```
                    1        10        20        30        40        50
CYNO_RAMP1    (1)  MARALCRLPQRGLWLLLAHHLFMATACQEANYGALLQELCLTQFQVDMEAVGET
HUMAN_RAMP1   (1)  MARALCRLPRRGLWLLLAHHLFMTTACQEANYGALLRELCLTQFQVDMEAVGET
RAT_RAMP1     (1)  MAPGLRGLPRRGLWLLLAHHLFMVTACRDPDYGTLIQELCLSRFKEDMETIGKT

                         60        70        80        90        100
CYNO_RAMP1   (55)  LWCDWGRTIGSYRELADCTWHMAEKLGCFWPNAEVDRFFLAVHGHYFRACPISG
HUMAN_RAMP1  (55)  LWCDWGRTIRSYRELADCTWHMAEKLGCFWPNAEVDRFFLAVHGRYFRSCPISG
RAT_RAMP1    (55)  LWCDWGKTIGSYGELTHCTKLVANKIGCFWPNPEVDKFFIAVHHRYFSKCPVSG

                    110       120       130       140
CYNO_RAMP1  (109)  RAVRDPPGSVLYPFIVVPITVTLLVTALVVWQSKHTEGIV
HUMAN_RAMP1 (109)  RAVRDPPGSILYPFIVVPITVTLLVTALVVWQSKRTEGIV
RAT_RAMP1   (109)  RALRDPPNSILCPFIVLPITVTLLMTALVVWRSKRTEGIV
```

Fig. 1

```
                1       10        20        30        40        50
CYNOCRLR   (1)  -MEKKCTLYFLVLLPFFMIFVTAELEESPEDSIQLGVTRNKIMTAQYECYQKIMQDP
HUCRLR     (1)  -MEKKCTLYFLVLLPFFMILVTAELEESPEDSIQLGVTRNKIMTAQYECYQKIMQDP
RATCRLR    (1)  MMDKKCTLCFLFLLLLNMALIAAESEEGANQT-DLGVTRNKIMTAQYECYQKIMQDP

                60        70        80        90        100       110
CYNOCRLR  (57)  IQQAEGVYCNRTWDGWLCWNNVAAGTESMQLCPDYFQDFDPSEKVTKICDQDGNWFR
HUCRLR    (57)  IQQAEGVYCNRTWDGWLCWNDVAAGTESMQLCPDYFQDFDPSEKVTKICDQDGNWFR
RATCRLR   (57)  IQQGEGLYCNRTWDGWLCWNDVAAGTESMQYCPDYFQDFDPSEKVTKICDQDGNWFR

                120       130       140       150       160       170
CYNOCRLR(114)  HPASNRTWTNYTQCNVNTHEKVKTALNLFYLTIIGHGLSIASLLISLGIFFYFKSLS
HUCRLR  (114)  HPASNRTWTNYTQCNVNTHEKVKTALNLFYLTIIGHGLSIASLLISLGIFFYFKSLS
RATCRLR (114)  HPDSNRTWTNYTLCNNSTHEKVKTALNLFYLTIIGHGLSIASLIISLIIFFYFKSLS

                180       190       200       210       220
CYNOCRLR(171)  CQRITLHKNLFFSFVCNSVVTIIHLTAVANNQALVATNPVSCKVSQFIHLYLMGCNY
HUCRLR  (171)  CQRITLHKNLFFSFVCNSVVTIIHLTAVANNQALVATNPVSCKVSQFIHLYLMGCNY
RATCRLR (171)  CQRITLHKNLFFSFVCNSIVTIIHLTAVANNQALVATNPVSCKVSQFIHLYLMGCNY

               230       240       250       260       270       280
CYNOCRLR(228)  FWMLCEGIYLHTLIVVAVFAEKQHLMWYYFLGWGFPLIPACIHAIARSLYYNDNCWI
HUCRLR  (228)  FWMLCEGIYLHTLIVVAVFAEKQHLMWYYFLGWGFPLIPACIHAIARSLYYNDNCWI
RATCRLR (228)  FWMLCEGIYLHTLIVVAVFAEKQHLMWYYFLGWGFPLLPACIHAIARSLYYNDNCWI

                290       300       310       320       330       340
CYNOCRLR(285)  SSDTHLLYIIHGPICAALLVNLFFLLNIVRVLITKLKVTHQAESNLYMKAVRATLIL
HUCRLR  (285)  SSDTHLLYIIHGPICAALLVNLFFLLNIVRVLITKLKVTHQAESNLYMKAVRATLIL
RATCRLR (285)  SSDTHLLYIIHGPICAALLVNLFFLLNIVRVLITKLKVTHQAESNLYMKAVRATLIL

                350       360       370       380       390
CYNOCRLR(342)  VPLLGIEFVLIPWRPEGKIAEEVYDYIMHILMHFQGLLVSTIFCFFNGEVQAILRRN
HUCRLR  (342)  VPLLGIEFVLIPWRPEGKIAEEVYDYIMHILMHFQGLLVSTIFCFFNGEVQAILRRN
RATCRLR (342)  VPLLGIEFVLFPWRPEGKVAEEVYDYVMHILMHYQGLLVSTIFCFFNGEVQAILRRN

               400       410       420       430       440       450
CYNOCRLR(399)  WNQYKIQFGNSFSNSEALRSASYTVSTISDGPGYSHDCPSEHLNGKSIHDIENVVLK
HUCRLR  (399)  WNQYKIQFGNSFSNSEALRSASYTVSTISDGPGYSHDCPSEHLNGKSIHDIENVLLK
RATCRLR (399)  WNQYKIQFGNGFSHSDALRSASYTVSTISDVQGYSHDCPTEHLNGKSIQDIENVALK

                460
CYNOCRLR(456)  PENLYN---
HUCRLR  (456)  PENLYN---
RATCRLR (456)  PEKMYDLVM
```

Fig. 2

Kappa K1	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
2E7	RASQGIRNDLG	48	AASSLQS	49	LQYNIYPWT	50
13H2	RASQGIRKDLG	66	GASSLQS	67	LQYNSFPWT	68
K1 Consensus	RASQGIRNDLG K	103	AASSLQS G	104	LQYNIYPWT SF	105

Kappa K4	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
32H7	RASQSVSSGYLT	69	GASSRAT	70	QQYGNSLCR	71
32H7a	RASQSVSSGYLT	69	GASSRAT	70	QQYGNSLSR	72
K4 Consensus	RASQSVSSGYLT	69	GASSRAT	70	QQYGNSLSR C	106

	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
Kappa K1,4 Cons	RASQSVSSGYLT GIRN D G K	107	GASSRAT A LQS	108	QQYGNSLCR L NTYPWT F S	109

Fig 3A

Kappa K2	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
4H6	RSSQSLLHSFGYNYLD	57	LGSNRAS	58	MQALQTPFT	59

Kappa K3	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
3C8	KSSQSLLHSAGKTYLY	54	EVSNRFS	55	MQSFPLPLT	56
5F5	KSSQSLLHSDGKTYLY	60	EVSNRFS	55	MQSFPLPLT	56
12E8	KSSQSLLHSDGRNYLY	65	EVSNRFS	55	MQSFPLPLT	56
K3 Consensus	KSSQSLLHSDGRNYLY A KT	110	EVSNRFS	55	MQSFPLPLT	56

	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
Kappa K2,3 Cons	RSSQSLLHSFGYNYLD K D RT Y A K	111	LGSNRAS EV F	112	MQALQTPFT SFPL L	113

Fig 3B

Lambda L1		SEQ		SEQ		SEQ
	CDR1	ID NO:	CDR2	ID NO:	CDR3	ID NO:
1E11	SGSSSNIGNNYVS	42	DNNKRPS	43	GTWDSRLSAVV	44
4E4	SGSSSNIGNNYVS	42	DNNKRPS	43	GTWDSRLSAVV	44
9D4	SGSSSNIGNNYVS	42	DNNKRPS	43	GTWDSRLSAVV	44
12G8	SGSSSNIGNNYVS	42	DNNKRPS	43	GTWDSRLSAVV	44
L1 Consensus	**SGSSSNIGNNYVS**	42	**DNNKRPS**	43	**GTWDSRLSAVV**	44

Lambda L2		SEQ		SEQ		SEQ
	CDR1	ID NO:	CDR2	ID NO:	CDR3	ID NO:
10E4	SGSSSNIGSNTVN	62	TNNQRPS	63	AARDESLNGVV	64

Lambda L3		SEQ		SEQ		SEQ
	CDR1	ID NO:	CDR2	ID NO:	CDR3	ID NO:
11D11	SGSSSNIGSNYVY	45	RNNQRPS	61	AAWDDSLSGWV	47
11H9	SGSSSNIGSNYVY	45	RNNQRPS	61	AAWDDSLSGWV	47
1H7	SGSSSNIGSNYVY	45	RSNQRPS	46	AAWDDSLSGWV	47
9F5	SGSSSNIGSNYVY	45	RNNQRPS	61	AAWDDSLSGWV	47
L3 Consensus	**SGSSSNIGSNYVY**	45	**RNNQRPS** S	114	**AAWDDSLSGWV**	47

Lambda L4		SEQ		SEQ		SEQ
	CDR1	ID NO:	CDR2	ID NO:	CDR3	ID NO:
3B6	QG DS LRSFYAS	51	GKNNRPS	52	NSRDSSVYHLV	53

		SEQ		SEQ		SEQ
	CDR1	ID NO:	CDR2	ID NO:	CDR3	ID NO:
Lam L1,2,3 Cons	SGSSSNIGNNYVS S T N Y	115	DNNKRPS TS Q R	116	GTWDSRLSAVV AAR DS NG	117

		SEQ		SEQ		SEQ
	CDR1	ID NO:	CDR2	ID NO:	CDR3	ID NO:
Lambda All Cons	SGSSSNIGNNYVS Q -D -LRSFTAN Y	118	DNNKRPS GK N TS Q R	119	GTWDSRLSAVV NSR DSVYHL AA NG	120

Fig 4

HC 1	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
3B6	GYYMH	82	WINPNSGGTNYAQKFQG	83	DQMSIIMLRGVFPPYYYGMDV	84
10E4	DYYMY	92	WISPNSGGTNYAQKFQG	93	GGYSGYA--GLYSHYY-GMDV	94
HC1 Consensus	GYYMH	121	WINPNSGGTNYAQKFQG	122	DQMSIIMLRGVFPPYYYGMDV	123
	D Y		S		GGY GYA-- LYSH -	

Fig 5A

HC2	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
11D11	NAWMS	76	RIKSKTDGGTTDYAAPVKG	95	DRTGYSISWSSYYYYYGMDV	78
9F5	NAWMS	76	RIKSKTDGGTTDYTAPVKG	91	DRTGYSISWSSYYYYYGMDV	78
11H9	NAWMS	76	RIKSKTDGGTTDYAAPVKG	95	DRTGYSISWSSYYYYYGMDV	78
1H7	NAWMS	76	RIKSTTDGGTTDYAAPVKG	77	DRTGYSISWSSYYYYYGMDV	78
HC2 Consensus	NAWMS	76	RIKSKTDGGTTDYTAPVKG	124	DRTGYSISWSSYYYYYGMDV	78
			T A			

Fig 5B

HC3	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
13H2	TYSMN	97	SISSSSSYRYYADSVKG	98	EGVSGSSPYSISWYDYYYGMDV	99
2E7	SYAMS	79	AISGSGGRTYYADSVKG	80	DQREVG-PYSSGWYDYYYGMDV	81
HC3 Consensus	TYSMN	125	SISSSSSYRYYADSVKG	126	EGVSGSSPYSISWYDYYYGMDV	127
	S A S		A G GGRT		DQREVG- SG	

HC4	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
3C8	SYGMH	85	VISYDGSHESYADSVKG	86	ERKRVTMSTLYYY-FYYGMDV	87
4E4	SFGMH	73	VISFDGSIKYSVDSVKG	74	DRLNYYDSSGYYHYKYYGMAV	75
9D4	SFGMH	73	VISFDGSIKYSVDSVKG	74	DRLNYYDSSGYYHYKYYGMAV	75
1E11	SFGMH	73	VISFDGSIKYSVDSVKG	74	DRLNYYDSSGYYHYKYYGMAV	75
12E8	SYGMH	85	VISYDGSHESYADSVKG	86	ERKRVTMSTLYYY-FYYGMDV	87
5F5	SYGMH	85	VISYDGSHESYADSVKG	86	ERKRVTMSTLYYY-FYYGMDV	87
12G8	SFGMH	73	VISFDGSIKYSVDSVKG	74	DRLNYYDSSGYYHYKYYGLAV	96
HC4 Consensus	SFGMH	128	VISFDGSIKYSVDSVKG	129	DRLNYYDSSGYYHYKYYGMAV	130
	Y		Y H YA		E KRVTM TL Y-F LD	

Fig 5C

HC5	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
4H6	DYAMS	88	FIRSRAYGGTPEYAASVKG	89	GRGIAARWDY	90

Fig 5D

HC6	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
32H7	SYGMH	100	VIWYDGSNKYYADSVKG	101	AGGIAAAGLYYYYGMDV	102

Fig 5E

	CDR1	SEQ ID NO:	CDR2	SEQ ID NO:	CDR3	SEQ ID NO:
HC Con A	NAWMS SYA H FG	131	RIKSKTDGGTTDYTAPVKG A SG--S SRKYSADS V WFT I V Y N H	132	DRTGYSISWSS-YYYYYGMDV AQREVGPYSGGWHDK-- LAV EGLNAYD--LYY -F GI AA T L KR TM	133
HC Con B	NAWMS GFYLH DYA S G A	134	RIKSKTDGGTTDYTAPVKG W NP--NSSGKNSAQKFQ A SGTAH RRY VDS V WFR S IPE S RY Y N F H Y	135	DRTGYSISWSS-YYYYYGMDV GGMSIIMLRGVFPPK-- LA AQYEGYA--LLYSHF E RNVGPYS GWHD LIAAD T Y - GR T K	136

Fig 5F

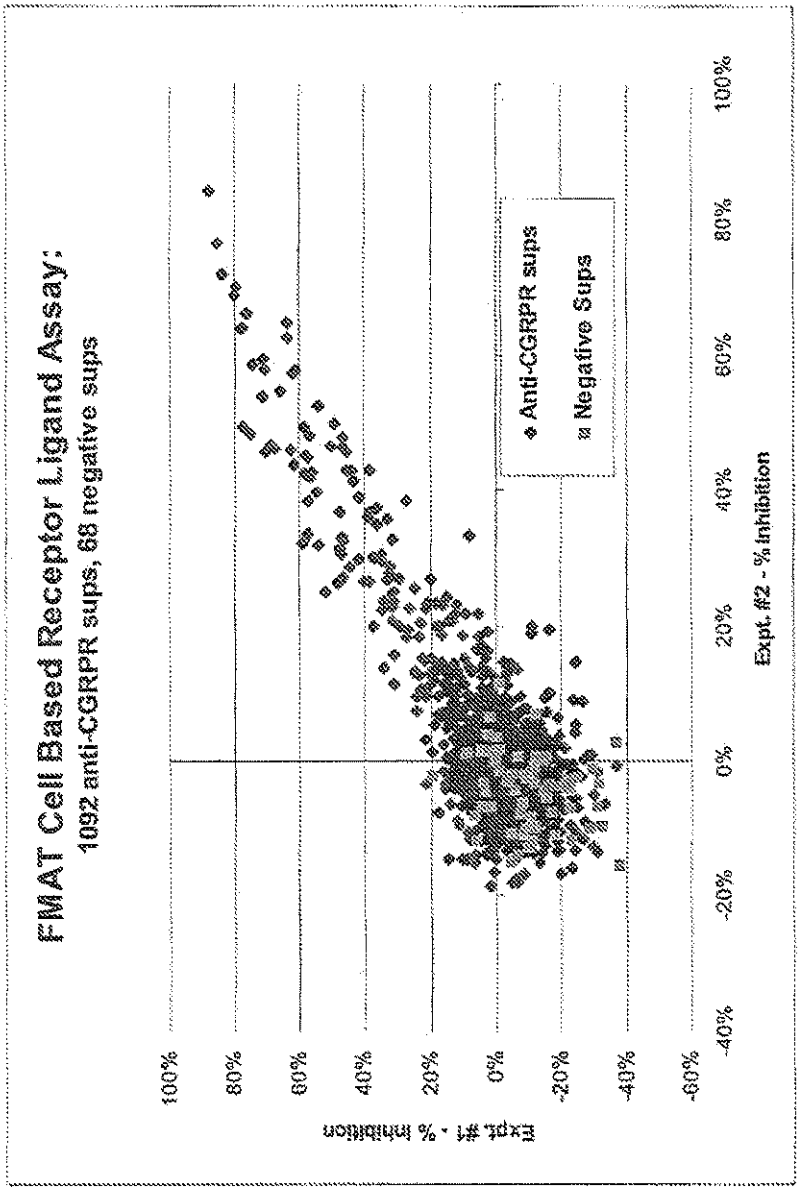

FMAT Cell Based Receptor Ligand Assay:
1092 anti-CGRPR sups, 68 negative sups
Expt. #1 - % Inhibition
Expt. #2 - % Inhibition
100%
80%
60%
40%
20%
0%
-20%
-40%
-60%
-40%
-20%
0%
20%
40%
60%
80%
100%
Anti-CGRPR sups
Negative Sups

Fig 6

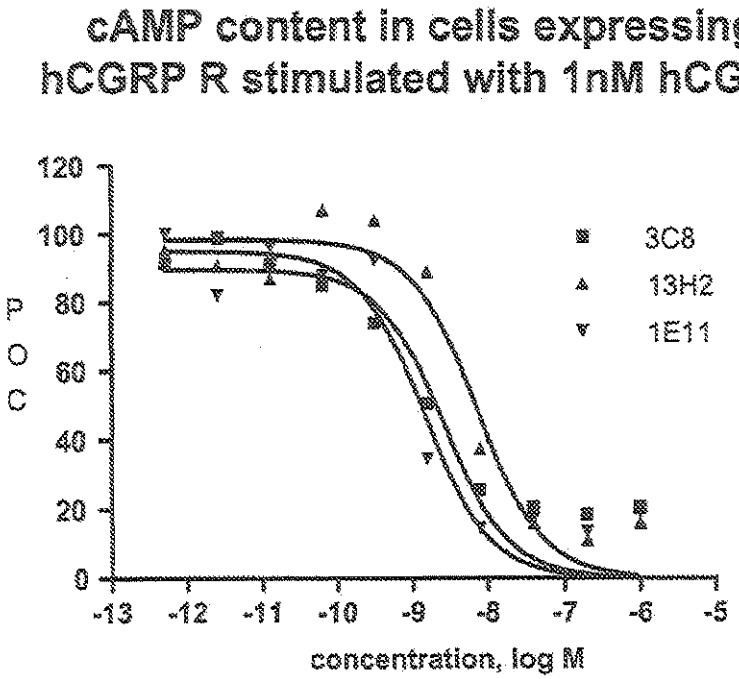

cAMP content in cells expressing
hCGRP R stimulated with 1nM hCGRP
120
100
80
60
40
20
0
p
O
C
-13
-12
-11
-10
-9
-8
-7
-6
-5
concentration, log M
3C8
13H2
1E11

Fig 7A

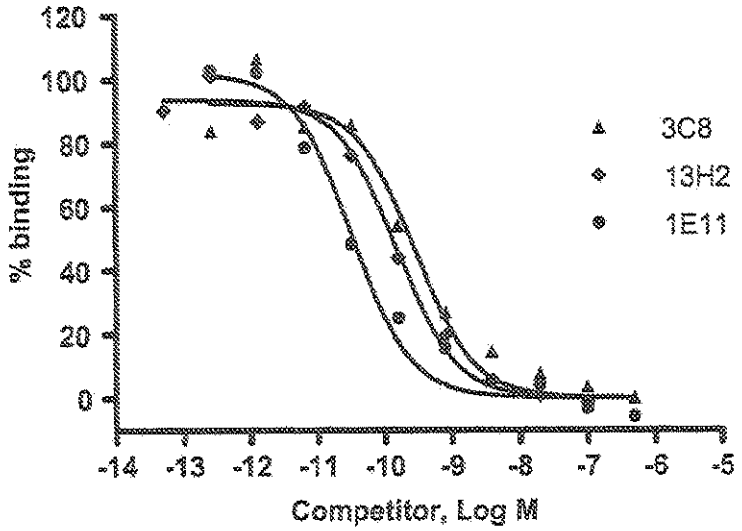

125I-CGRP binding to human CGRP receptor
120
100
80
60
40
20
0
% binding
-14
-13
-12
-11
-10
-9
-8
-7
-6
-5
Competitor, Log M
3C8
13H2
1E11

Fig 8

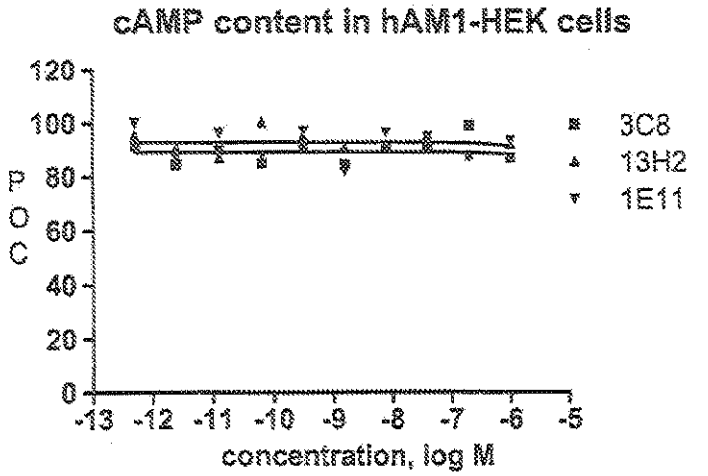


Fig 7B

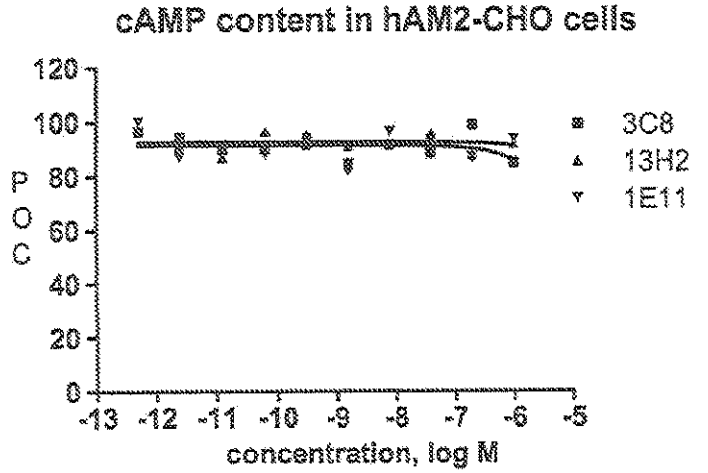


Fig 7C

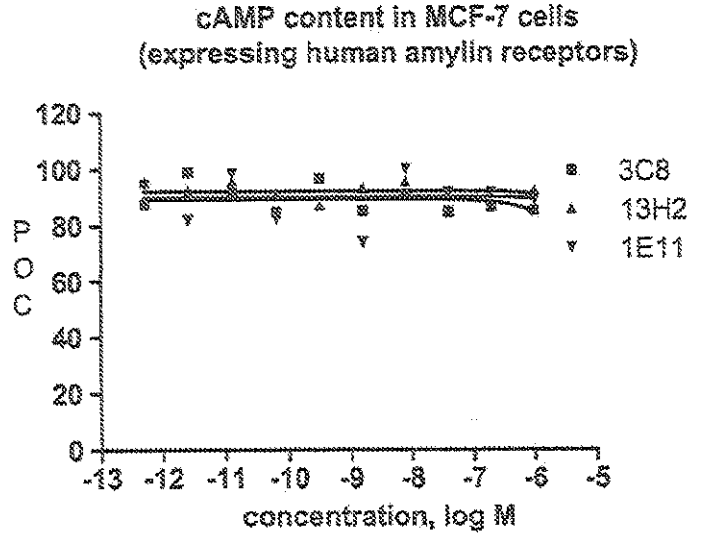


Fig 7D

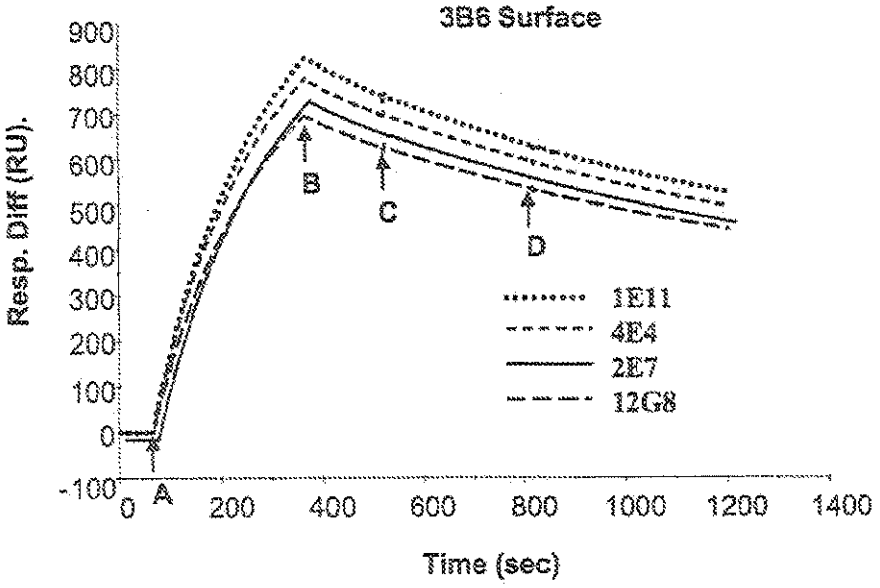

3B6 Surface
Resp. Diff (RU).
900
800
700
600
500
400
300
200
100
0
-100
A
B
C
D
1E11
4E4
2E7
12G8
0
200
400
600
800
1000
1200
1400
Time (sec)

Fig 9A

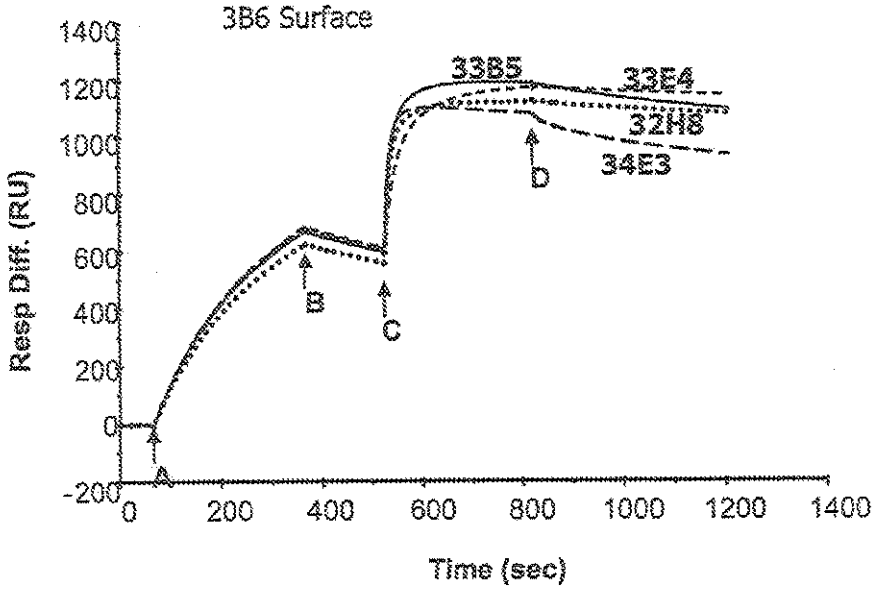

3B6 Surface
Resp Diff. (RU)
1400
1200
1000
800
600
400
200
0
-200
A
B
C
D
33B5
33E4
32H8
34E3
0
200
400
600
800
1000
1200
1400
Time (sec)

Fig 9B

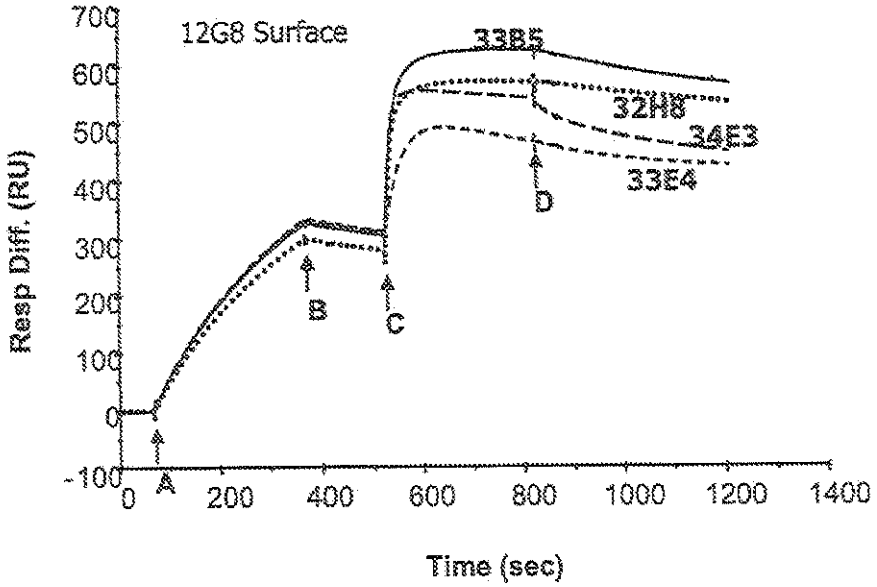

12G8 Surface
33B5
32H8
34E3
33E4
A
B
C
D
Resp Diff. (RU)
Time (sec)
700
600
500
400
300
200
100
0
-100
0
200
400
600
800
1000
1200
1400

Fig 9C

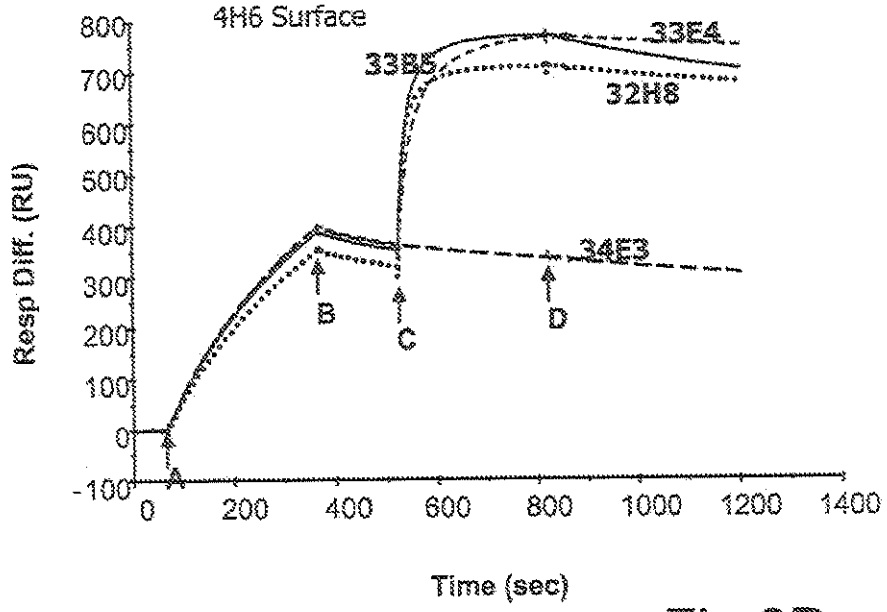

4H6 Surface
33E4
33B5
32H8
34E3
A
B
C
D
Resp Diff. (RU)
Time (sec)
800
700
600
500
400
300
200
100
0
-100
0
200
400
600
800
1000
1200
1400

Fig 9D

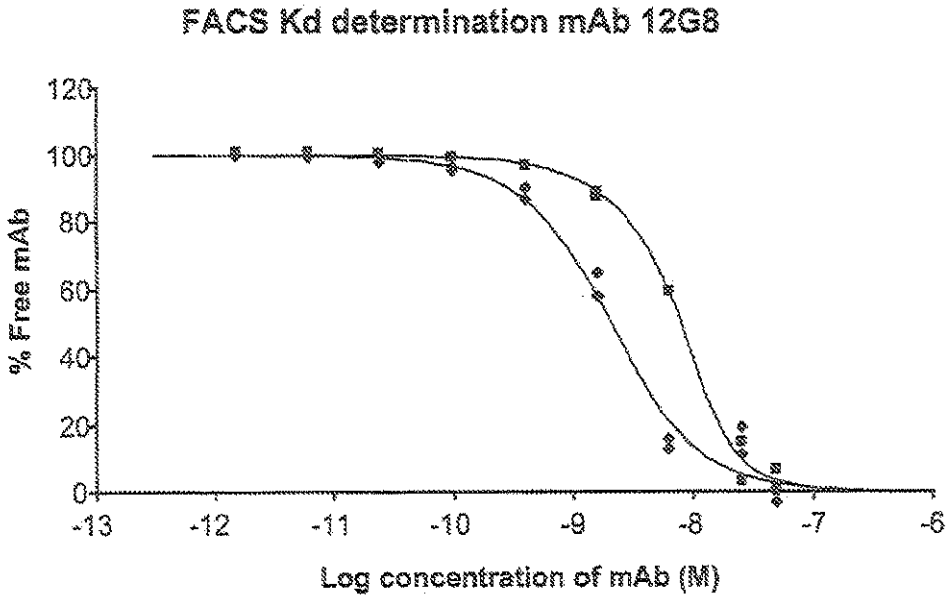
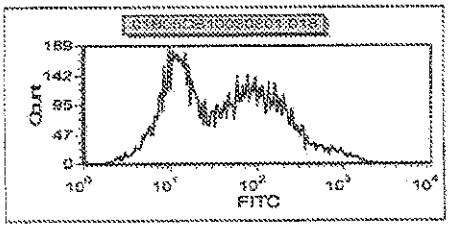
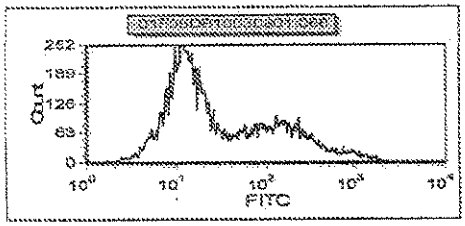


Fig 10



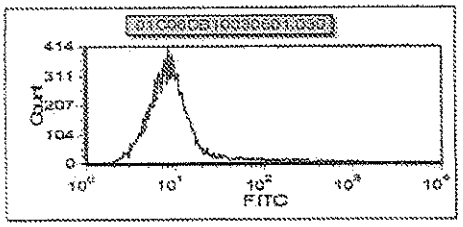
CRLR: RAMP1 Wild Type

Fig 13A



CRLR L24-Q33: RAMP1

Fig 13B



CRLR: RAMP1 Q28-A34

Fig 13C

```
                          1                                                  50
cyno_RAMP1                MARALCRLPQ RGLWLLLAHH LFMATACQEA NYGALLQELC LTQFQVDMEA
human_RAMP1               MARALCRLPR RGLWLLLAHH LFMTTACQEA NYGALLRELC LTQFQVDMEA
huRAMP1(Q28-A34))         MARALCRLPR RGLWLLLAHH LFMTTACRDP DYGTLLRELC LTQFQVDMEA
huRAMP1(Q43-E53)          MARALCRLPR RGLWLLLAHH LFMTTACQEA NYGALLRELC LTRFKEDMET
huRAMP1(R67-E78)          MARALCRLPR RGLWLLLAHH LFMTTACQEA NYGALLRELC LTQFQVDMEA
rat_RAMP1                 MAPGLRGLPR RGLWLLLAHH LFMVTACRDP DYGTLIQELC LSRFKEDMET
rhesus_RAMP1              MARALCRLPQ RGLWLLLAHH LFMATACQEA NYGALLQELC LTQFQVDMEA

                          51                                                 100
cyno_RAMP1                VGETLWCDWG RTIGSYRELA DCTWHMAEKL GCFWPNAEVD RFFLAVHGHY
human_RAMP1               VGETLWCDWG RTIRSYRELA DCTWHMAEKL GCFWPNAEVD RFFLAVHGRY
huRAMP1(Q28-A34))         VGETLWCDWG RTIRSYRELA DCTWHMAEKL GCFWPNAEVD RFFLAVHGRY
huRAMP1(Q43-E53)          IGKTLWCDWG RTIRSYRELA DCTWHMAEKL GCFWPNAEVD RFFLAVHGRY
huRAMP1(R67-E78)          VGETLWCDWG RTIRSYGELT HCTKLVANKL GCFWPNAEVD RFFLAVHGRY
rat_RAMP1                 IGKTLWCDWG KTIGSYGELT HCTKLVANKI GCFWPNPEVD KFFIAVHHRY
rhesus_RAMP1              VGETLWCDWG RTIGSYRELA DCTWHMAEKL GCFWPNAEVD RFFLAVHGHY

                          101                                                148
cyno_RAMP1                FRACPISGRA VRDPPGSVLY PFIVVPITVT LLVIALVVWQ SKHTEGIV
human_RAMP1               FRSCPISGRA VRDPPGSILY PFIVVPITVT LLVTALVVWQ SKRTEGIV
huRAMP1(Q28-A34))         FRSCPISGRA VRDPPGSILY PFIVVPITVT LLVTALVVWQ SKRTEGIV
huRAMP1(Q43-E53)          FRSCPISGRA VRDPPGSILY PFIVVPITVT LLVTALVVWQ SKRTEGIV
huRAMP1(R67-E78)          FRSCPISGRA VRDPPGSILY PFIVVPITVT LLVTALVVWQ SKRTEGIV
rat_RAMP1                 FSKCPVSGRA LRDPPNSILC PFIVLPITVT LLMTALVVWR SKRTEGIV
rhesus_RAMP1              FRACPISGRA VRDPPGSVLY PFIVVPITVT LLVTALVVWQ SKHTEGIV
```

Fig. 11

```
                1                                                   50
        huCRLR  MEKKCTLYF LVLLPFFMIL VTAELEESPE DSIQLGVTRN KIMTAQYECY
      cynoCRLR  MEKKCTLYF LVLLPFFMIF VTAELEESPE DSIQLGVTRN KIMTAQYECY
    rhesusCRLR  MEKKCTLYF LVLLPFFMIF VTAELEESPE DSIQLGVTRN KIMTAQYECY
       ratCRLR MMDKKCTLCF LFLLLLNMAL IAAESEEGAN QT-DLGVTRN KIMTAQYECY
huCRLR(L24-Q33)  MEKKCTLYF LVLLPFFMIL VTAESEEGAN QT-DLGVTRN KIMTAQYECY
     Consensus  MeKKCTLyF LvLLpffMil -tAE-EE--- ----LGVTRN KIMTAQYECY

                51                                                  100
        huCRLR QKIMQDPIQQ AEGVYCNRTW DGWLCWNDVA AGTESMQLCP DYFQDFDPSE
      cynoCRLR QKIMQDPIQQ AEGVYCNRTW DGWLCWNNVA AGTESMQLCP DYFQDFDPSE
    rhesusCRLR QKIMQDPIQQ AEGVYCNRTW DGWLCWNNVA AGTESMQLCP DYFQDFDPSE
       ratCRLR QKIMQDPIQQ GEGLYCNRTW DGWLCWNDVA AGTESMQYCP DYFQDFDPSE
huCRLR(L24-Q33)  QKIMQDPIQQ AEGVYCNRTW DGWLCWNDVA AGTESMQLCP DYFQDFDPSE
     Consensus  QKIMQDPIQQ aEG-YCNRTW DGWLCWN-VA AGTESMQlCP DYFQDFDPSE

                101                                                 150
        huCRLR KVTKICDQDG NWFRHPASNR TWTNYTQCNV NTHEKVKTAL NLFYLTIIGH
      cynoCRLR KVTKICDQDG NWFRHPASNR TWTNYTQCNV NTHEKVKTAL NLFYLTIIGH
    rhesusCRLR KVTKICDQDG NWFRHPASNR TWTNYTQCNV NTHEKVKTAL NLFYLTIIGH
       ratCRLR KVTKICDQDG NWFRHPDSNR TWTNYTLCNN STHEKVKTAL NLFYLTIIGH
huCRLR(L24-Q33)  KVTKICDQDG NWFRHPASNR TWTNYTQCNV NTHEKVKTAL NLFYLTIIGH
     Consensus  KVTKICDQDG NWFRHPaSNR TWTNYTqCNv nTHEKVKTAL NLFYLTIIGH

                151                                                 200
        huCRLR GLSIASLLIS LGIFFYFKSL SCQRITLHKN LFFSFVCNSV VTIIHLTAVA
      cynoCRLR GLSIASLLIS LGIFFYFKSL SCQRITLHKN LFFSFVCNSV VTIIHLTAVA
    rhesusCRLR GLSIASLLIS LGIFFYFKSL SCQRITLHKN LFFSFVCNSV VTIIHLTAVA
       ratCRLR GLSIASLIIS LIIFFYFKSL SCQRITLHKN LFFSFVCNSI VTIIHLTAVA
huCRLR(L24-Q33)  GLSIASLLIS LGIFFYFKSL SCQRITLHKN LFFSFVCNSV VTIIHLTAVA
     Consensus  GLSIASL-IS LgIFFYFKSL SCQRITLHKN LFFSFVCNS- VTIIHLTAVA

                201                                                 250
        huCRLR NNQALVATNP VSCKVSQFIH LYLMGCNYFW MLCEGIYLHT LIVVAVFAEK
      cynoCRLR NNQALVATNP VSCKVSQFIH LYLMGCNYFW MLCEGIYLHT LIVVAVFAEK
    rhesusCRLR NNQALVATNP VSCKVSQFIH LYLMGCNYFW MLCEGIYLHT LIVVAVFAEK
       ratCRLR NNQALVATNP VSCKVSQFIH LYLMGCNYFW MLCEGIYLHT LIVVAVFAEK
huCRLR(L24-Q33)  NNQALVATNP VSCKVSQFIH LYLMGCNYFW MLCEGIYLHT LIVVAVFAEK
     Consensus  NNQALVATNP VSCKVSQFIH LYLMGCNYFW MLCEGIYLHT LIVVAVFAEK

                251                                                 300
        huCRLR QHLMWYYFLG WGFPLIPACI HAIARSLYYN DNCWISSDTH LLYIIHGPIC
      cynoCRLR QHLMWYYFLG WGFPLIPACI HAIARSLYYN DNCWISSDTH LLYIIHGPIC
    rhesusCRLR QHLMWYYFLG WGFPLIPACI HAIARSLYYN DNCWISSDTH LLYIIHGPIC
       ratCRLR QHLMWYYFLG WGFPLLPACI HAIARSLYYN DNCWISSDTH LLYIIHGPIC
huCRLR(L24-Q33)  QHLMWYYFLG WGFPLIPACI HAIARSLYYN DNCWISSDTH LLYIIHGPIC
     Consensus  QHLMWYYFLG WGFPL-PACI HAIARSLYYN DNCWISSDTH LLYIIHGPIC
```

Fig. 12A

```
                301                                                 350
        huCRLR  AALLVNLFFL LNIVRVLITK LKVTHQAESN LYMKAVRATL ILVPLLGIEF
      cynoCRLR  AALLVNLFFL LNIVRVLITK LKVTHQAESN LYMKAVRATL ILVPLLGIEF
    rhesusCRLR  AALLVNLFFL LNIVRVLITK LKVTHQAESN LYMKAVRATL ILVPLLGIEF
       ratCRLR  AALLVNLFFL LNIVRVLITK LKVTHQAESN LYMKAVRATL ILVPLLGIEF
huCRLR(L24-Q33) AALLVNLFFL LNIVRVLITK LKVTHQAESN LYMKAVRATL ILVPLLGIEF
     Consensus  AALLVNLFFL LNIVRVLITK LKVTHQAESN LYMKAVRATL ILVPLLGIEF

                 351                                                400
        huCRLR  VLIPWRPEGK IAEEVYDYIM HILMHFQGLL VSTIFCFFNG EVQAILRRNW
      cynoCRLR  VLIPWRPEGK IAEEVYDYIM HILMHFQGLL VSTIFCFFNG EVQAILRRNW
    rhesusCRLR  VLIPWRPEGK IAEEVYDYIM HILMHFQGLL VSTIFCFFNG EVQAILRRNW
       ratCRLR  VLFPWRPEGK VAEEVYDYVM HILMHYQGLL VSTIFCFFNG EVQAILRRNW
huCRLR(L24-Q33) VLIPWRPEGK IAEEVYDYIM HILMHFQGLL VSTIFCFFNG EVQAILRRNW
     Consensus  VLiPWRPEGK -AEEVYDY-M HILMH-QGLL VSTIFCFFNG EVQAILRRNW

                 401                                                450
        huCRLR  NQYKIQFGNS FSNSEALRSA SYTVSTISDG PGYSHDCPSE HLNGKSIHDI
      cynoCRLR  NQYKIQFGNS FSNSEALRSA SYTVSTISDG PGYSHDCPSE HLNGKSIHDI
    rhesusCRLR  NQYKIQFGNS FSNSEALRSA SYTVSTISDG PGYSHDCPSE HLNGKSIHDI
       ratCRLR  NQYKIQFGNG FSHSDALRSA SYTVSTISDV QGYSHDCPTE HLNGKSIQDI
huCRLR(L24-Q33) NQYKIQFGNS FSNSEALRSA SYTVSTISDG PGYSHDCPSE HLNGKSIHDI
     Consensus  NQYKIQFGNs FSnSeALRSA SYTVSTISDg pGYSHDCP-E HLNGKSIhDI

                 451             465
        huCRLR  ENVLLKPENL YN---
      cynoCRLR  ENVVLKPENL YN---
    rhesusCRLR  ENVVLKPENL YN---
       ratCRLR  ENVALKPEKM YDLVM
huCRLR(L24-Q33) ENVLLKPENL YN---
     Consensus  ENV-LKPEn- Y----
```

Fig. 12B

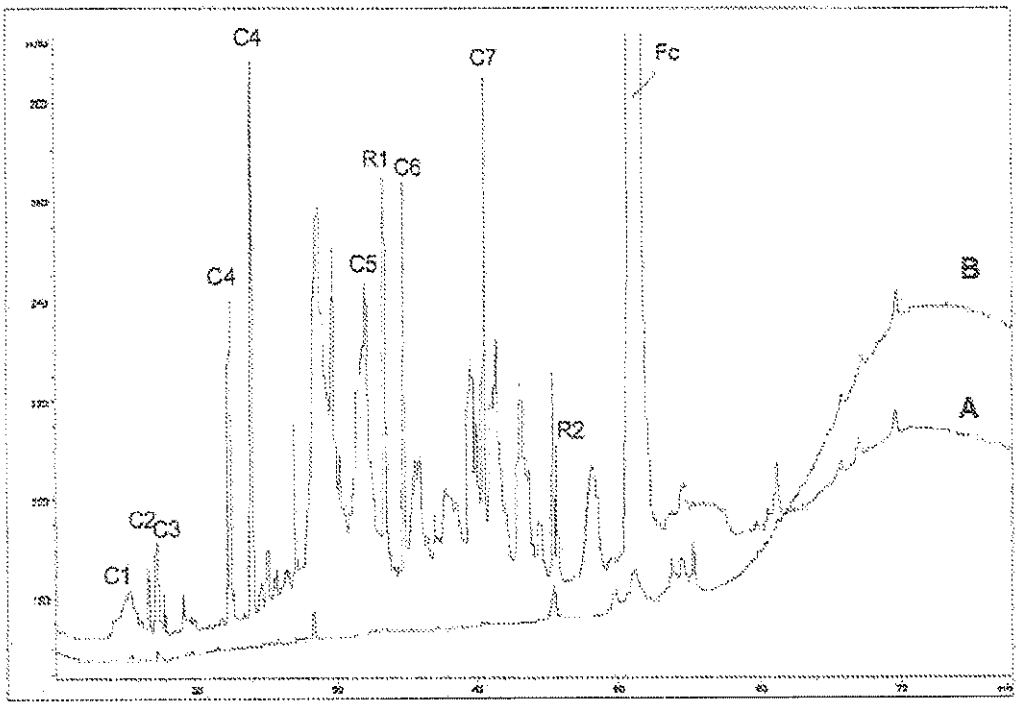

C4
C7
Fc
R1
C6
C5
C4
B
A
R2
C2
C3
C1

Fig 14

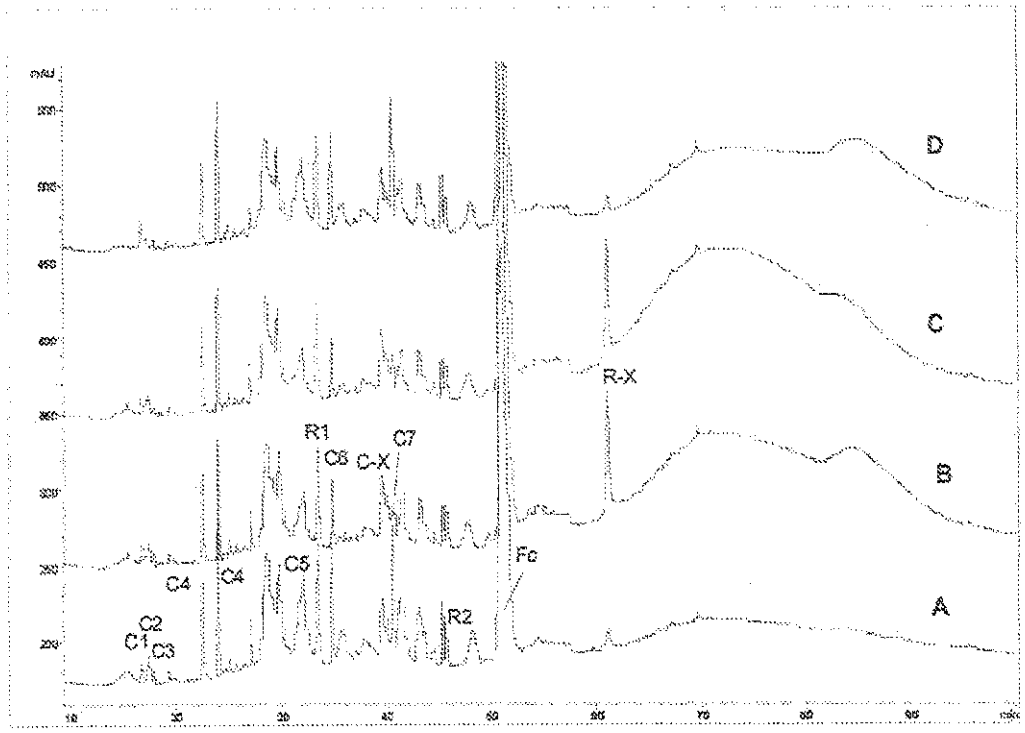

D
C
R-X
R1
C6
C-X
C7
B
Fc
C4
C4
C5
A
R2
C2
C1
C3

Fig 15

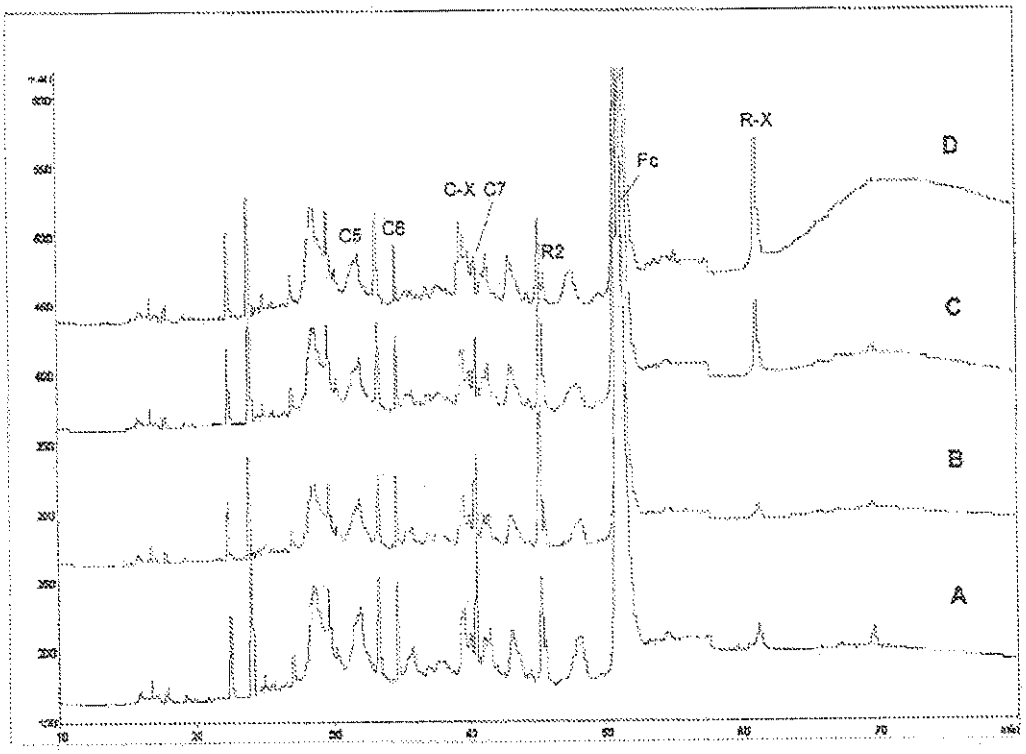

C5
C6
C-X C7
R2
Fc
R-X
D
C
B
A

Fig 16

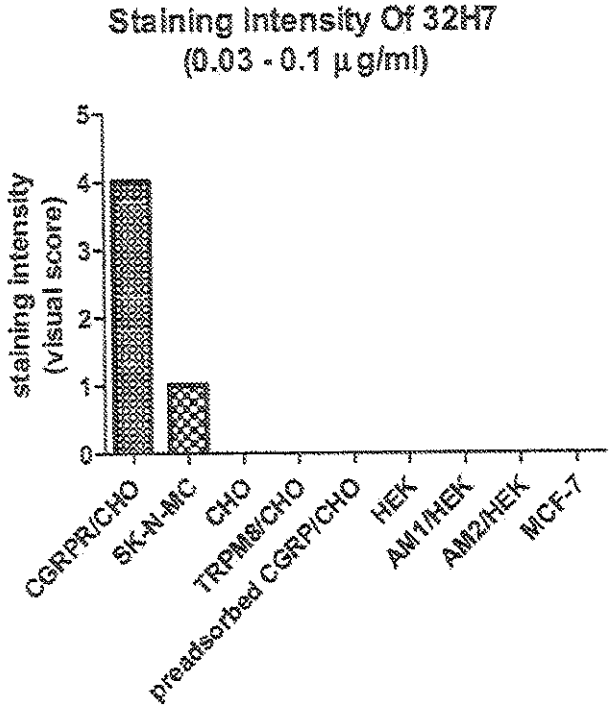

Staining Intensity Of 32H7
(0.03 - 0.1 µg/ml)
staining intensity
(visual score)
0
1
2
3
4
5
CGRPR/CHO
SK-N-MC
CHO
TRPM8/CHO
preadsorbed CGRP/CHO
HEK
AM1/HEK
AM2/HEK
MCF-7

Fig 17