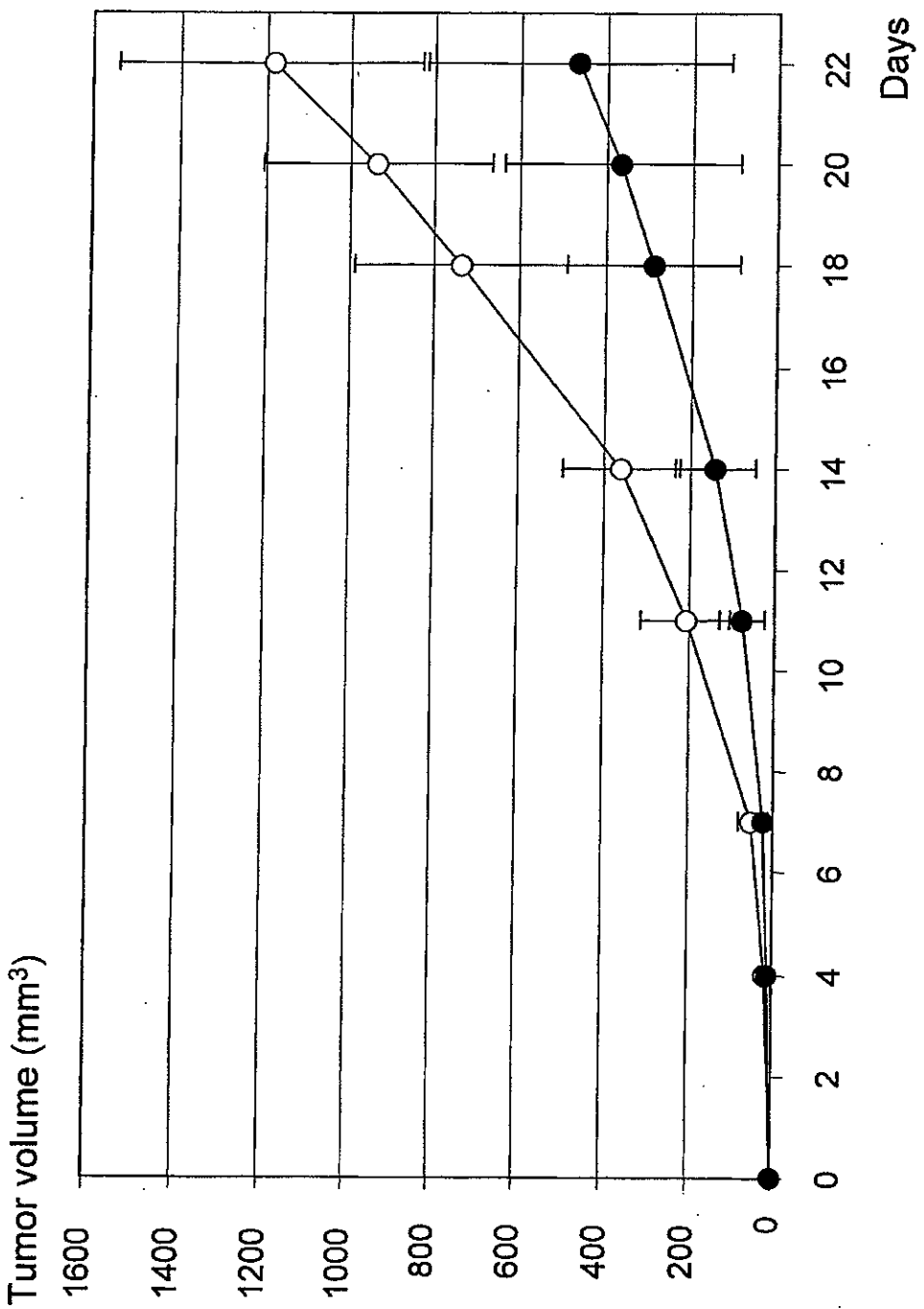

Tumor volume (mm3)
1600
1400
1200
1000
800
600
400
200
0
0
2
4
6
8
10
12
14
16
18
20
22
Days

Fig. 15

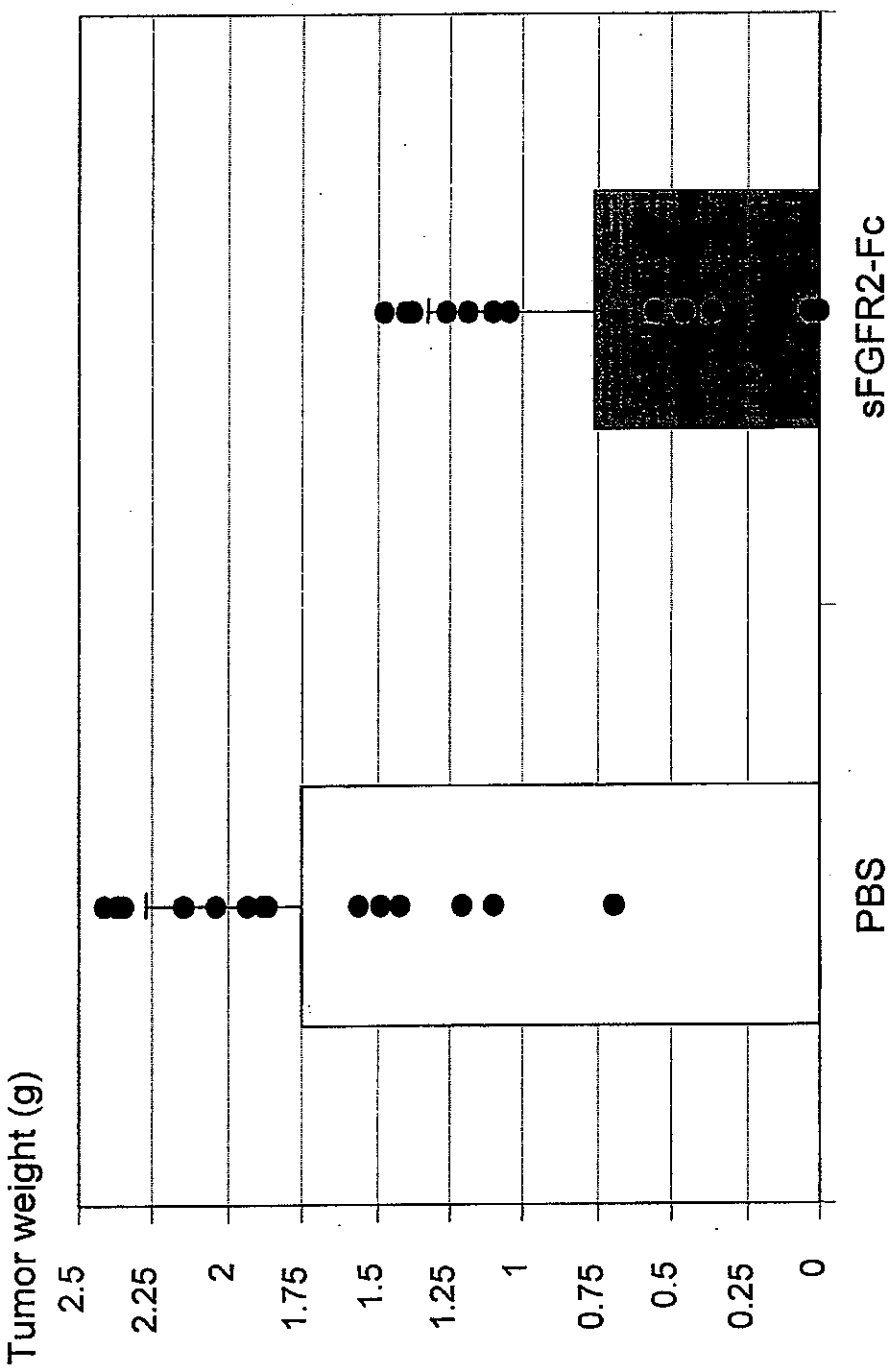
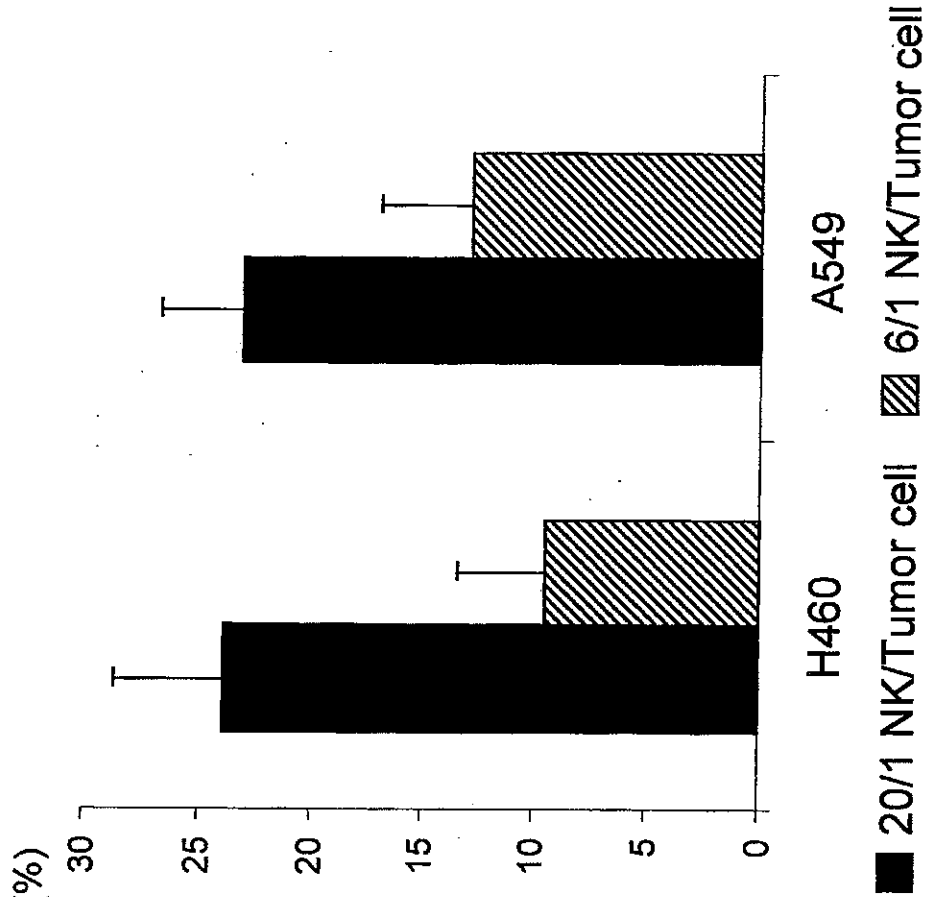


Fig. 16


Tumor lysis (%)
30
25
20
15
10
5
0
H460
A549
20/1 NK/Tumor cell
6/1 NK/Tumor cell

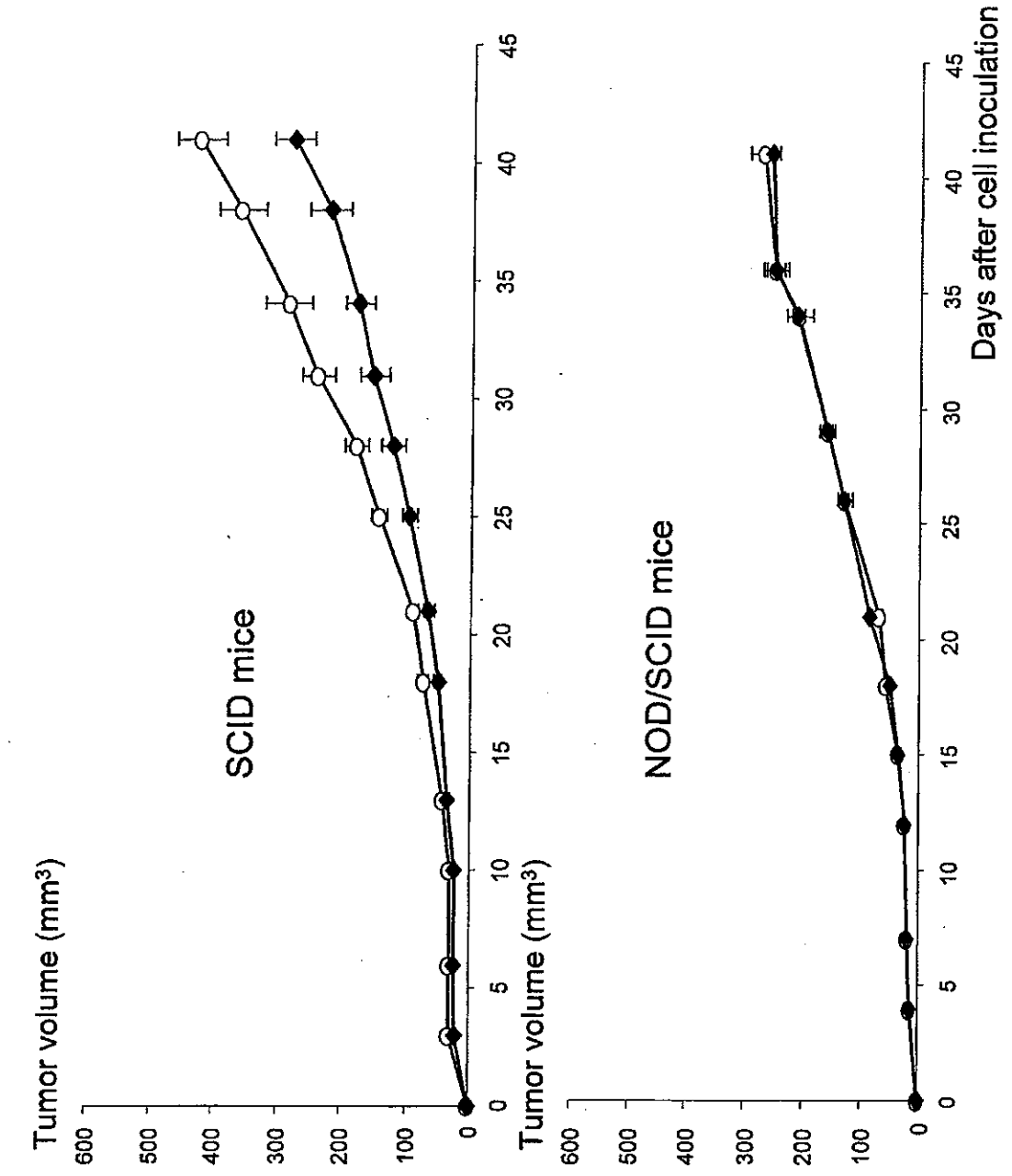
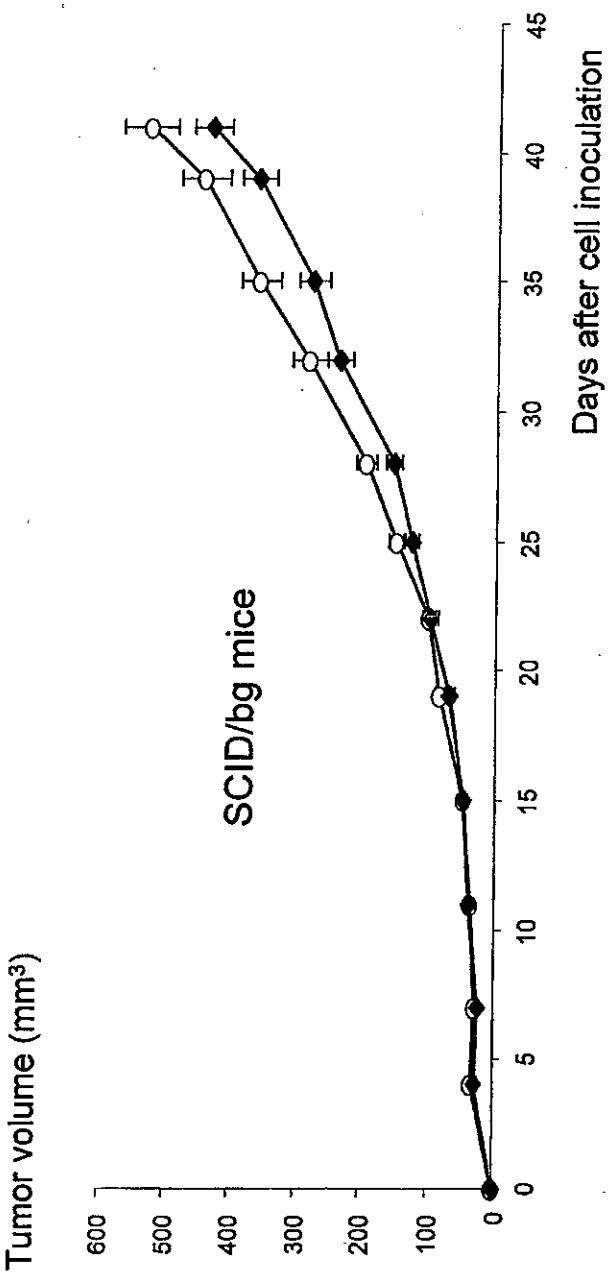


Fig. 17A

Fig. 17B

Fig. 17C


Tumor volume (mm³)
600
500
400
300
200
100
0
SCID/bg mice
0
5
10
15
20
25
30
35
40
45
Days after cell inoculation

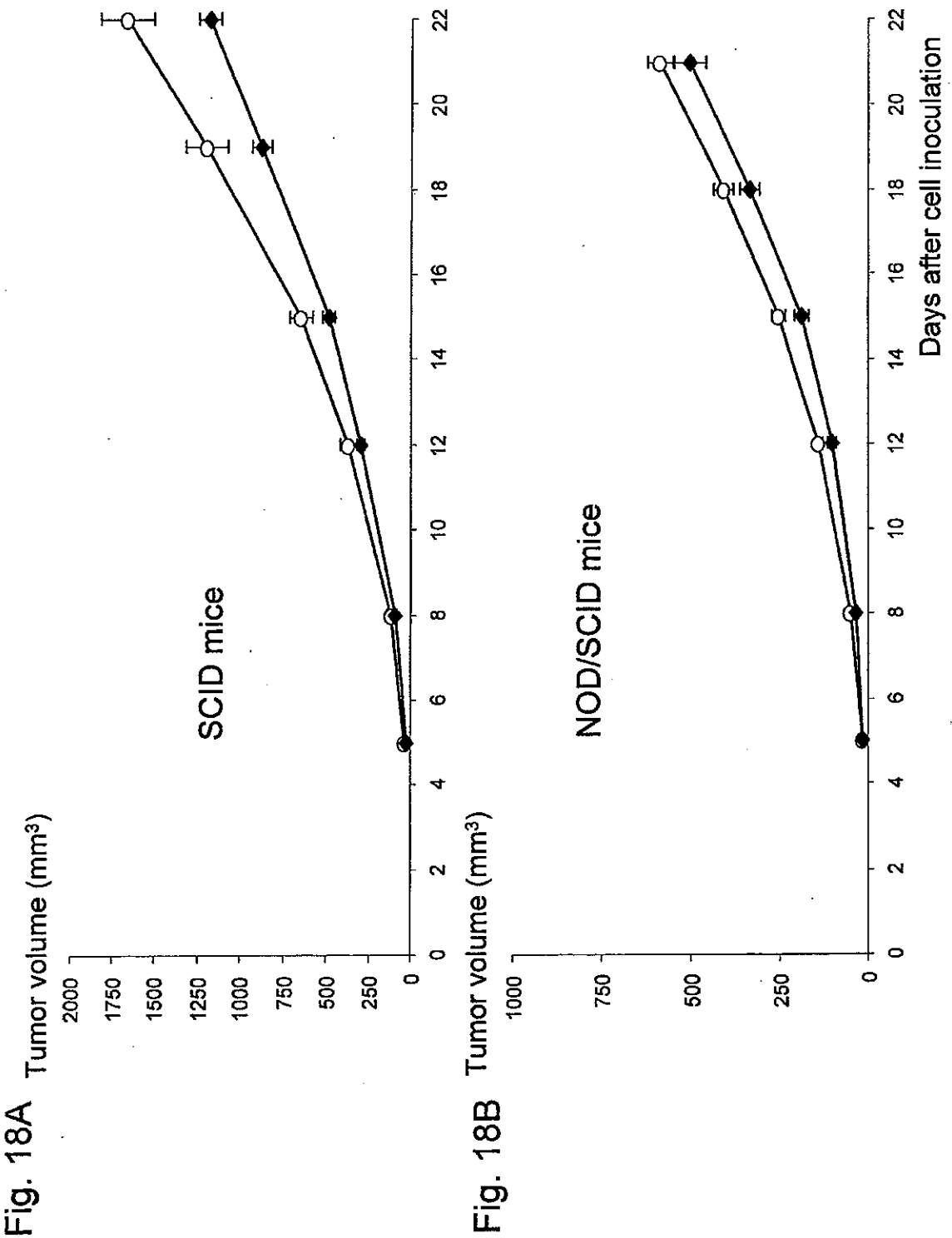


Fig. 18A

Fig. 18B

Fig. 18C

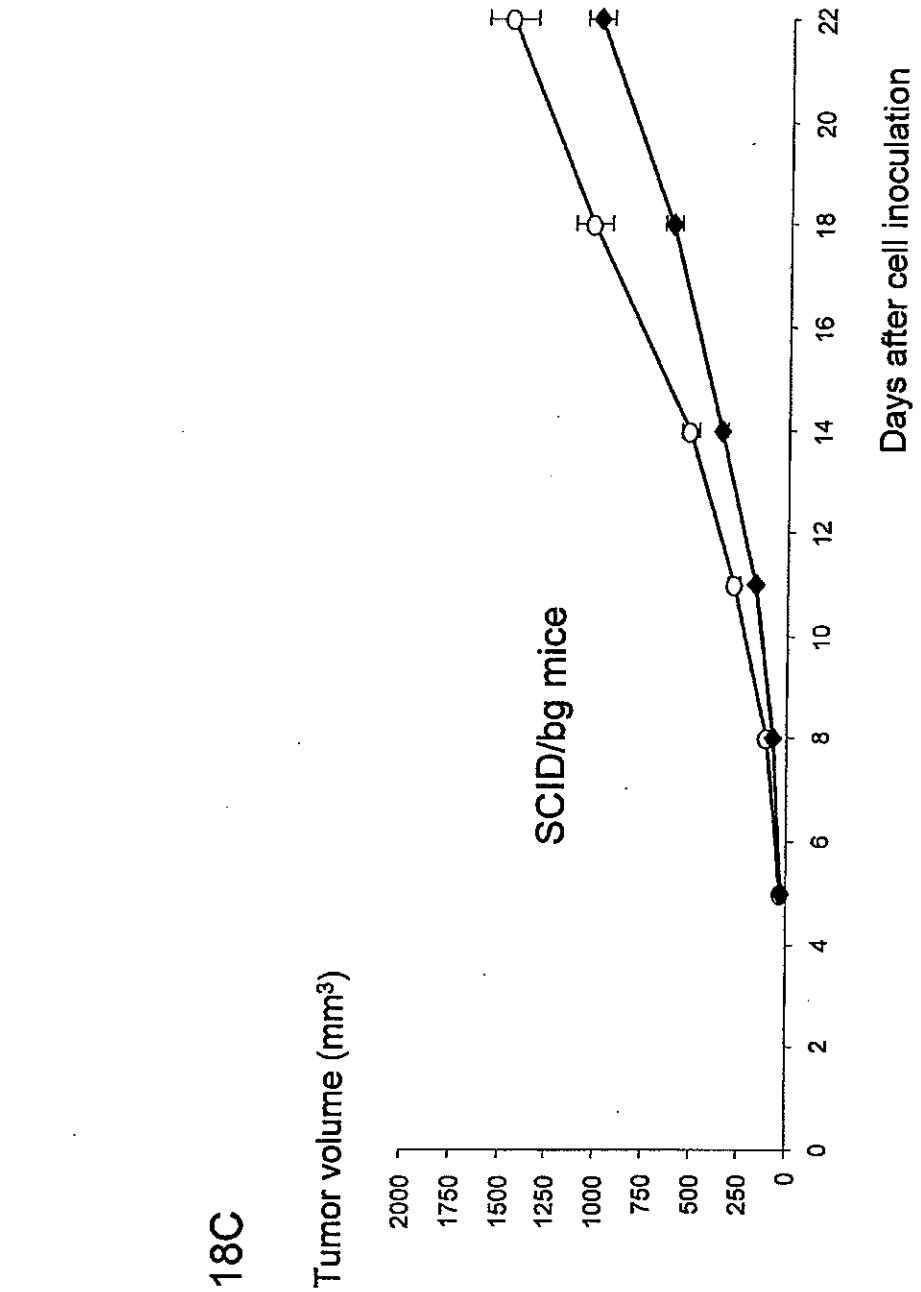

Tumor volume (mm3)
2000
1750
1500
1250
1000
750
500
250
0
SCID/bg mice
0
2
4
6
8
10
12
14
16
18
20
22
Days after cell inoculation

Fig. 19A

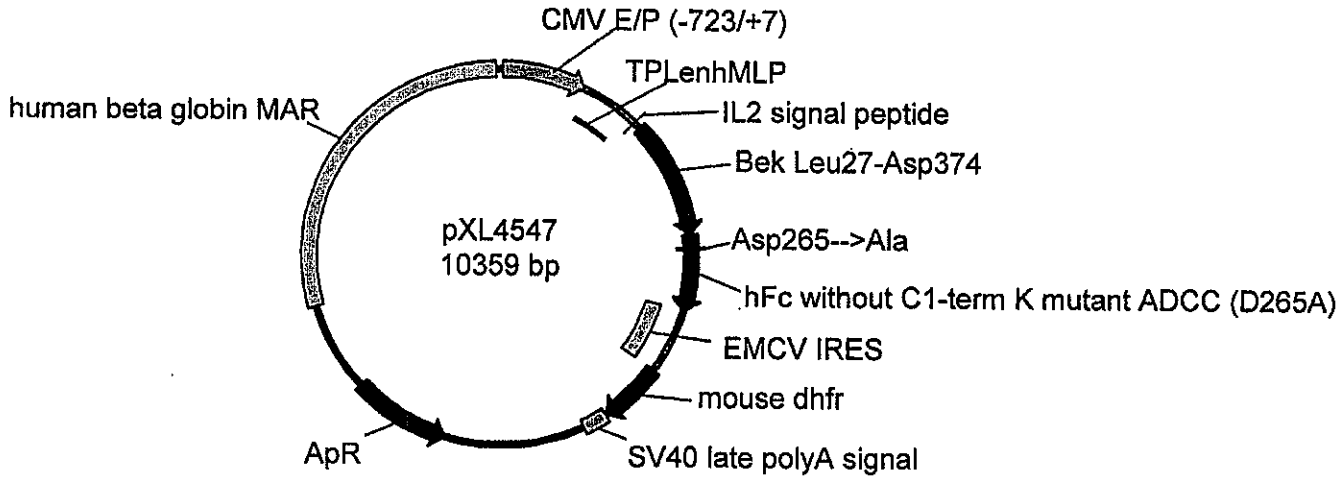
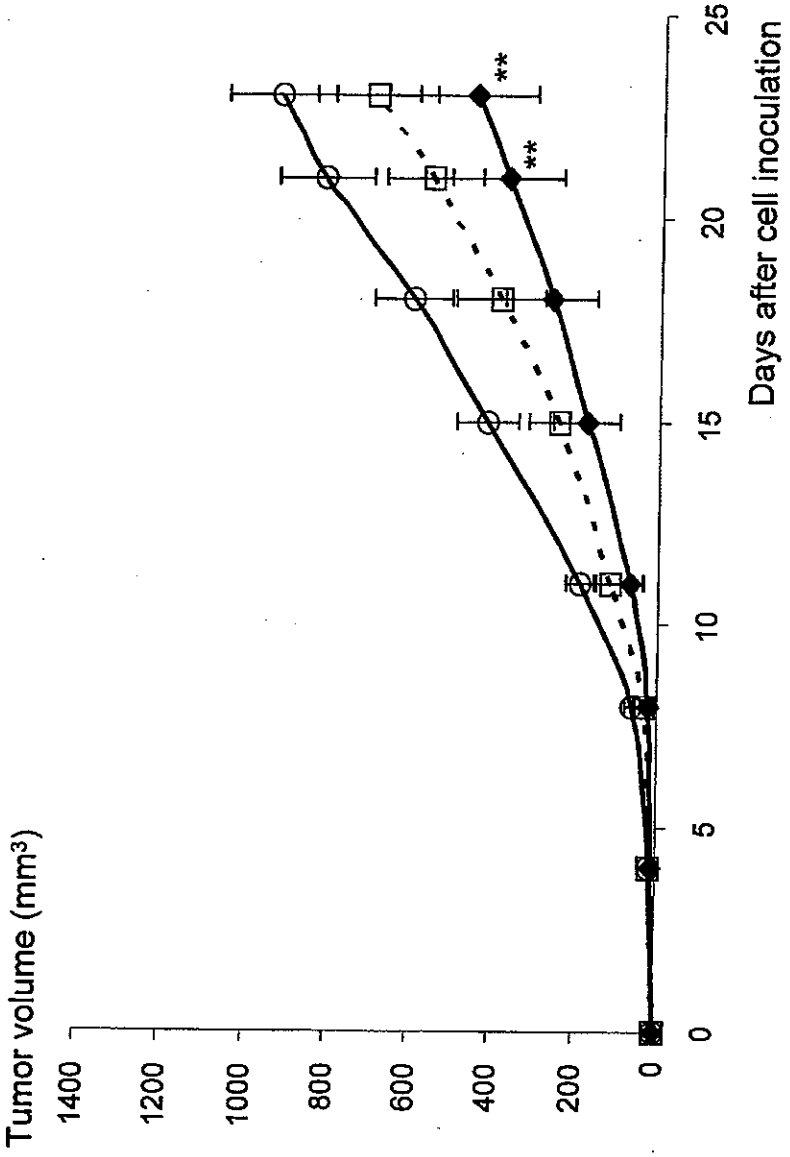


Fig. 19B

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  1    LVEDTTLEPE EPPTKYQISQ PEVYVAAPGE SLEVRCLLKD AAVISWTKDG
 51    VHLGPNNRTV LIGEYLQIKG ATPRDSGLYA CTASRTVDSE TWYFMVNVTD
101    AISSGDDEDD TDGAEDFVSE NSNNKRAPYW TNTEKMEKRL HAVPAANTVK
151    FRCPAGGNPM PTMRWLKNGK EFKQEHRIGG YKVRNQHWSL IMESVVPSDK
201    GNYTCVVENE YGSINHTYHL DVVERSPHRP ILQAGLPANA STVVGGDVEF
251    VCKVYSDAQP HIQWIKHVEK NGSKYGPDGL PYLKVLKAAG VNTTDKEIEV
301    LYIRNVTFED AGEYTCLAGN SIGISFHSAW LTVLPAPGRE KEITASPDKT
351    HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VAVSHEDPEV
401    KFNWYVDGVE VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV
451    SNKALPAPIE KTISKAKGQP REPQVYTLPP SRDELTKNQV SLTCLVKGFY
501    PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSKLTVD KSRWQQGNVF
551    SCSVMHEALH NHYTQKSLSL SPG
```

Fig. 20


Tumor volume (mm3)
1400
1200
1000
800
600
400
200
0
0
5
10
15
20
25
Days after cell inoculation
**
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