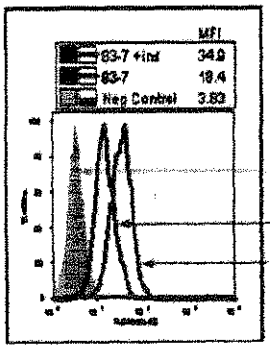
Figure 1

positive control (83.7 mAb)

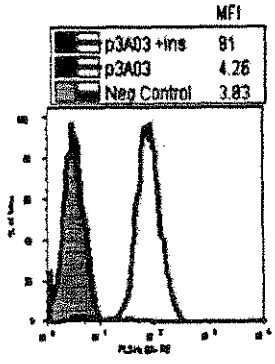


Background binding

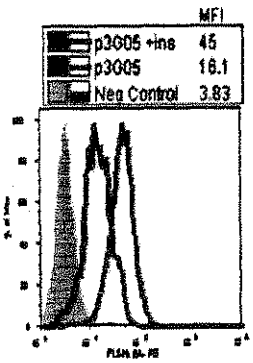
Binding to free receptor

Binding to INSR/INS complex

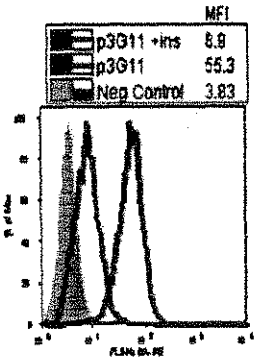
Binds exclusively to INS/INSR complex



Preferentially binds INS/INSR complex



Preferentially binds INSR



Binds equally to INSR and INS/INSR complex

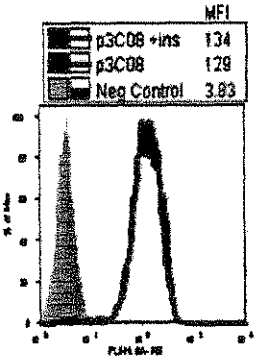


Figure 2

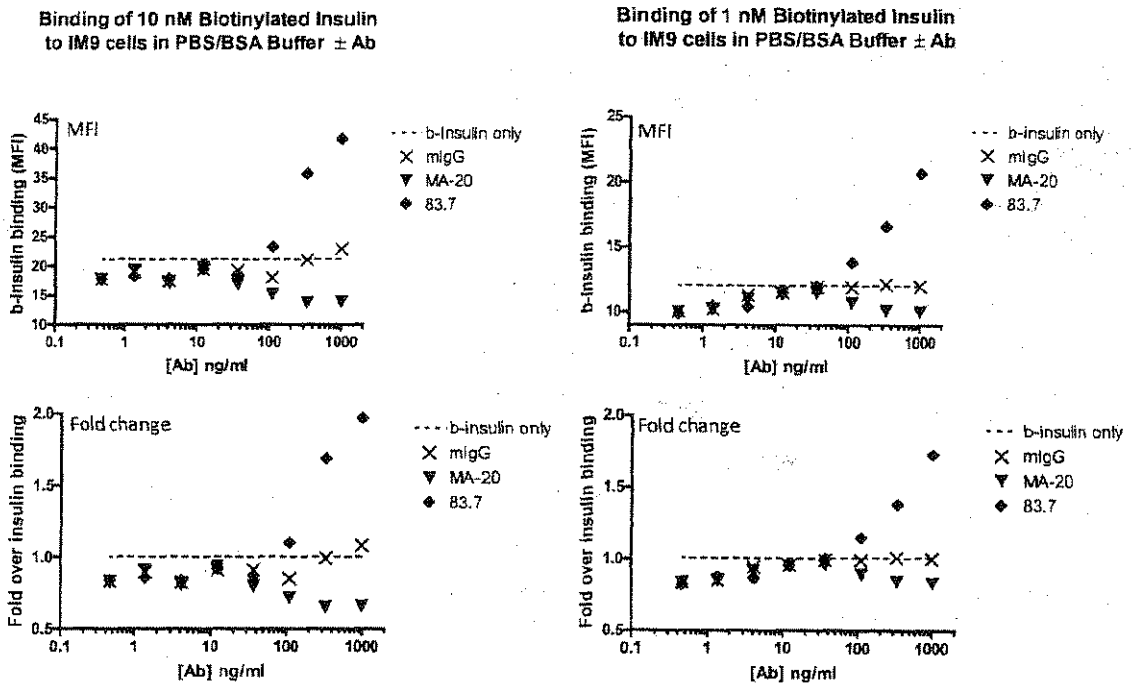

Binding of 10 nM Biotinylated Insulin to IM9 cells in PBS/BSA Buffer ± Ab
MFI
b-Insulin binding (MFI)
[Ab] ng/ml
b-insulin only
mIgG
MA-20
83.7
Fold change
Fold over insulin binding
Binding of 1 nM Biotinylated Insulin to IM9 cells in PBS/BSA Buffer ± Ab

Figure 3

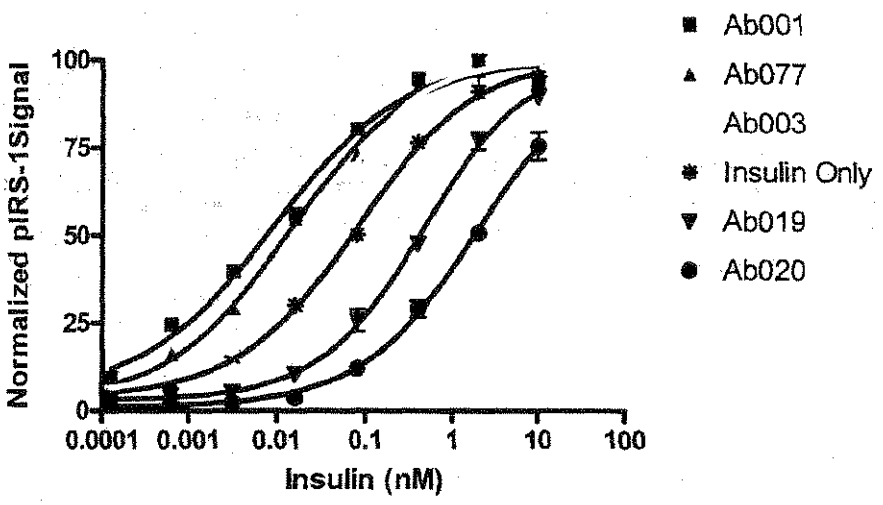
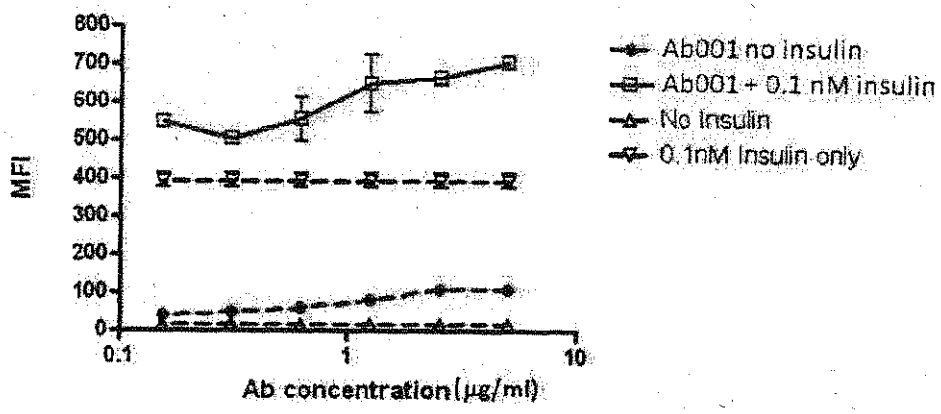

Normalized pIRS-1Signal
100
75
50
25
0
0.0001
0.001
0.01
0.1
1
10
100
Insulin (nM)
Ab001
Ab077
Ab003
Insulin Only
Ab019
Ab020

Figure 4

Figure 4A. Positive modulator



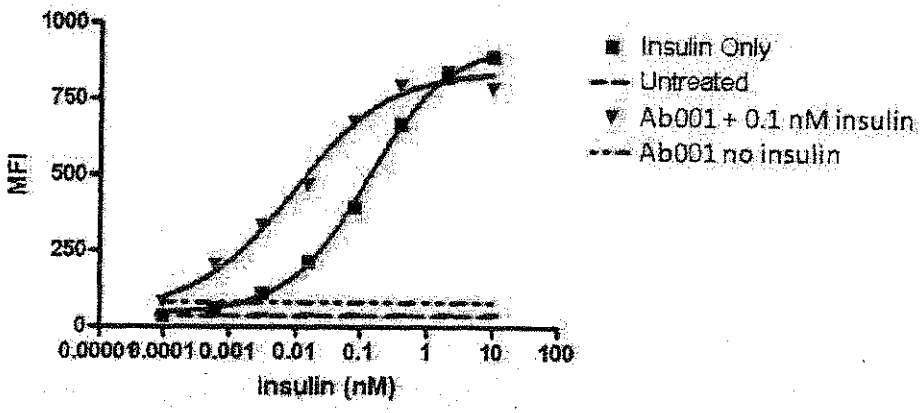


Figure 4B. Positive modulator with significant agonism

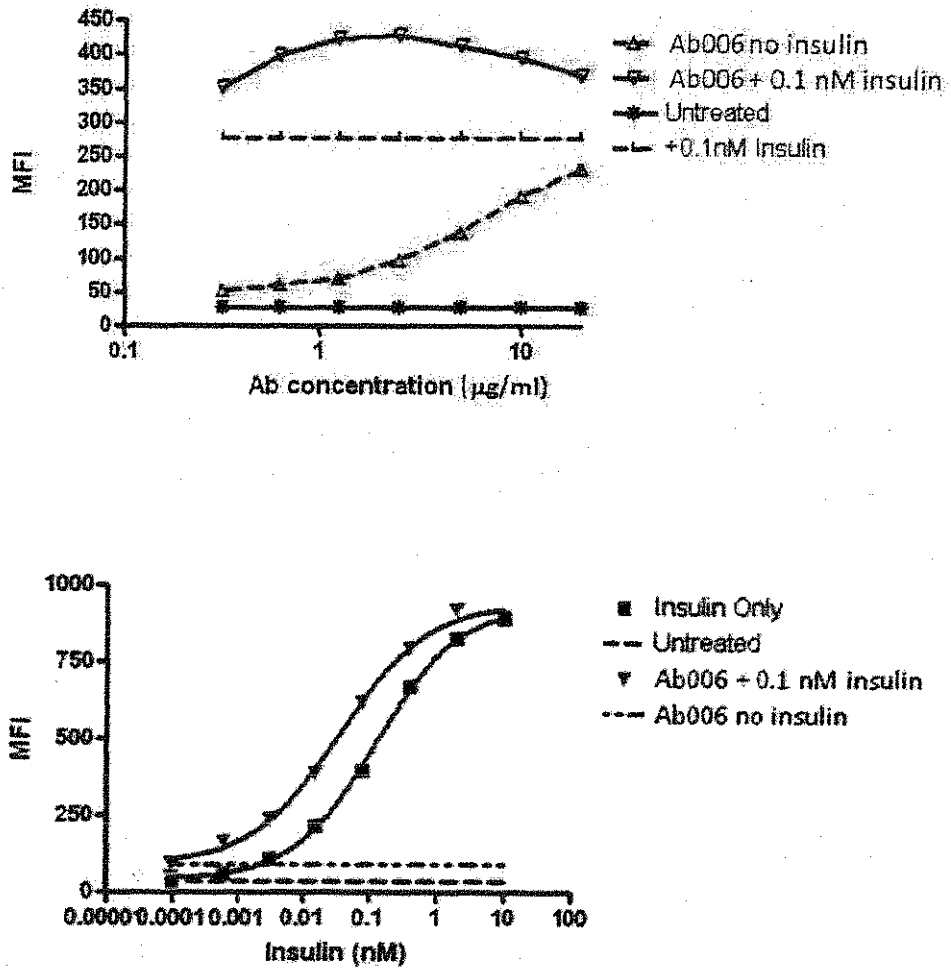


Figure 4C. Non-modulator

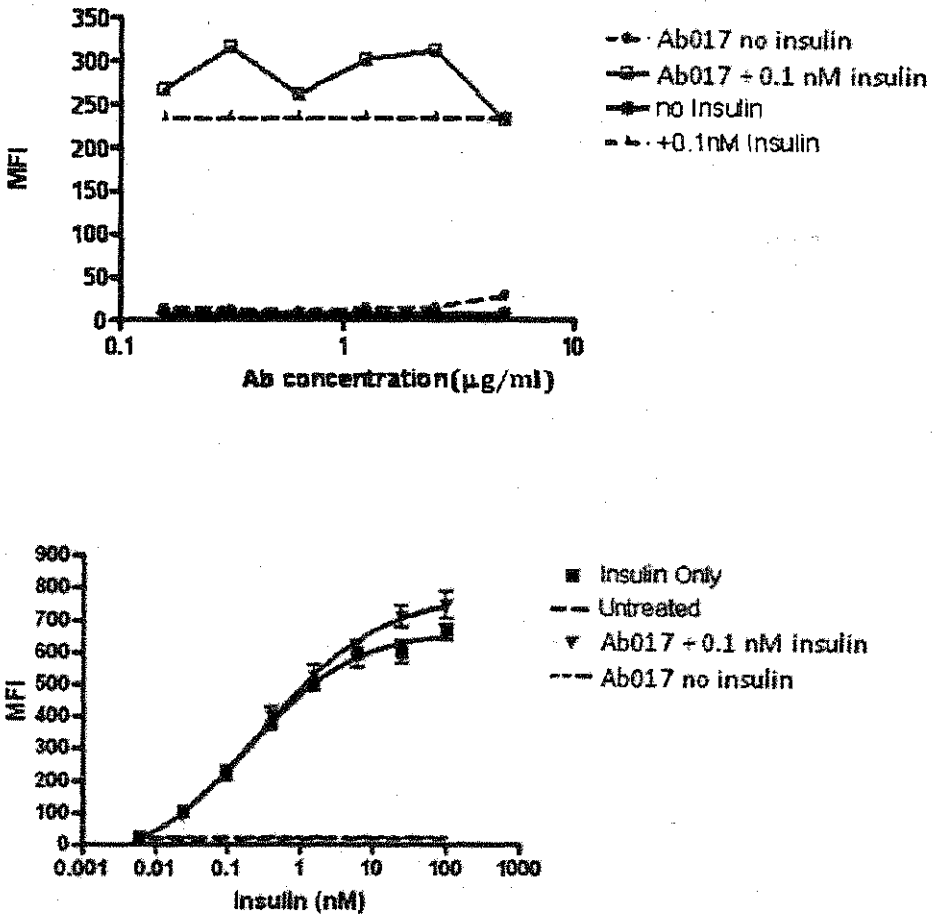


Figure 4D. Agonist Abs

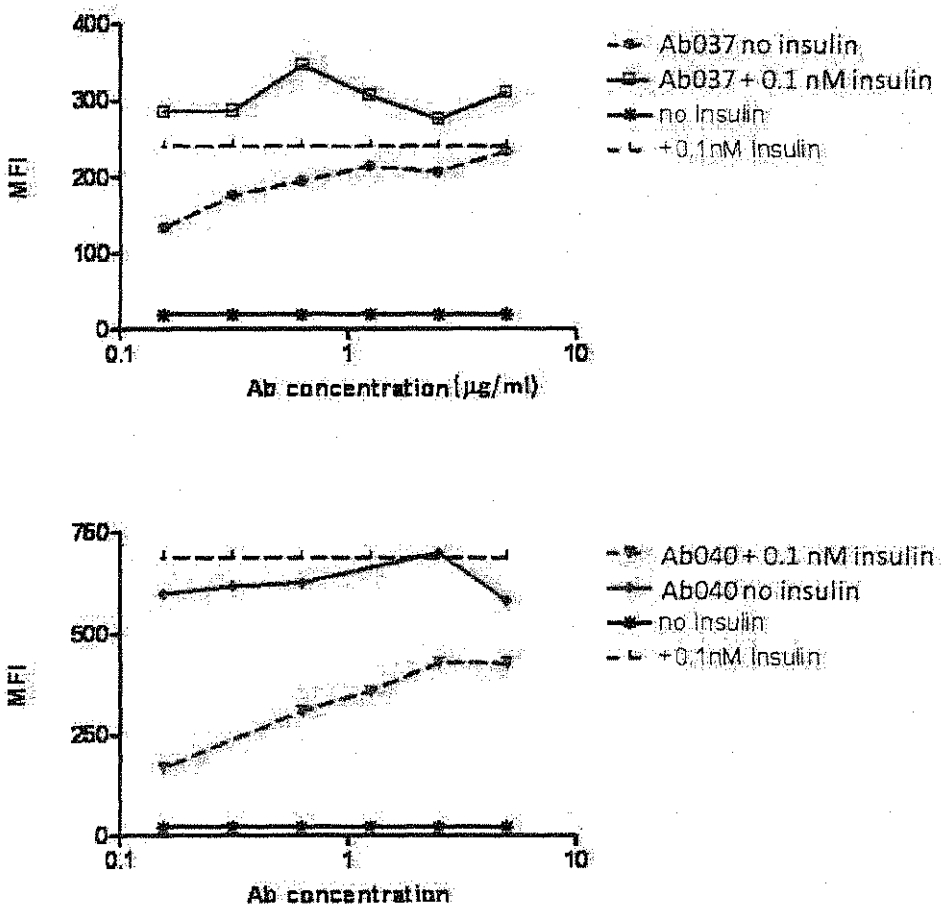


Figure 4E. Negative modulator

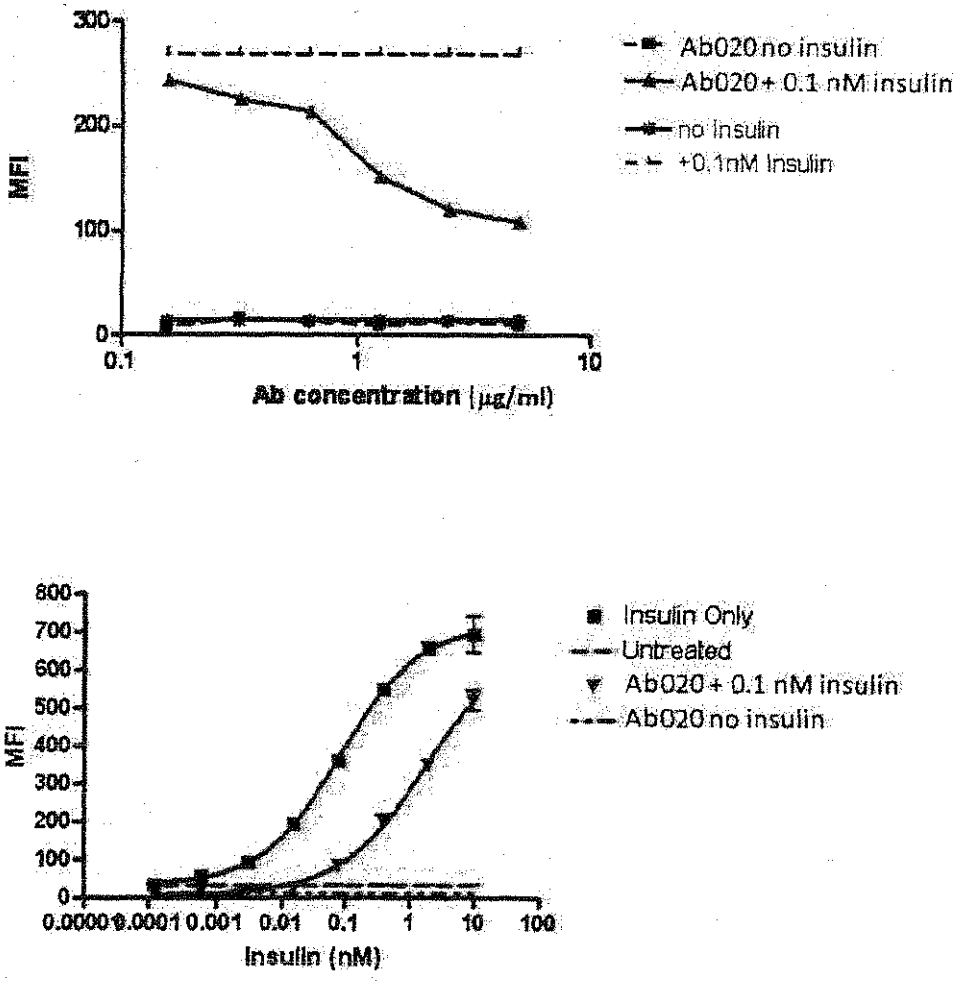


Figure 5

Ab	*Ab type*	*[Ab] (ug/ml)*	*Insulin EC50 (nM)*		*Fold change in insulin EC50*			*Ab property*
			insulin alone	*Insulin + antibody*	*-Ab EC50/+Ab EC50*	*+Ab EC50/-Ab EC50*	*absolute change*	
Ab001	IgG2	5.00	0.11	0.0048	23.32	0.04	23.32	Abs with significant positive modulation
Ab002	IgG2	2.50	0.12	0.0166	7.32	0.14	7.32	
Ab003	IgG2	2.25	0.12	0.0171	7.11	0.14	7.11	
Ab004	IgG2	5.00	0.13	0.0239	5.34	0.19	5.34	
Ab005	Fab	2.50	0.08	0.0188	4.48	0.22	4.48	
Ab006	IgG2	1.25	0.13	0.0367	3.47	0.29	3.47	
Ab007	IgG2	5.00	0.11	0.0346	3.22	0.31	3.22	
Ab008	Fab	0.63	0.08	0.0270	3.11	0.32	3.11	
Ab009	IgG2	5.00	0.13	0.0461	2.77	0.36	2.77	
Ab010	IgG2	2.50	0.12	0.0463	2.62	0.38	2.62	
Ab011	IgG2	2.50	0.13	0.0719	1.78	0.56	1.78	Abs without significant modulation
Ab012	IgG2	2.50	0.08	0.0504	1.67	0.60	1.67	
Ab013	IgG2	1.25	0.08	0.0540	1.56	0.64	1.56	
Ab014	IgG2	5.00	0.11	0.0984	1.13	0.88	1.13	
Ab015	IgG2	1.25	0.20	0.2450	0.82	1.23	1.23	
Ab016	IgG2	1.25	0.20	0.2714	0.74	1.36	1.36	
Ab017	IgG2	2.50	0.20	0.2747	0.73	1.37	1.37	
Ab018	IgG2	5.00	0.09	0.2969	0.29	3.48	3.48	Abs with significant negative modulation
Ab019	Fab	5.00	0.09	0.4527	0.19	5.31	5.31	
Ab020	IgG2	5.00	0.09	1.8570	0.05	21.79	21.79	

Figure 6

Figure 6A. Positive modulator with very low agonism

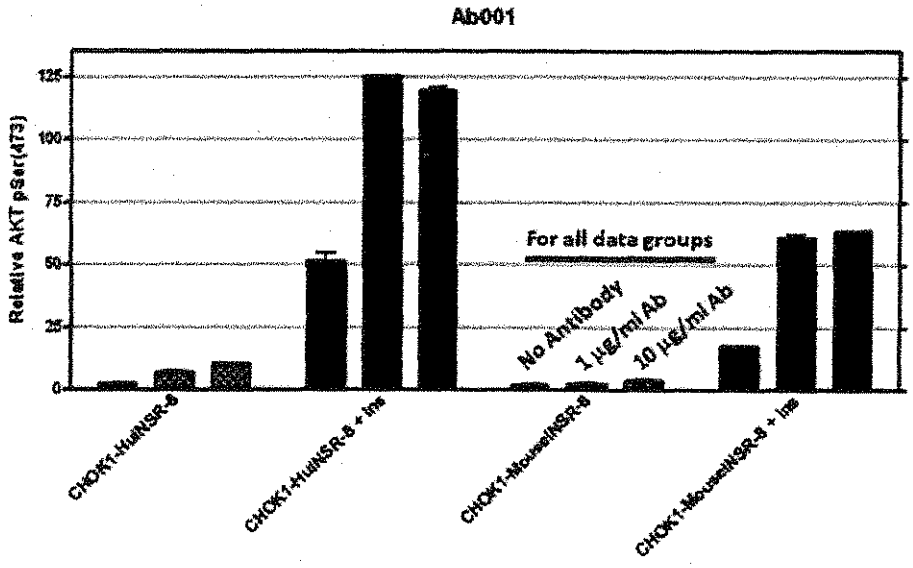


Figure 6B. Positive modulator with agonism

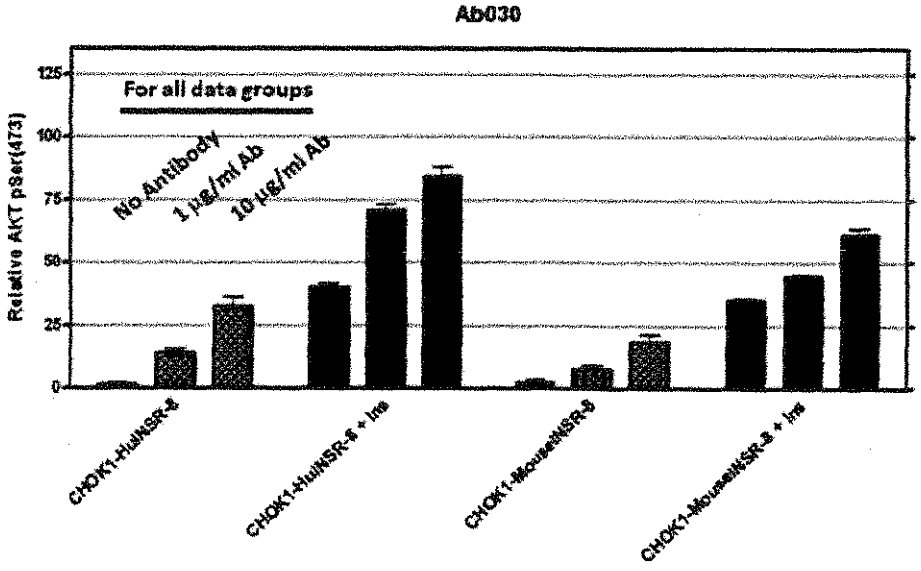


Figure 6C. Agonist Abs

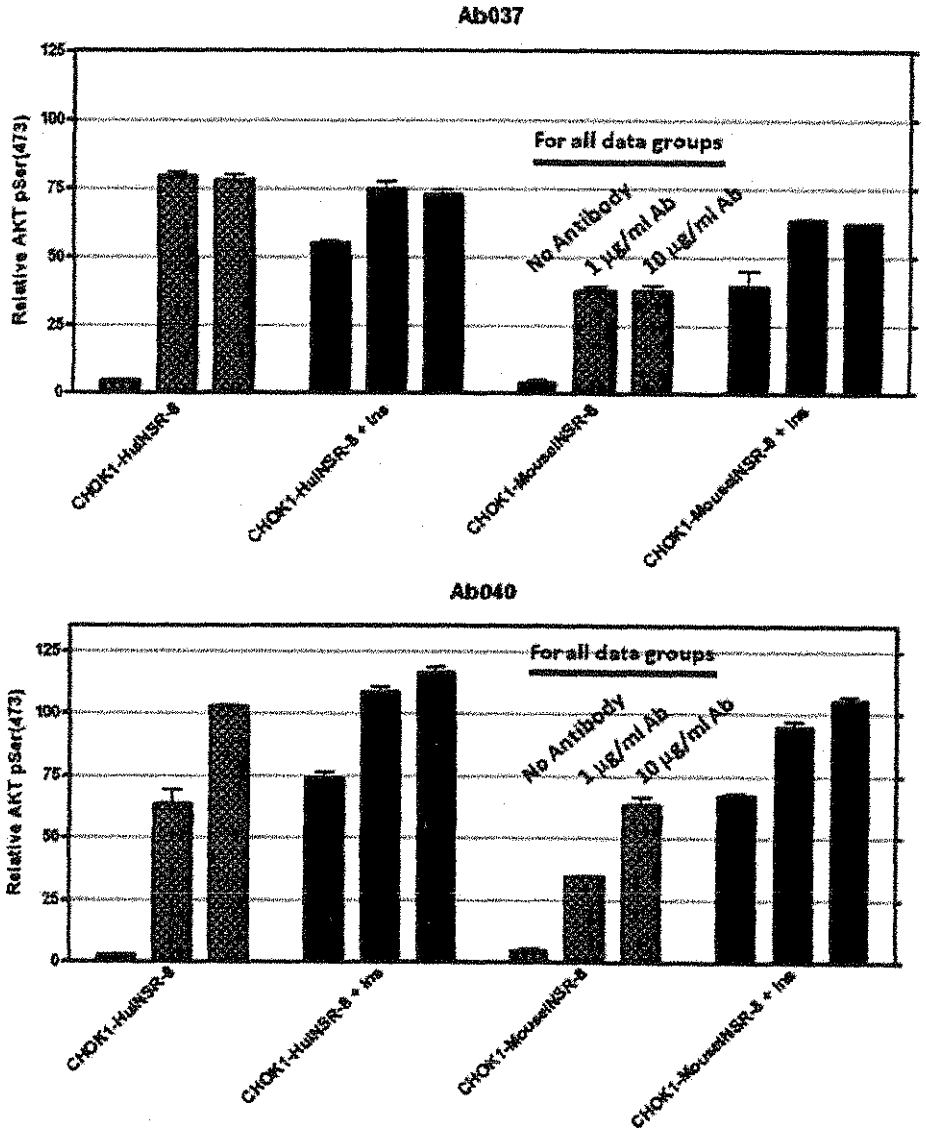


Figure 6D. 83-7

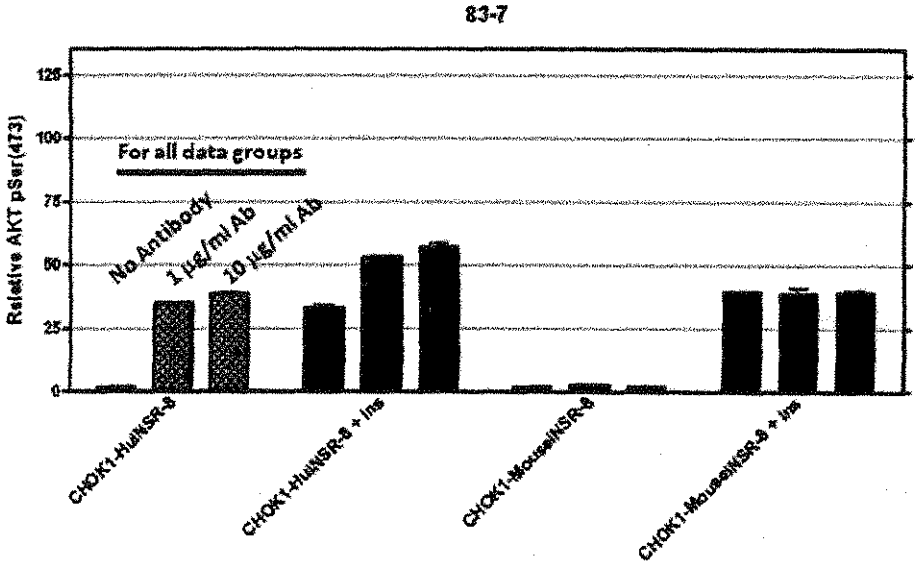


Figure 6E. Insulin and background response in the absence of antibody

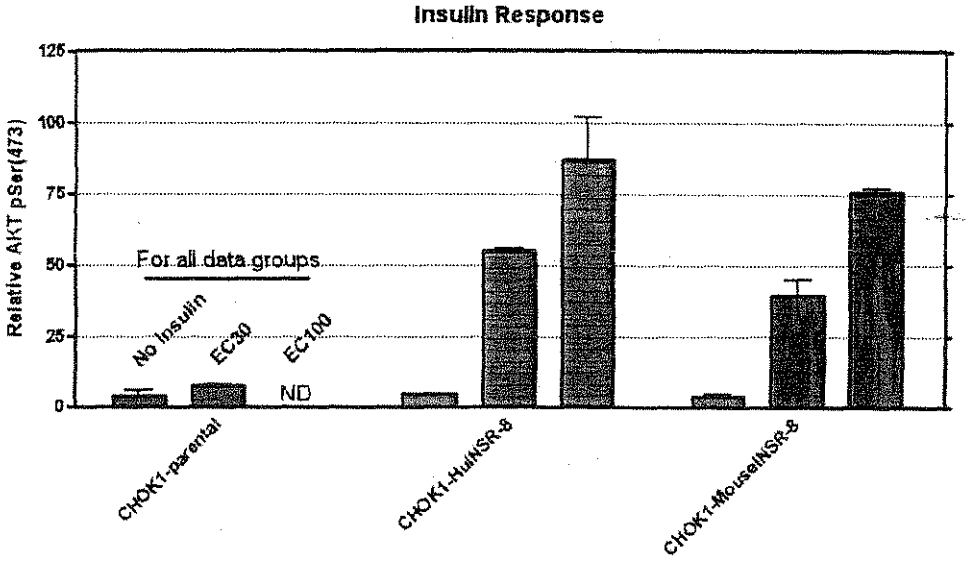


Figure 7

Agonism class	*Antibody*	*agonist of human INSR by pIRS-1*	*agonist of human INSR by pAkt*	*agonist of mouse INSR by pAkt*	*cross reactive to mouse INSR by FACS*	*cross reactive to mouse INSR by pAkt*
Abs with weak or very weak agonism	Ab021	yes	nd	nd	nd	nd
	Ab022	yes	nd	nd	nd	nd
	Ab023	yes	nd	nd	nd	nd
	Ab024	yes	nd	nd	no	nd
	Ab025	yes	nd	nd	no	nd
	Ab026	yes	nd	nd	no	nd
	Ab027	yes	nd	nd	no	nd
	Ab028	yes	nd	nd	no	nd
	Ab013	yes	nd	nd	no	nd
	Ab011	yes	nd	nd	yes	nd
	Ab001	yes	yes	no	yes	yes
	Ab015	yes	yes	no	no	no
	Ab002	yes	yes	no	no	no
Abs with moderate agonism	Ab029	yes	nd	nd	nd	nd
	Ab017	yes	yes	no	yes	no
	Ab030	yes	yes	yes	yes	yes
	Ab031`	yes	nd	nd	no	nd
	Ab009	yes	yes	yes	yes	yes
	Ab032	yes	yes	yes	yes	yes
	Ab018	yes	nd	nd	yes	nd
	Ab033	yes	nd	nd	yes	nd
	Ab012	yes	yes	no	no	yes
	Ab014	yes	yes	yes	yes	yes
	Ab034	yes	nd	nd	nd	nd
	Ab010G1	yes	yes	no	no	no
	Ab010G2	yes	yes	no	yes	yes
	Ab003	yes	nd	nd	nd	nd
Abs with strong agonism	Ab006	yes	yes	yes	yes	yes
	Ab035	yes	nd	nd	no	nd
	Ab036	yes	yes	yes	yes	yes
	Ab037	yes	yes	yes	yes	yes
	Ab038	yes	yes	no	yes	no
	Ab039	yes	yes	yes	yes	yes
	Ab040	yes	yes	yes	yes	yes
	Ab041	yes	nd	nd	nd	nd
	Ab042	yes	nd	nd	no	nd
	Ab043	yes	yes	yes	yes	yes

Agonism class	*Antibody*	*agonist of human INSR by pIRS-1*	*agonist of human INSR by pAkt*	*agonist of mouse INSR by pAkt*	*cross reactive to mouse INSR by FACS*	*cross reactive to mouse INSR by pAkt*
	Ab044	yes	nd	nd	yes	nd
	Ab045	yes	nd	nd	yes	nd
	Ab046	yes	yes	yes	yes	yes
	Ab047	yes	nd	nd	no	nd
	Ab048	yes	yes	no	yes	no
	Ab049	yes	yes	no	no	no

nd = not determined

Figure 7 (cont'd)

Figure 8

Figure 8A

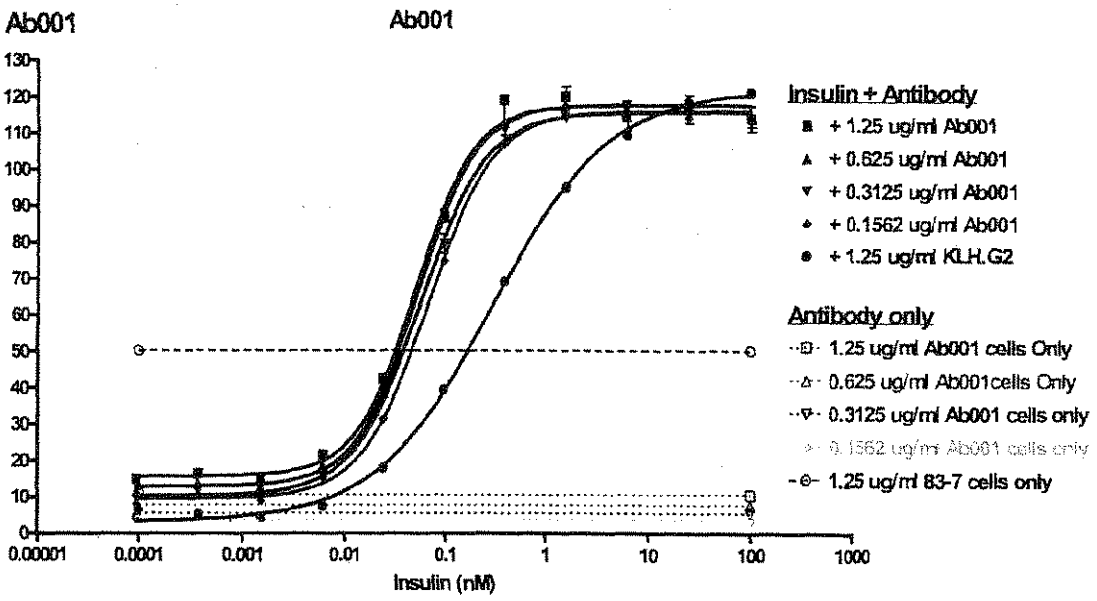


Figure 8B

Ab Concentration (ug/mL)	HILLSLOPE	EC50 (pM)	Fold-change in EC50
1.25 Ab001	1.49	51	5.9
0.62 Ab001	1.44	53	5.7
0.31 Ab001	1.32	57	5.3
0.15 Ab001	1.33	68	4.4
1.25 anti-KLH	0.76	301	

Figure 9

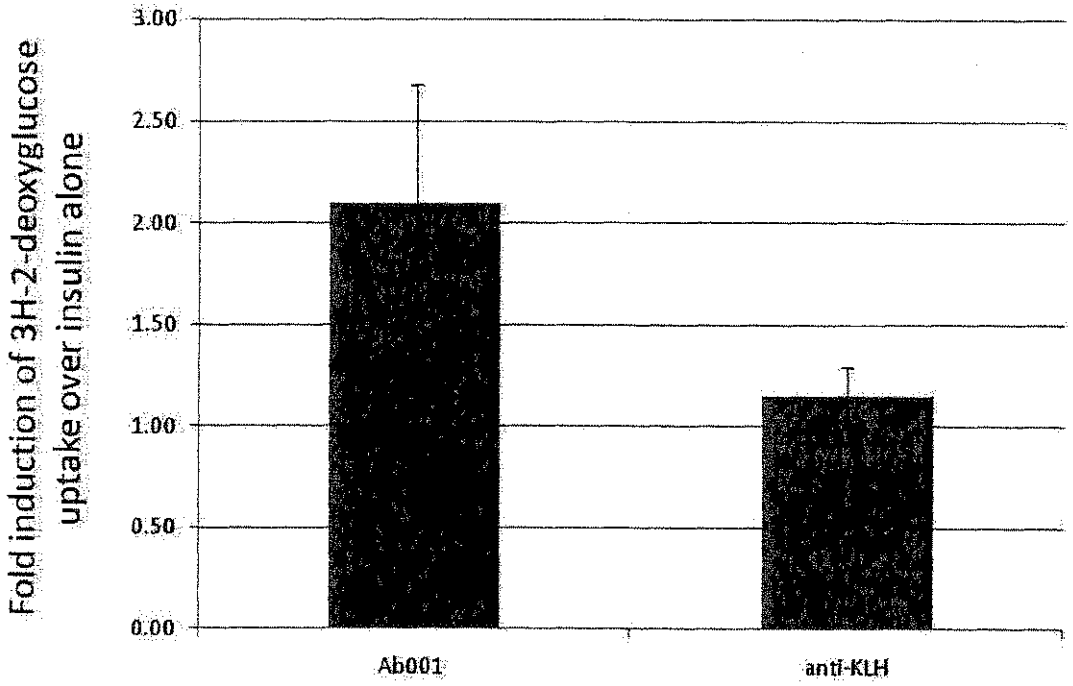
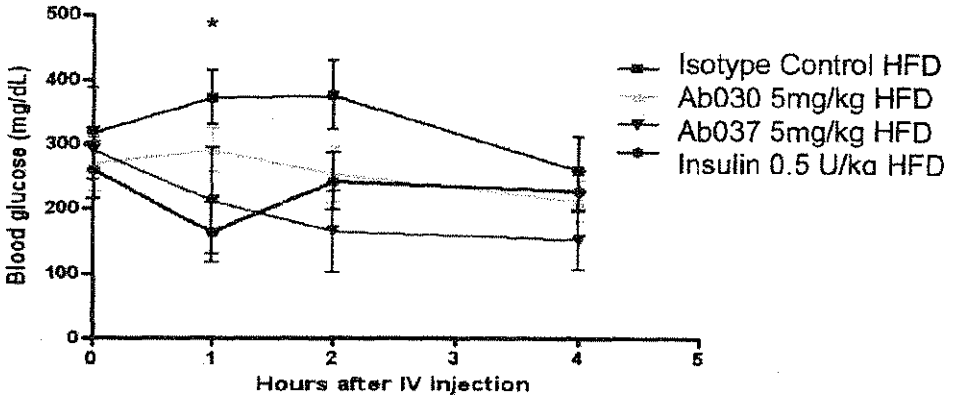

Fold induction of 3H-2-deoxyglucose uptake over insulin alone
3.00
2.50
2.00
1.50
1.00
0.50
0.00
Ab001
anti-KLH

Figure 10

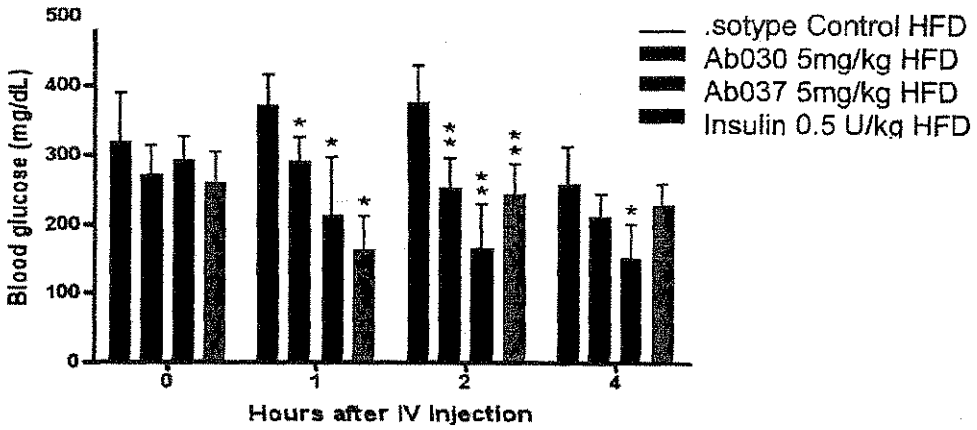
Blood Glucose Levels in DIO Mice Treated with Partial Agonist Anti-INSR Antibodies

A.



* $p < 0.01$ (one-tailed) ND/isotype compared to HFD/isotype

B.

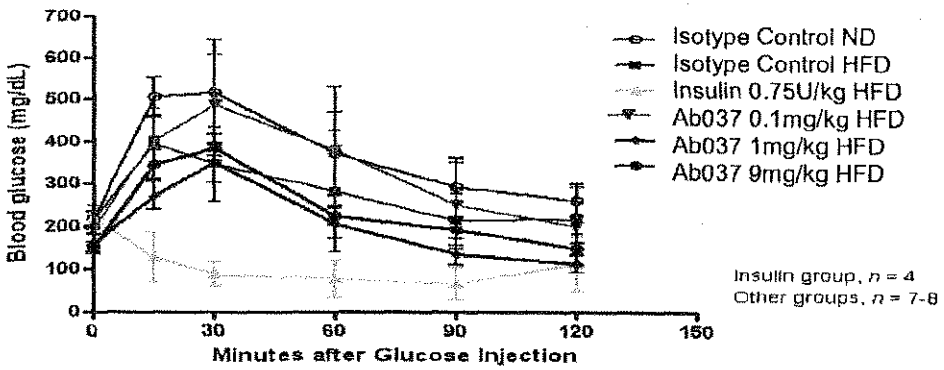


* $p \leq 0.01$ (two-tailed) compared to HFD/isotype

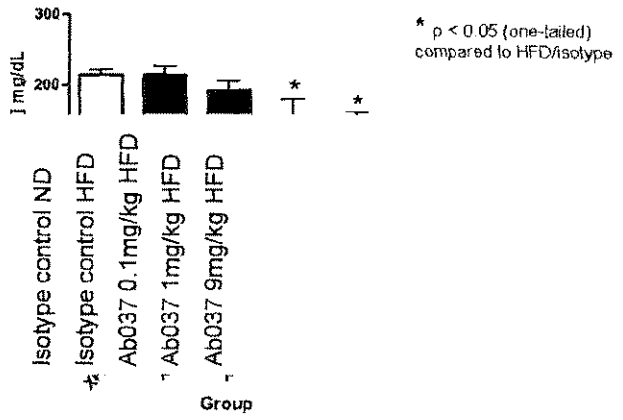
** $p < 0.001$ (two tailed) compared to HFD/isotype

Figure 11

A.



B.



C.

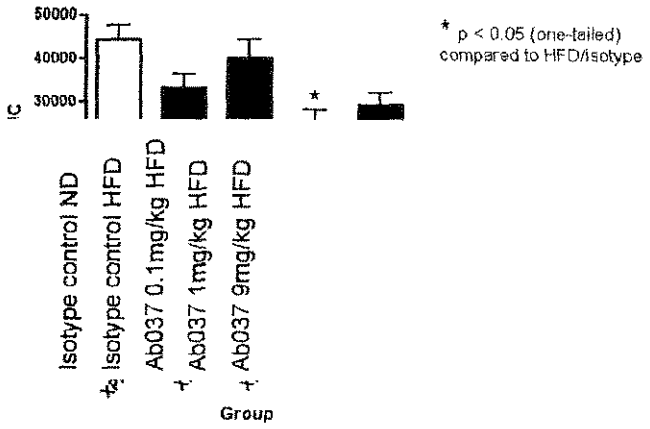
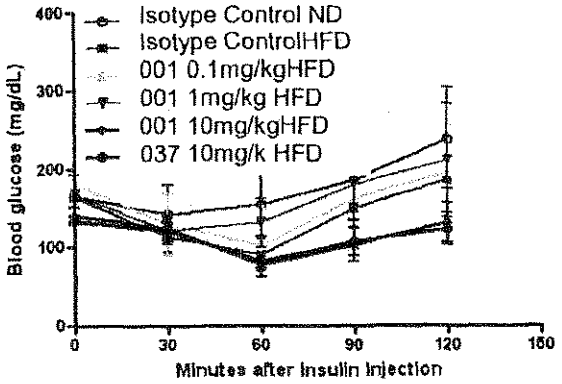
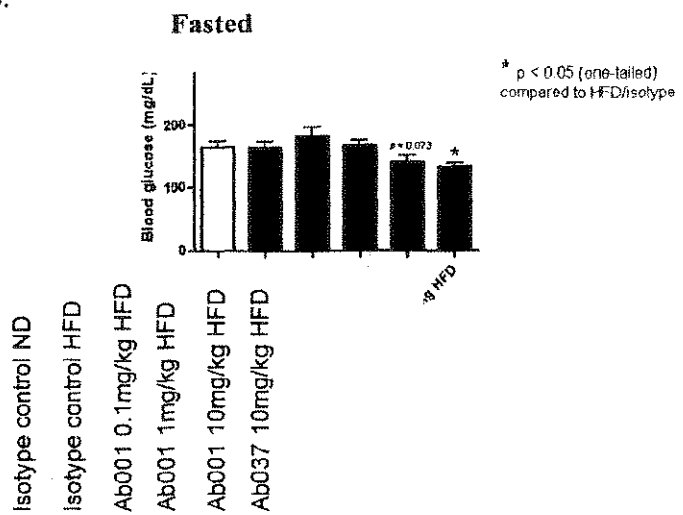


Figure 12

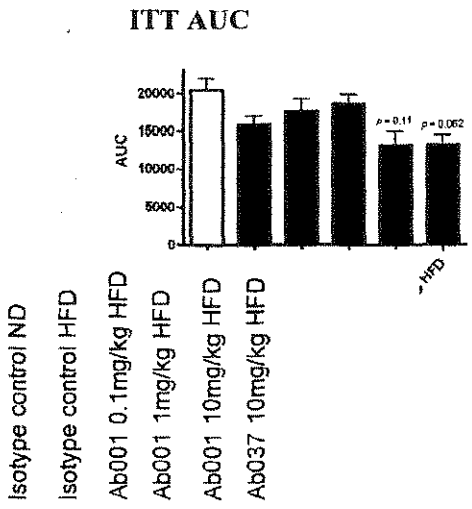
A.



B.



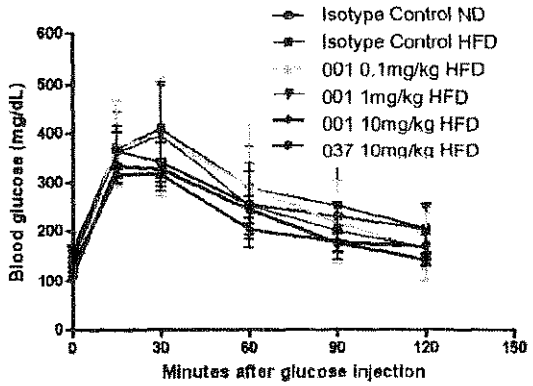
C.



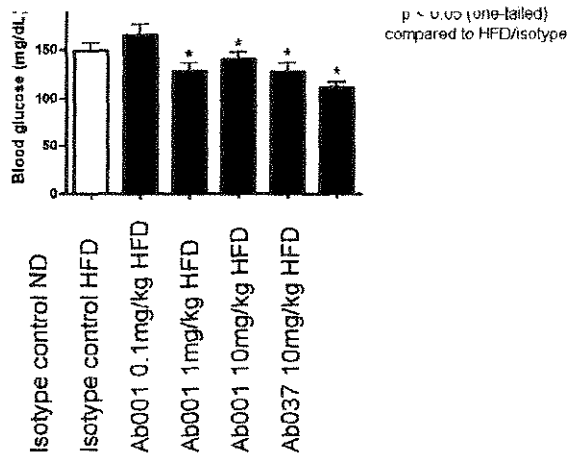
19/82

Figure 13

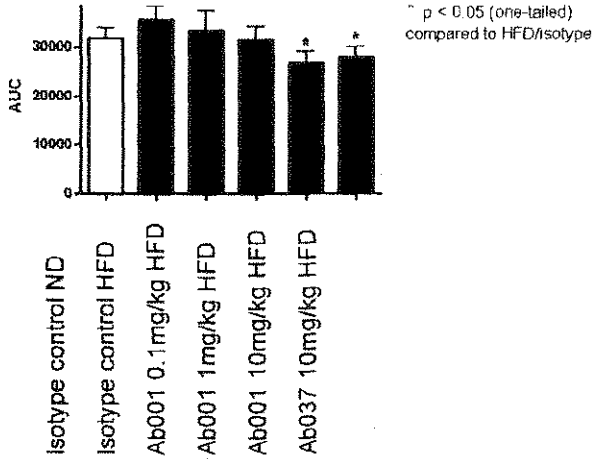
A.



B.



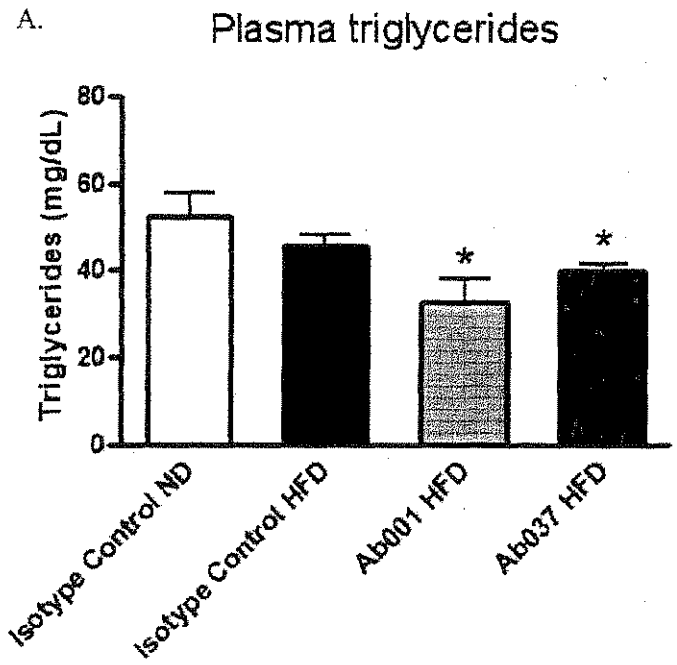
C.



20/82

Figure 14

A.


Plasma triglycerides
Triglycerides (mg/dL)
80
60
40
20
0
*
*
Isotype Control ND
Isotype Control HFD
Ab001 HFD
Ab037 HFD

B.

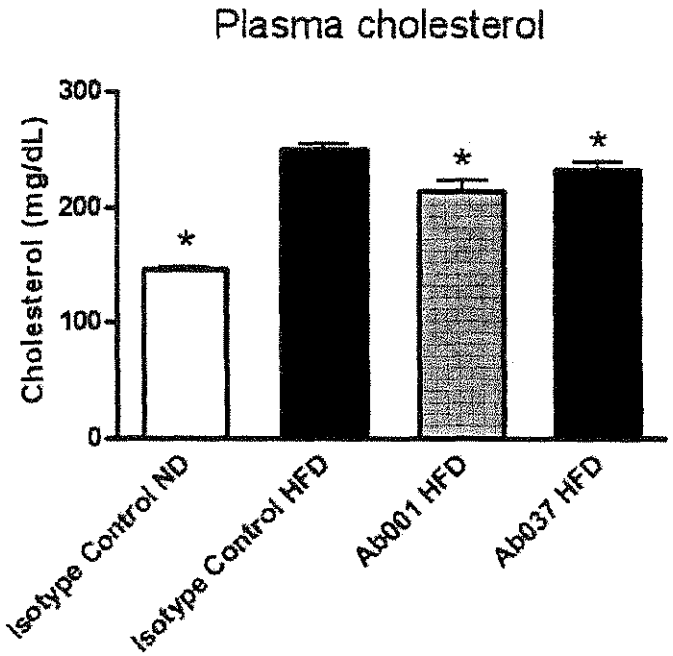
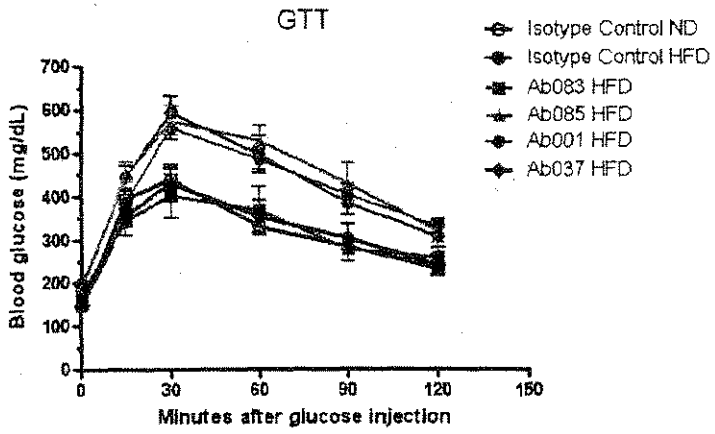
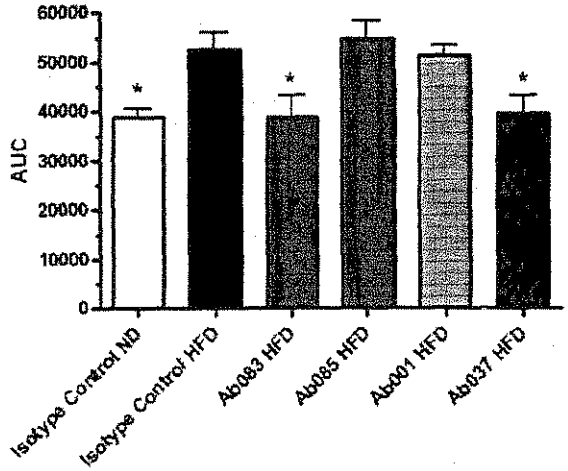

Plasma cholesterol
Cholesterol (mg/dL)
300
200
100
0
*
*
*
Isotype Control ND
Isotype Control HFD
Ab001 HFD
Ab037 HFD

Figure 15

A.



B.



C.

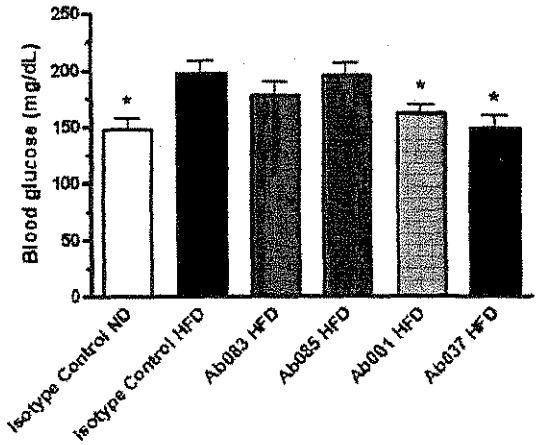
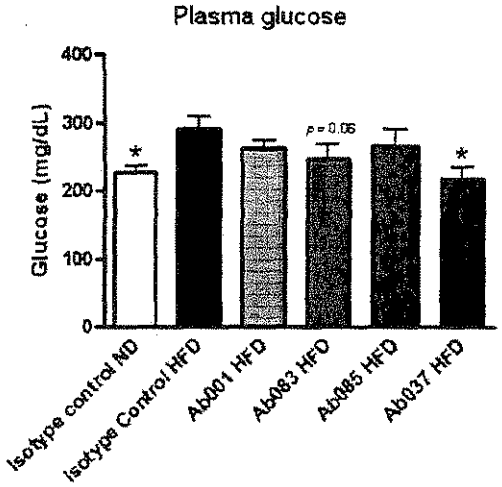
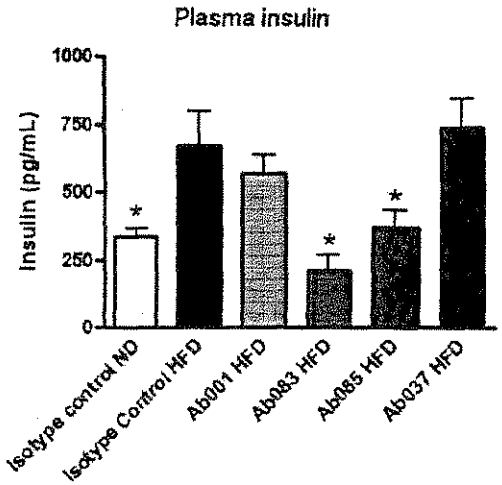


Figure 16

A.



B.



C.

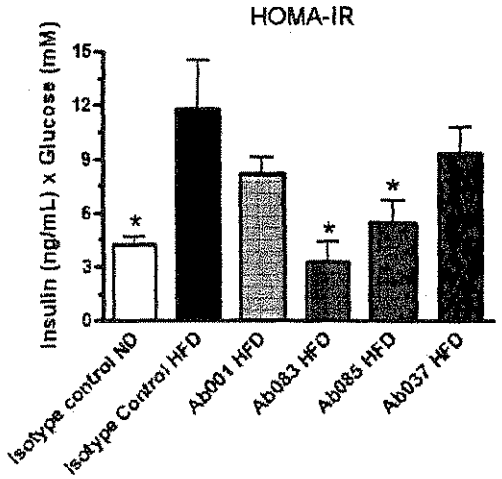
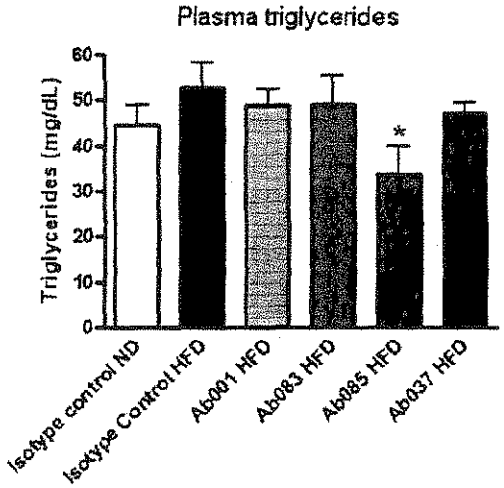
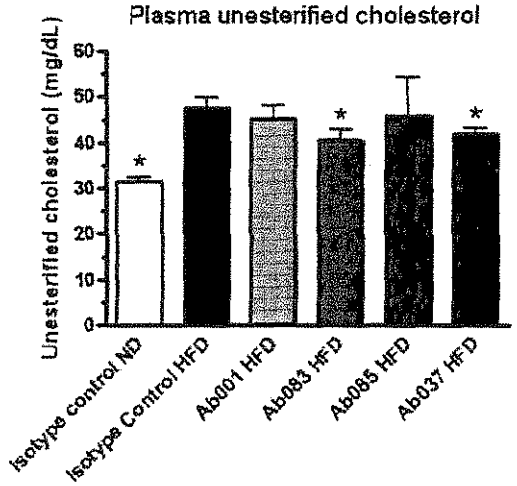


Figure 16 (Cont'd)

D.



E.



F.

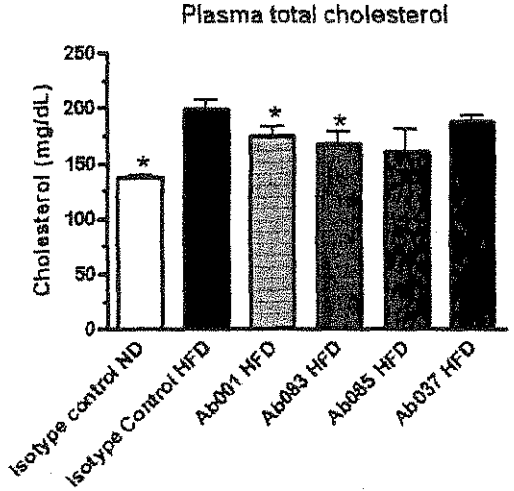
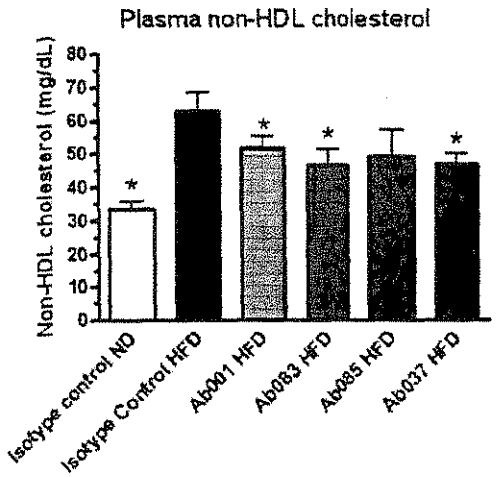


Figure 16 (Cont'd)

G.



H.

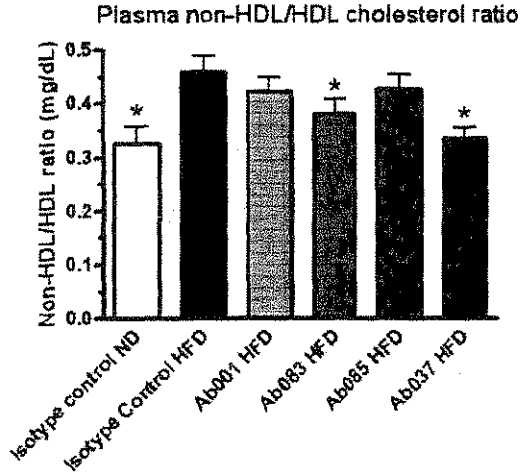
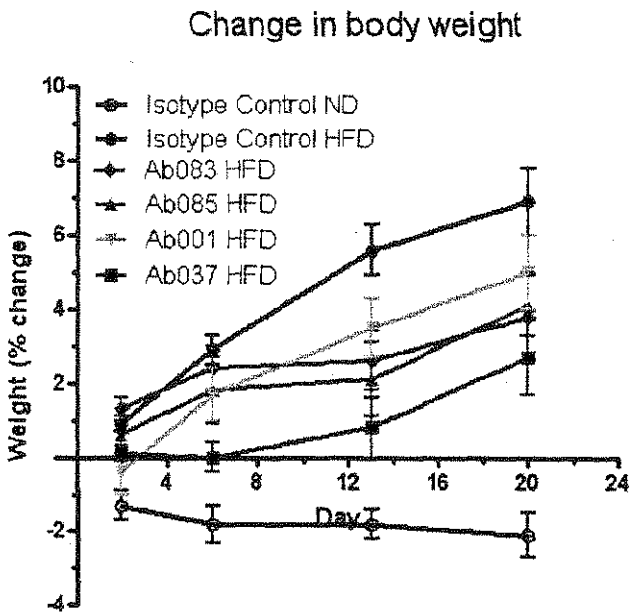


Figure 17

A.


Change in body weight
Isotype Control ND
Isotype Control HFD
Ab083 HFD
Ab085 HFD
Ab001 HFD
Ab037 HFD
Weight (% change)
Day
10
8
6
4
2
-2
-4
4
8
12
16
20
24

B.

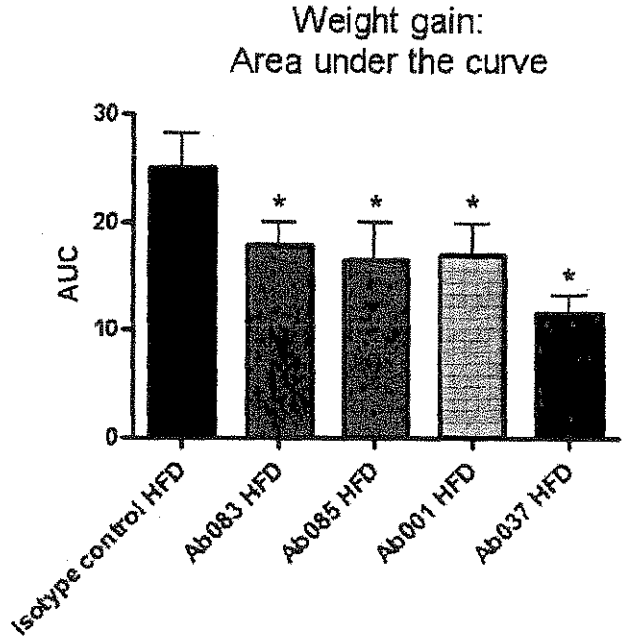
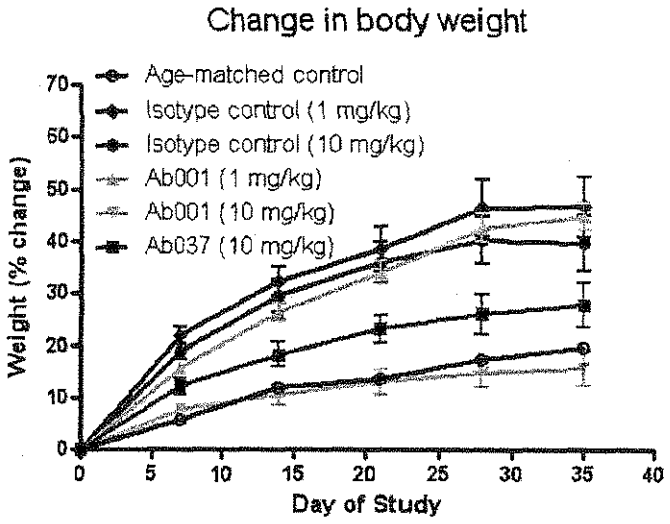

Weight gain:
Area under the curve
AUC
30
20
10
0
*
*
*
*
Isotype control HFD
Ab083 HFD
Ab085 HFD
Ab001 HFD
Ab037 HFD

Figure 18

A.


Change in body weight
Age-matched control
Isotype control (1 mg/kg)
Isotype control (10 mg/kg)
Ab001 (1 mg/kg)
Ab001 (10 mg/kg)
Ab037 (10 mg/kg)
Weight (% change)
Day of Study

B.

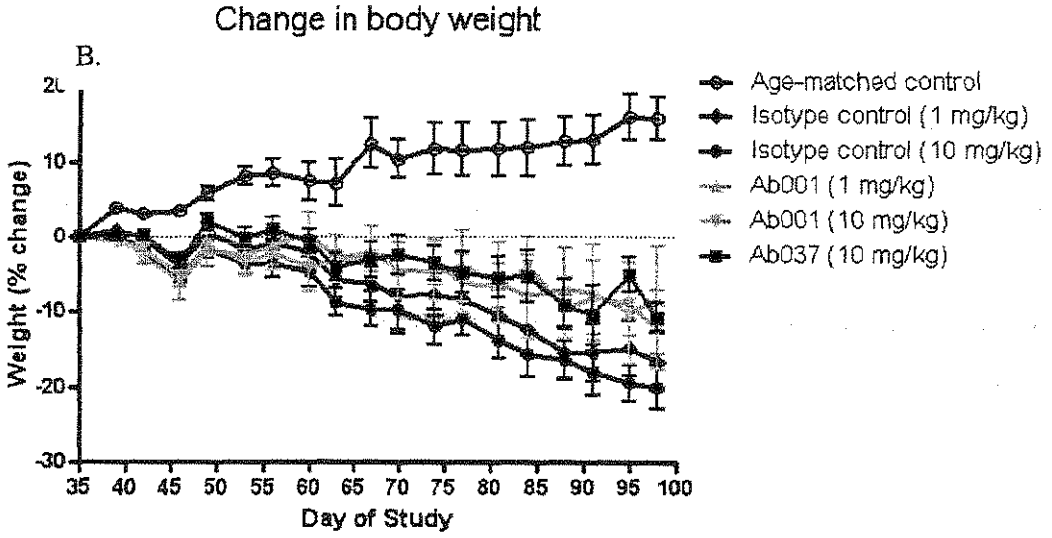
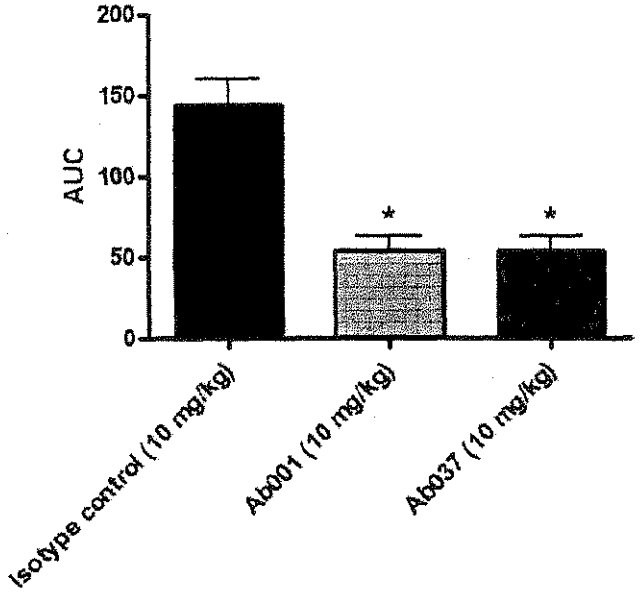

Change in body weight
Age-matched control
Isotype control (1 mg/kg)
Isotype control (10 mg/kg)
Ab001 (1 mg/kg)
Ab001 (10 mg/kg)
Ab037 (10 mg/kg)
Weight (% change)
Day of Study

Figure 18 (cont'd)

C. Weight gain: Area under the curve



D. Weight reduction: Area under the curve

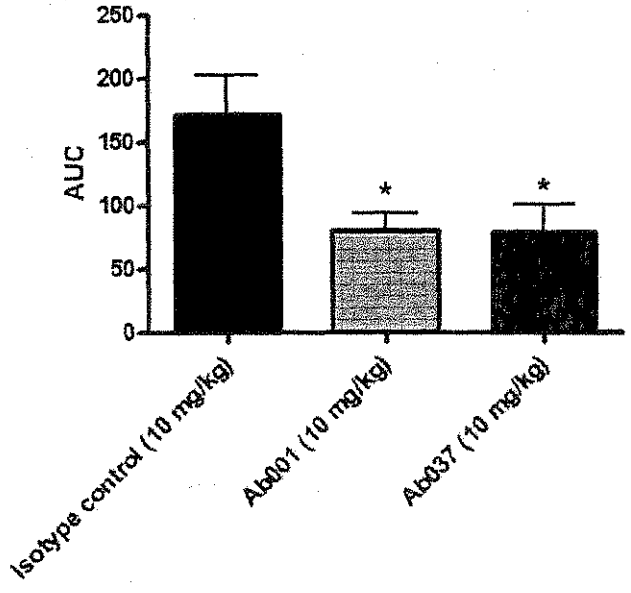
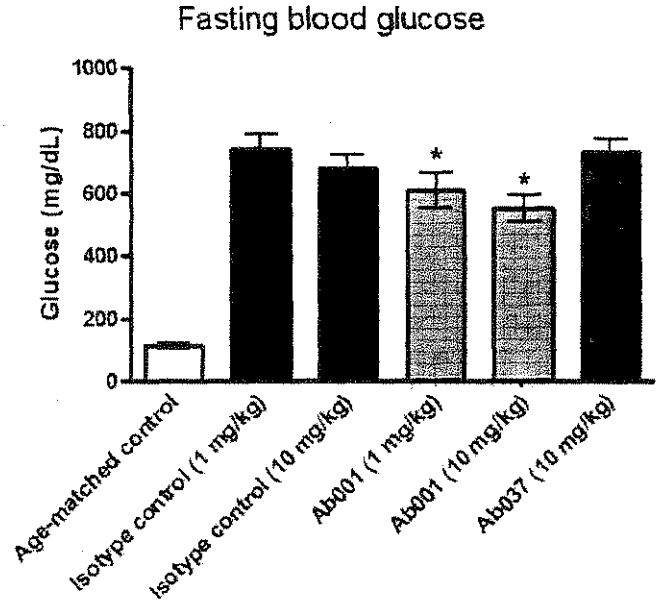


Figure 19

A.


Fasting blood glucose
Glucose (mg/dL)
1000
800
600
400
200
0
*
*
Age-matched control
Isotype control (1 mg/kg)
Isotype control (10 mg/kg)
Ab001 (1 mg/kg)
Ab001 (10 mg/kg)
Ab037 (10 mg/kg)

B.

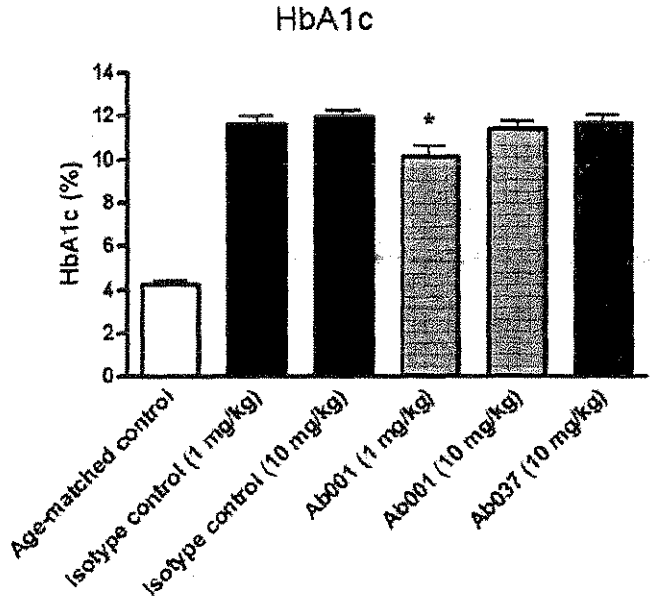
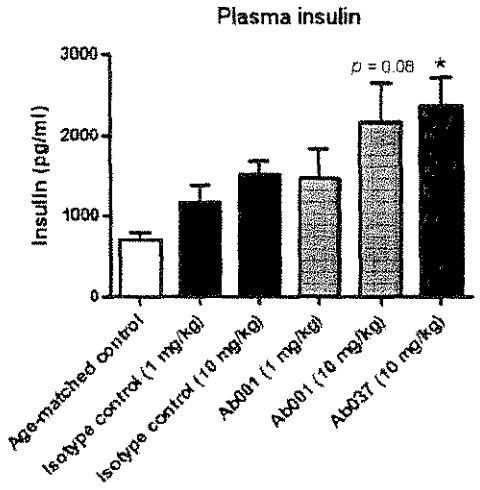
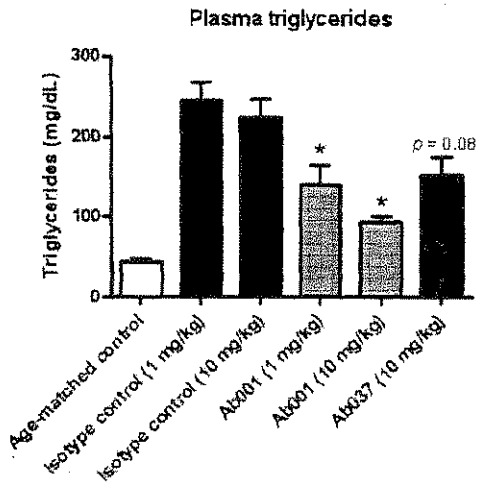

HbA1c
HbA1c (%)
14
12
10
8
6
4
2
0
*
Age-matched control
Isotype control (1 mg/kg)
Isotype control (10 mg/kg)
Ab001 (1 mg/kg)
Ab001 (10 mg/kg)
Ab037 (10 mg/kg)

Figure 20

A.



B.



C.

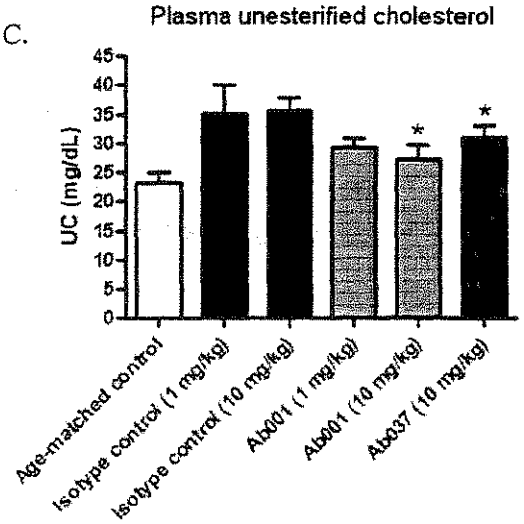
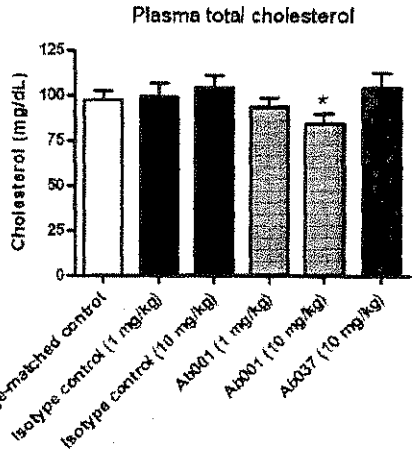
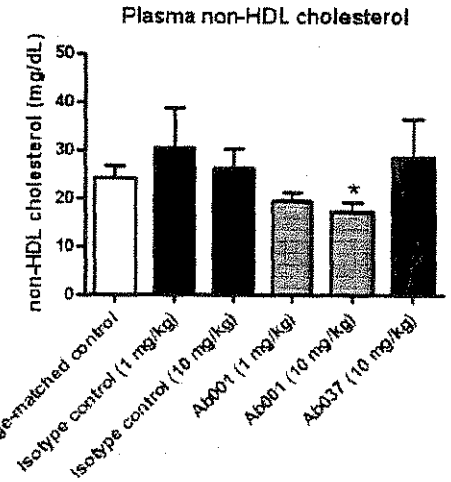


Figure 20 (Cont'd)

D.



E.



F.

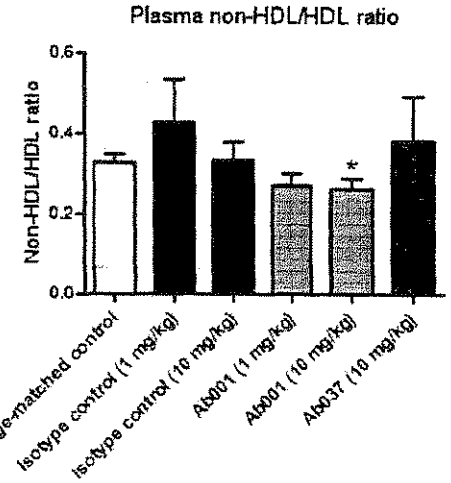


Figure 21

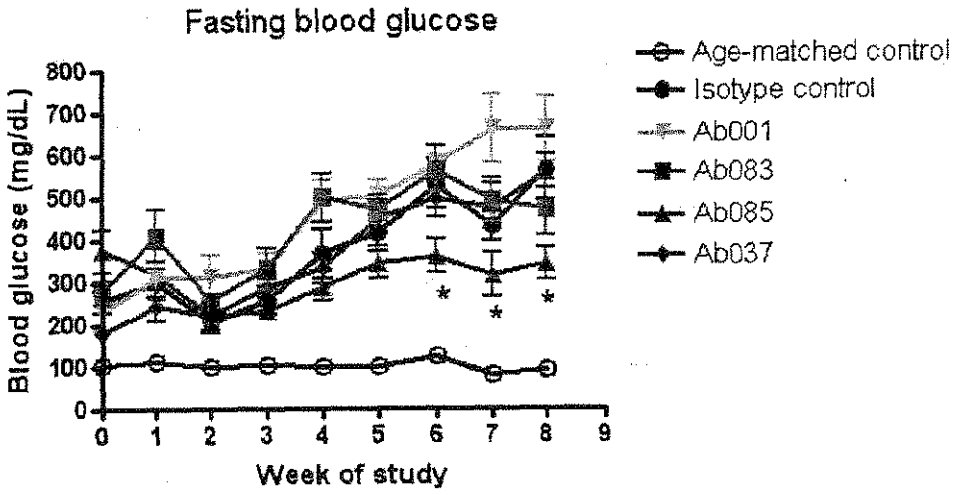


Figure 22

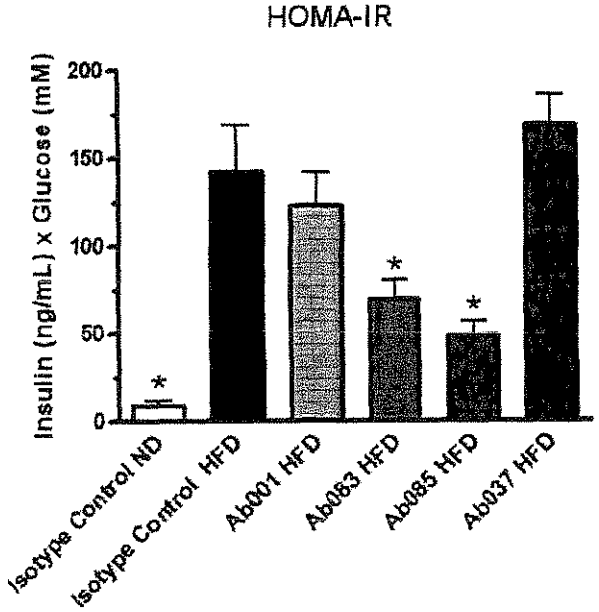
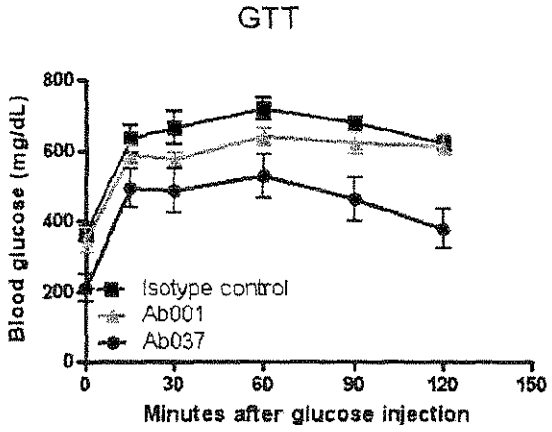
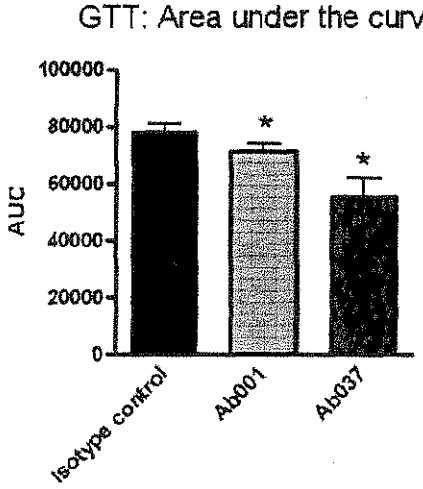


Figure 23

A.



B.



C.

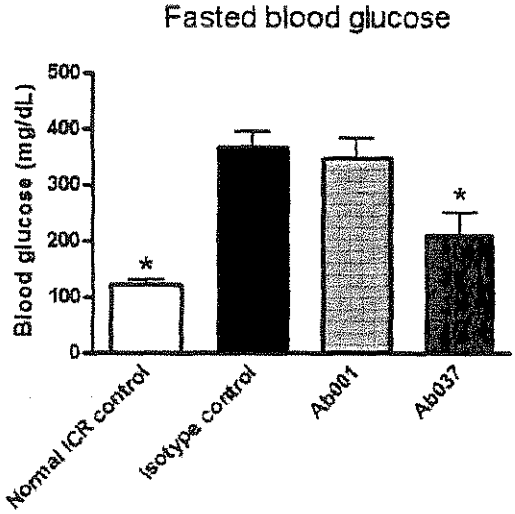
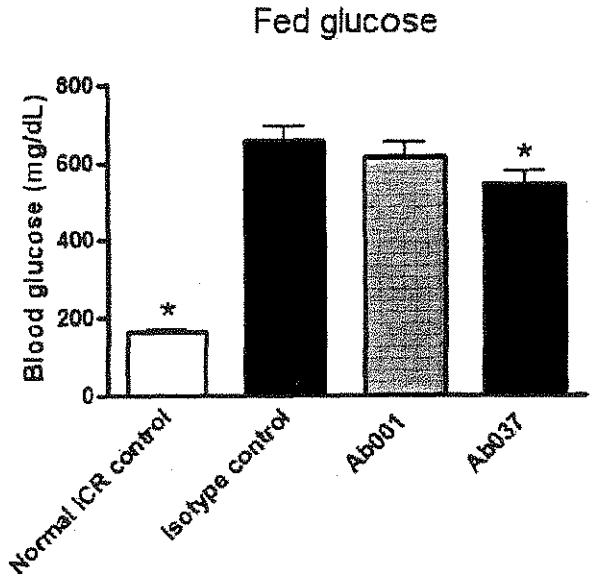


Figure 24

A.


Fed glucose
Blood glucose (mg/dL)
800
600
400
200
0
*
*
Normal ICR control
Isotype control
Ab001
Ab037

B.

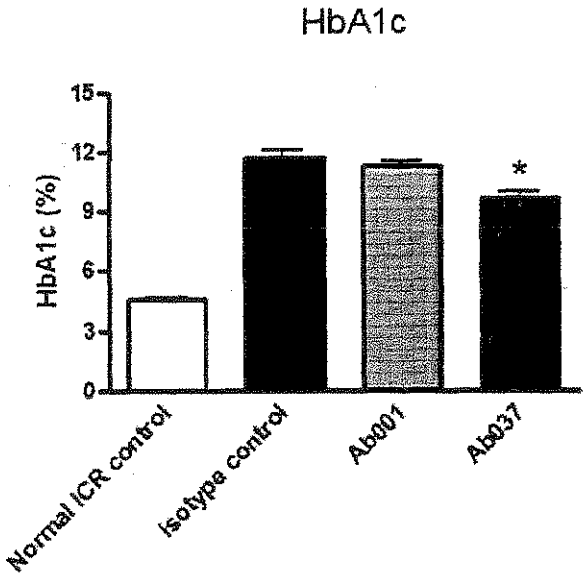
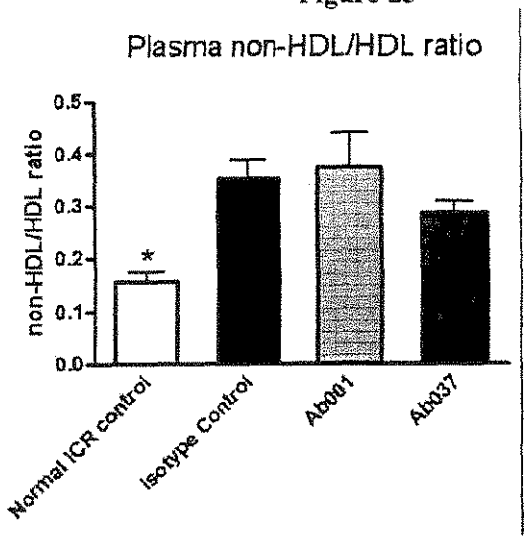
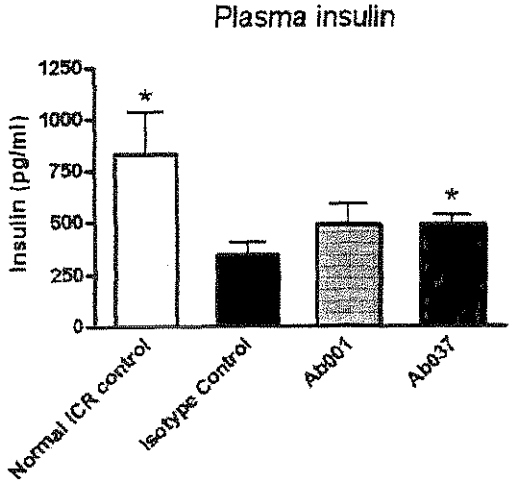

HbA1c
HbA1c (%)
15
12
9
6
3
0
*
Normal ICR control
Isotype control
Ab001
Ab037

Figure 25

A.



B.



C.

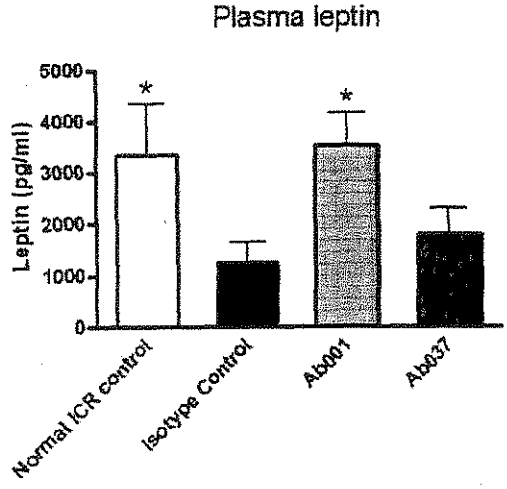
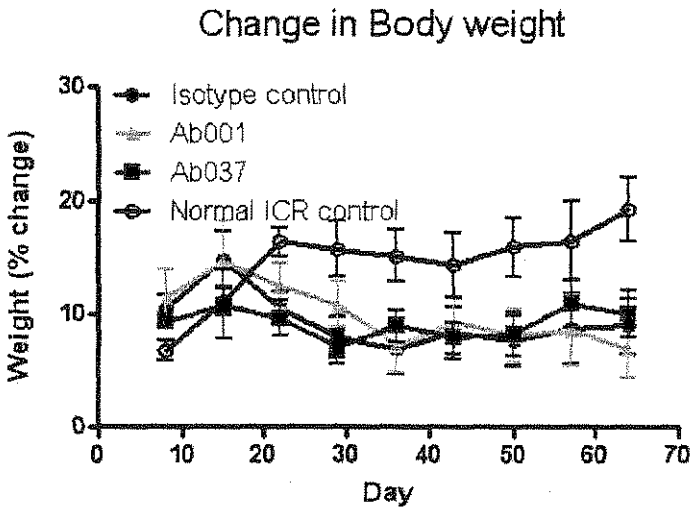
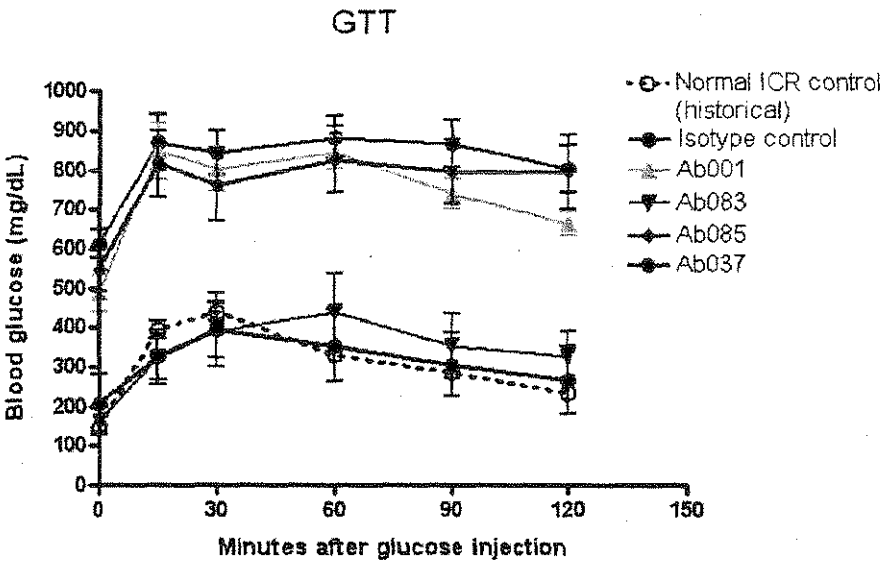


Figure 26


Change in Body weight
Isotype control
Ab001
Ab037
Normal ICR control
Weight (% change)
30
20
10
0
0
10
20
30
40
50
60
70
Day

A. ıre 27


GTT
Normal ICR control (historical)
Isotype control
Ab001
Ab083
Ab085
Ab037
Blood glucose (mg/dL)
1000
900
800
700
600
500
400
300
200
100
0
0
30
60
90
120
150
Minutes after glucose injection

B.

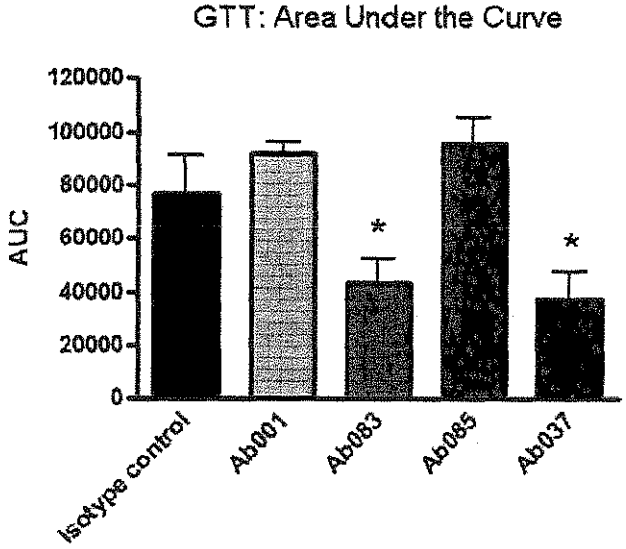

GTT: Area Under the Curve
AUC
120000
100000
80000
60000
40000
20000
0
*
*
Isotype control
Ab001
Ab083
Ab085
Ab037

Figure 28

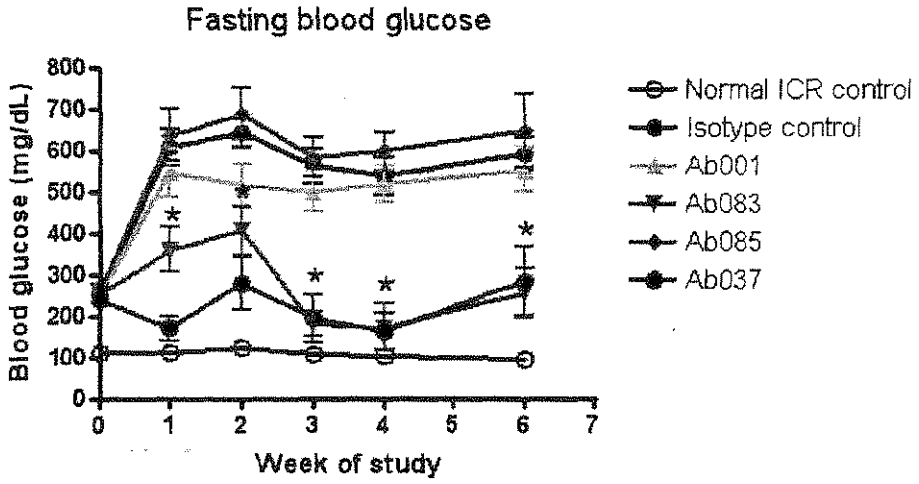
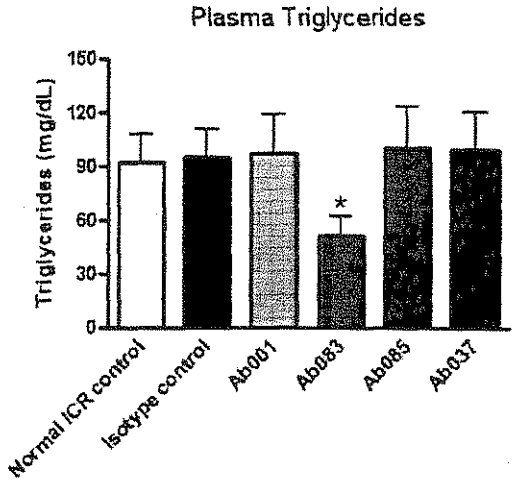
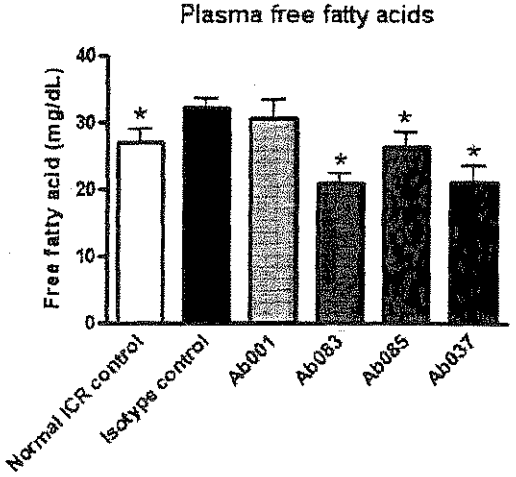

Fasting blood glucose
Blood glucose (mg/dL)
800
700
600
500
400
300
200
100
0
0
1
2
3
4
5
6
7
Week of study
Normal ICR control
Isotype control
Ab001
Ab083
Ab085
Ab037
*
*
*
*
*

Figure 29

A.



B.



C.

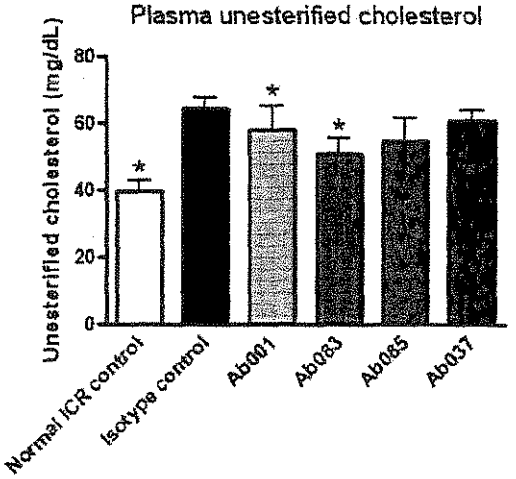
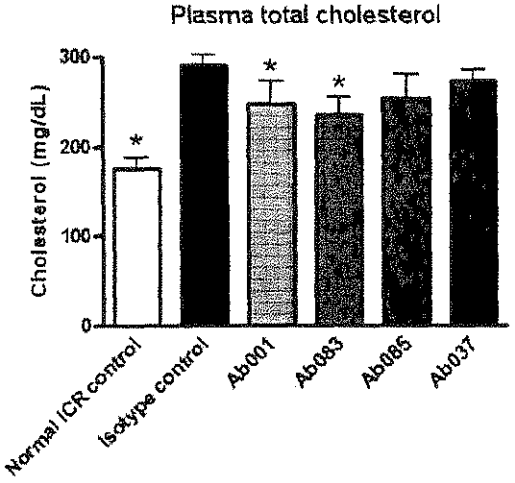
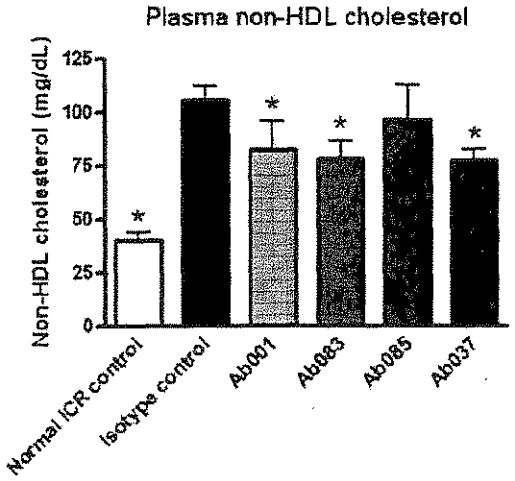


Figure 29 cont'd

D.



E.



F.

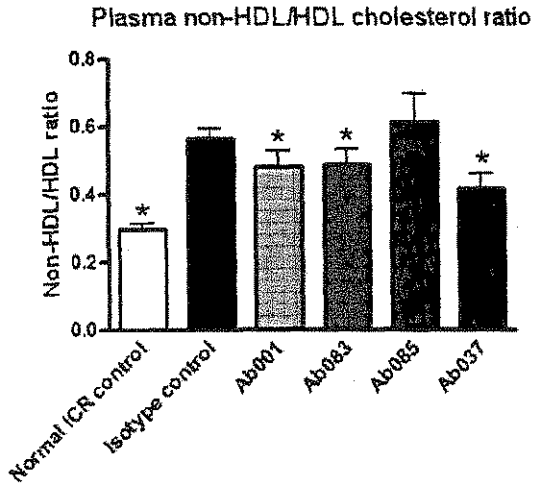


Figure 30

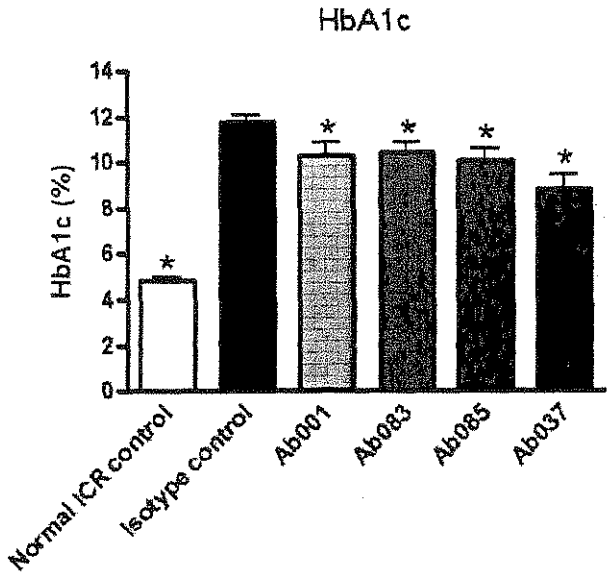


Figure 31

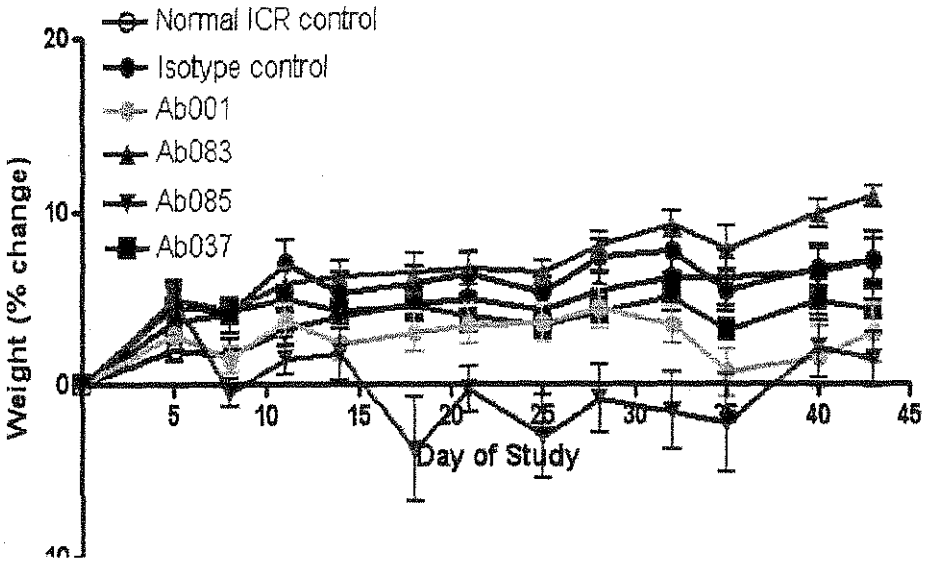
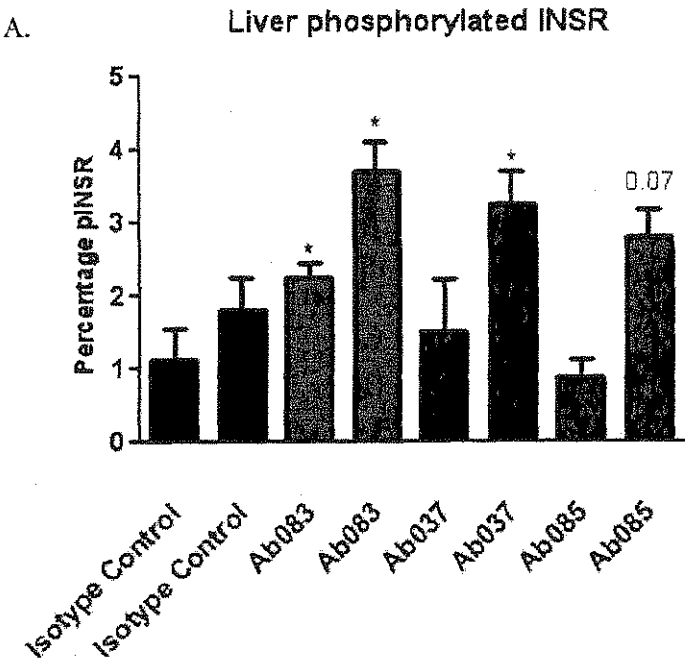


Figure 32

A.


Liver phosphorylated INSR
Percentage pINSR
0
1
2
3
4
5
0.07
Isotype Control
Isotype Control
Ab083
Ab083
Ab037
Ab037
Ab085
Ab085

B.

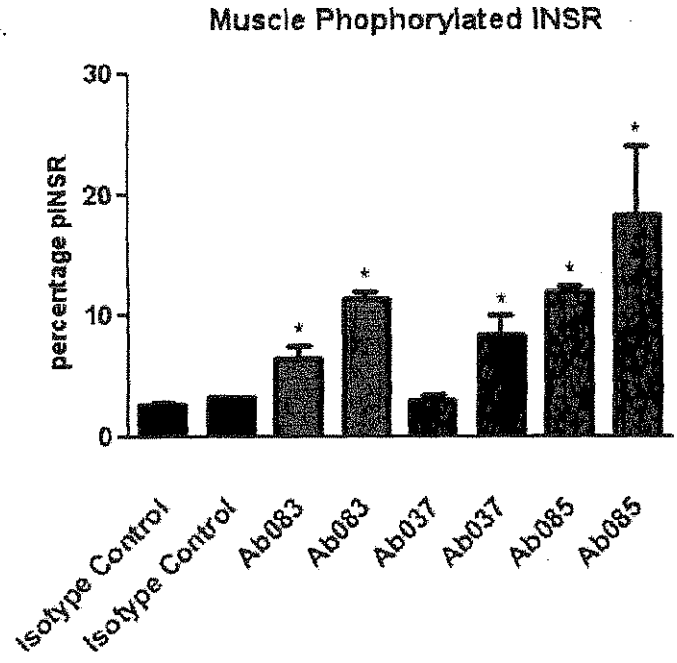

Muscle Phophorylated INSR
percentage pINSR
0
10
20
30
Isotype Control
Isotype Control
Ab083
Ab083
Ab037
Ab037
Ab085
Ab085

Figure 33

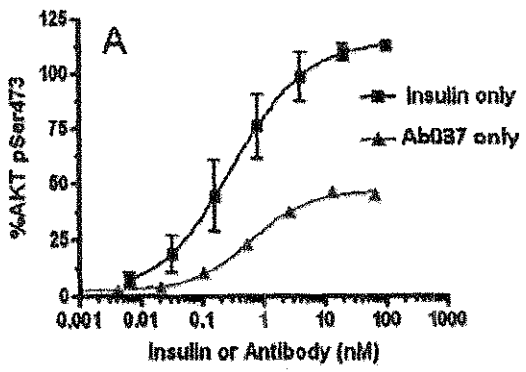
Antibody tested	*FACS area under log transformed data MFI of clones binding to INSR CHO-K1 cells following serum starvation*				*FACS area under log transformed data MFI ratio of clones binding to human INSR CHO-K1 with insulin and without insulin (+insulin/-insulin)*	
	human INSR, no insulin	*mouse INSR, no insulin*	*human INSR, with insulin*	*mouse INSR, with insulin*	*human INSR*	*mouse INSR*
Ab050	252	424	81	170	0.32	0.40
Ab051	554	663	378	470	0.68	0.71
Ab052	445	892	134	397	0.30	0.45
Ab053	1331	1131	451	574	0.34	0.51
Ab054	1128	1027	356	519	0.32	0.51
Ab055	1192	1300	759	1050	0.64	0.81
Ab056	1110	21	927	41	0.84	1.98
Ab057	155	409	87	250	0.56	0.61
Ab058	1407	812	370	388	0.26	0.48
Ab059	22	14	764	13	34.25	ND
Ab060	460	210	308	388	0.67	1.85
Ab061	204	462	59	170	0.29	0.37
Ab062	1398	1448	790.3	1009	0.57	0.70
Ab063	943	1025	674	733	0.71	0.72
Ab064	1710	1019	1271	813	0.74	0.80
Ab065	205	483	57	177	0.28	0.37
Ab066	1564	1516	1157	1145	0.74	0.76
Ab067	1537	1281	1063	786	0.69	0.61
Ab068	1422	803	1028	445	0.72	0.55
Ab069	357	642	146	383	0.41	0.60

Antibody tested	*FACS area under log transformed data MFI of clones binding to INSR CHO-K1 cells following serum starvation*				*FACS area under log transformed data MFI ratio of clones binding to human INSR CHO-K1 with insulin and without insulin (+insulin/-insulin)*	
	human INSR, no insulin	*mouse INSR, no insulin*	*human INSR, with insulin*	*mouse INSR, with insulin*	*human INSR*	*mouse INSR*
Ab070	283	587	150	389	0.53	0.66
Ab071	490	818	194	518	0.40	0.63
Ab072	226	508	84	267	0.37	0.53
Ab073	729	307	341	321	0.47	1.05
Ab074	596	932	260	503	0.44	0.54
Ab075	692	425	353	446	0.51	1.05
Ab076	552	268	543	391	0.98	1.46
Ab077	127	45	268	103	2.12	2.28
Ab078	11	12	704	217	66	17.6
Ab079	296	154	385	215	1.30	1.39
Ab080	282	157	386	191	1.37	1.22
Ab081	176	189	75	125	0.42	0.66
Ab082	399	257	236	267	0.59	1.04
Ab083	97	81	294	179	3.03	2.21
Ab084	532	196	508	344	0.95	1.75
Ab001+anti-human IgG APC p1	294	34	565	127	1.92	3.68
Ab001+anti-human IgG APC p2	687	443	1017	1062	1.48	2.40
Ab001+anti-human IgG APC p3						
Ab001+anti-human IgG APC p5	534	176	1006	485	1.89	2.76
Ab001+anti-human IgG APC p6 cropped	693	232	1030	518	1.49	2.24

Figure 33 (cont'd)

ND = not determine

Figure 34



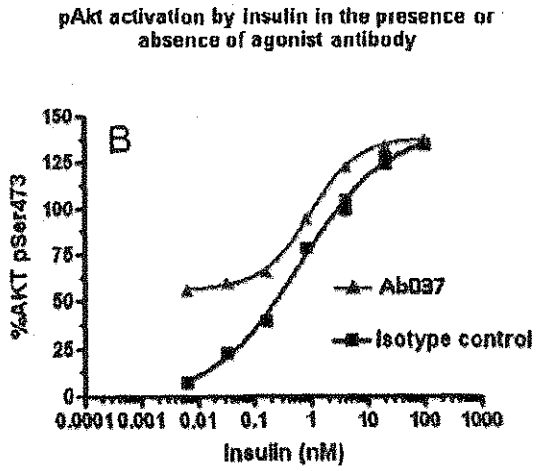
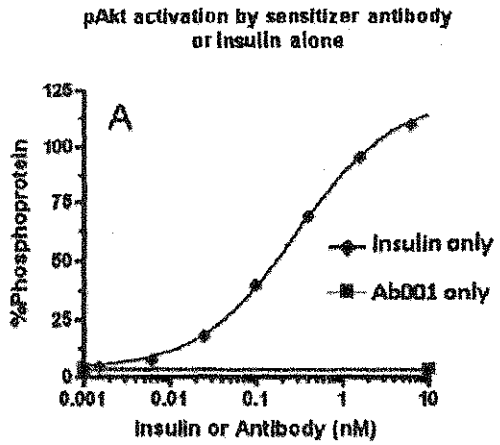


Figure 35



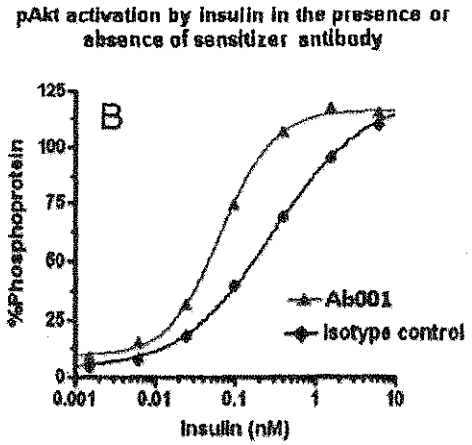


Figure 36

Engineered insulin receptor cell line used in the assay	*Assay parameter determined from sigmoidal dose-response curve fit*	*Human Insulin*	*Ab037*	*Ab030*	*Ab040*	*Ab018*
Human INSR CHO-K1	*Relative maximum activation of pAkt by insulin or antibody alone*	100%	44%	47%	19%	36%
	EC_{50} (nM) of insulin or antibody alone	0.6	0.8	12	4	1
	Hill coefficient of insulin or antibody alone	0.8	0.9	1.8	1.4	1.4
Mouse INSR CHO-K1	*Relative maximum activation of pAkt by insulin or antibody alone*	100%	29%	37%	25%	26%
	EC_{50} (nM) of insulin or antibody alone	3.4	1.4	11	4	3
	Hill coefficient of insulin or antibody alone	0.7	1	1.7	1.3	1

Figure 37

Engineered insulin receptor cell line used in the assay	*Assay parameter determined from sigmoidal dose-response curve fit*	*Assay 1*		*Assay 2*	
		Hu Insulin with 10 ug/ml control antibody	***Hu Insulin with 10 ug/ml Ab037***	***Hu Insulin with 10 ug/ml control antibody***	***Hu Insulin with 10 ug/ml Ab040***
Human INSR CHO-K1	Relative maximum activation of pAkt in the presence of 10 ug/ml antibody	100 ± 5%	93 ± 2%	100 ± 3%	85 ± 1%
	EC50 of insulin in the presence of 10 ug/ml antibody (nM)	0.7 ± 0.3	1 ± 0.3	0.8 ± 0.2	0.3 ± 0.1
Mouse INSR CHO-K1	Relative maximum activation of pAkt in the presence of 10 ug/ml antibody	100 ± 2%	99 ± 1%	100 ± 3%	98 ± 1%
	EC50 of insulin in the presence of 10 ug/ml antibody (nM)	3.3 ± 0.6	2.1 ± 0.4	3 ± 1	0.6 ± 0.2

Figure 38

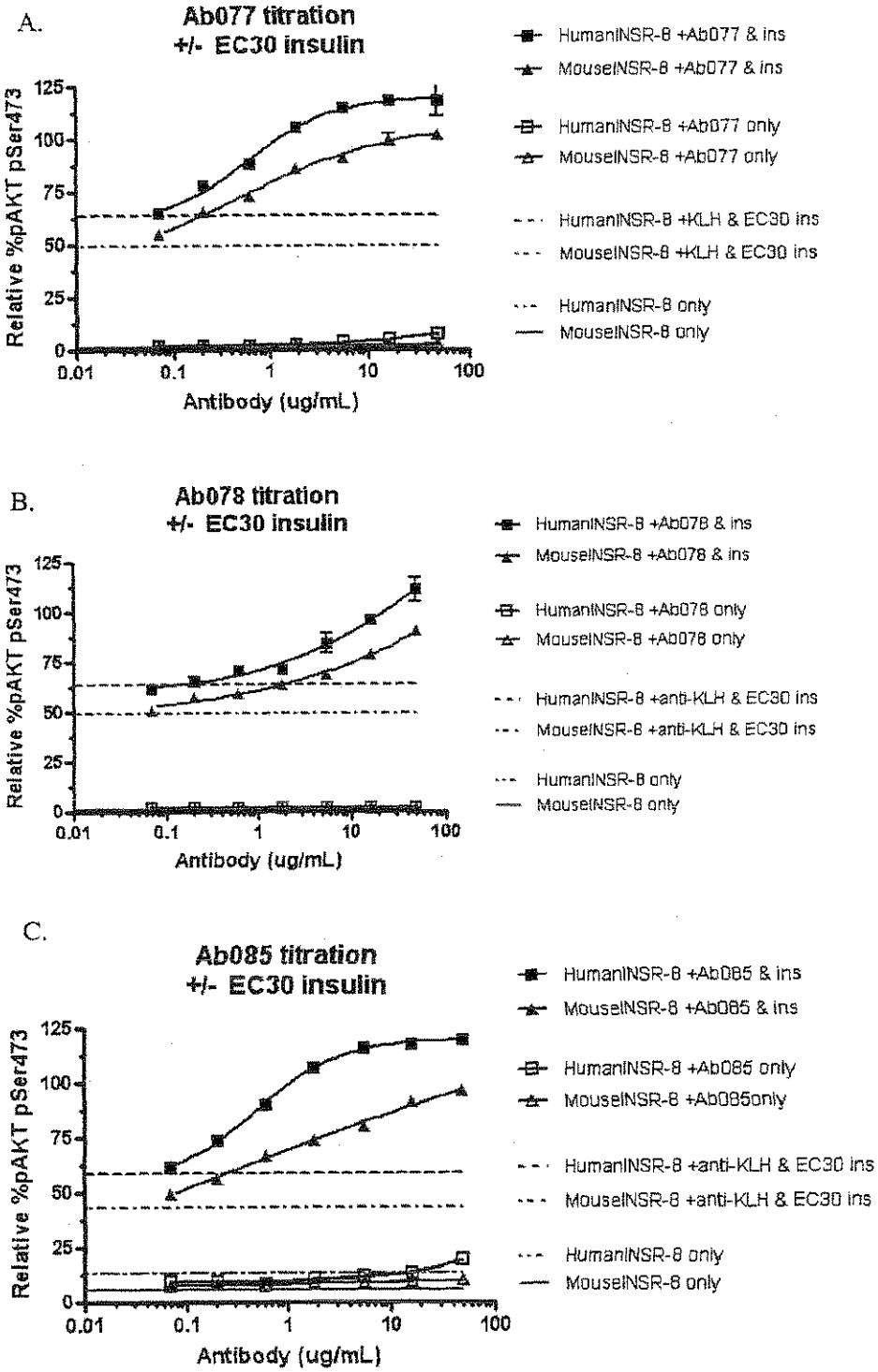
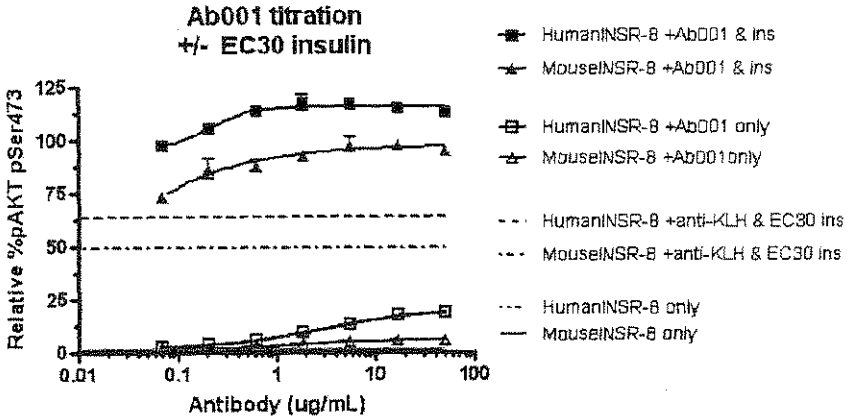
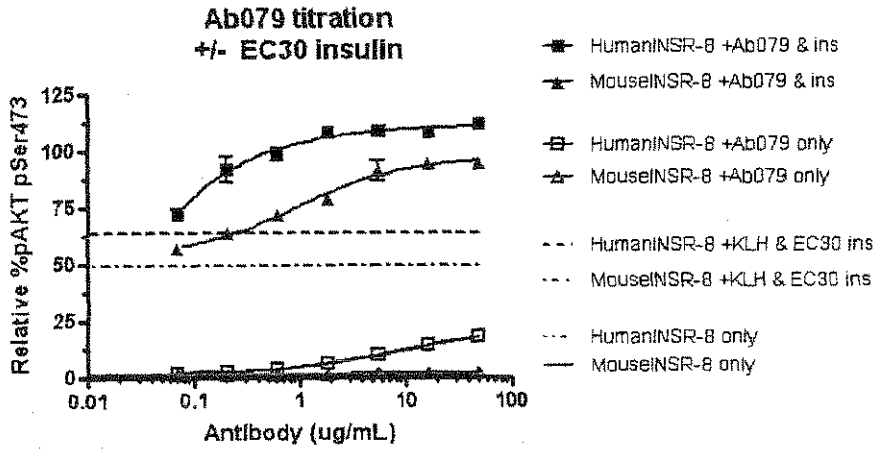

A.
Ab077 titration
+/- EC30 insulin
Relative %pAKT pSer473
Antibody (ug/mL)
HumaniNSR-8 +Ab077 & ins
MouseINSR-8 +Ab077 & ins
HumaniNSR-8 +Ab077 only
MouseINSR-8 +Ab077 only
HumaniNSR-8 +KLH & EC30 ins
MouseINSR-8 +KLH & EC30 ins
HumaniNSR-8 only
MouseINSR-8 only
B.
Ab078 titration
+/- EC30 insulin
Relative %pAKT pSer473
Antibody (ug/mL)
HumaniNSR-8 +Ab078 & ins
MouseINSR-8 +Ab078 & ins
HumaniNSR-8 +Ab078 only
MouseINSR-8 +Ab078 only
HumaniNSR-8 +anti-KLH & EC30 ins
MouseINSR-8 +anti-KLH & EC30 ins
HumaniNSR-8 only
MouseINSR-8 only
C.
Ab085 titration
+/- EC30 insulin
Relative %pAKT pSer473
Antibody (ug/mL)
HumaniNSR-8 +Ab085 & ins
MouseINSR-8 +Ab085 & ins
HumaniNSR-8 +Ab085 only
MouseINSR-8 +Ab085only
HumaniNSR-8 +anti-KLH & EC30 ins
MouseINSR-8 +anti-KLH & EC30 ins
HumaniNSR-8 only
MouseINSR-8 only

Figure 39

A.



B.



C.

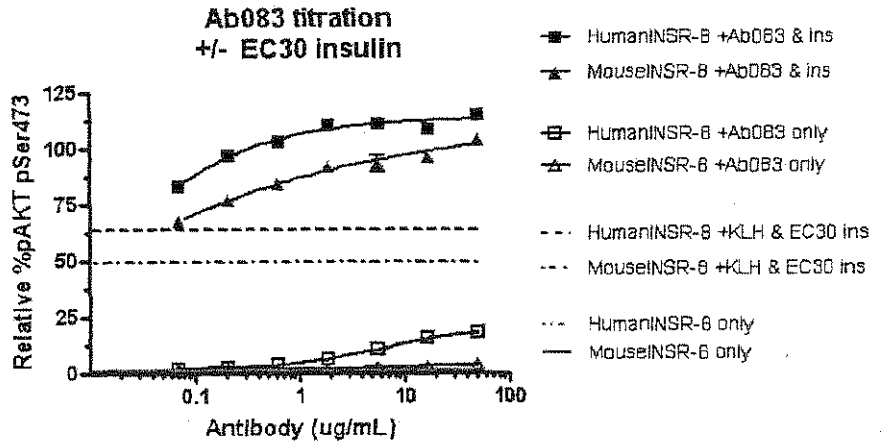


Figure 40

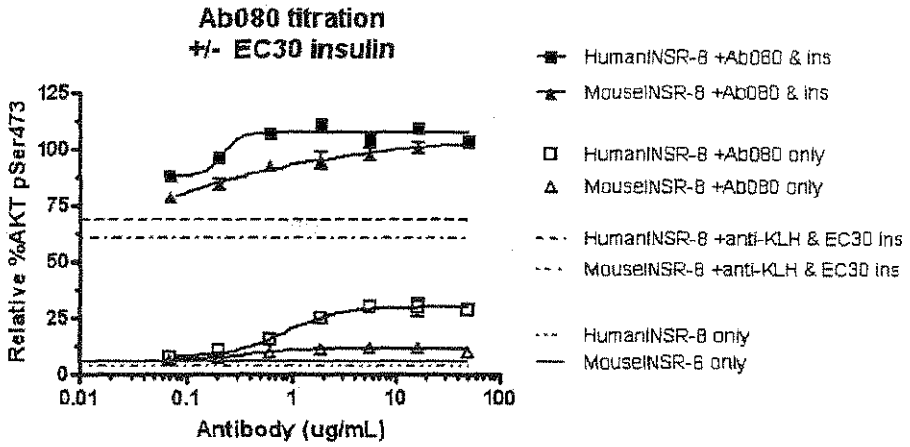

Ab080 titration
+/- EC30 insulin
Relative %AKT pSer473
125
100
75
50
25
0
0.01
0.1
1
10
100
Antibody (ug/mL)
HumanINSR-8 +Ab080 & ins
MouseINSR-8 +Ab080 & ins
HumanINSR-8 +Ab080 only
MouseINSR-8 +Ab080 only
HumanINSR-8 +anti-KLH & EC30 ins
MouseINSR-8 +anti-KLH & EC30 ins
HumanINSR-8 only
MouseINSR-8 only

Figure 41

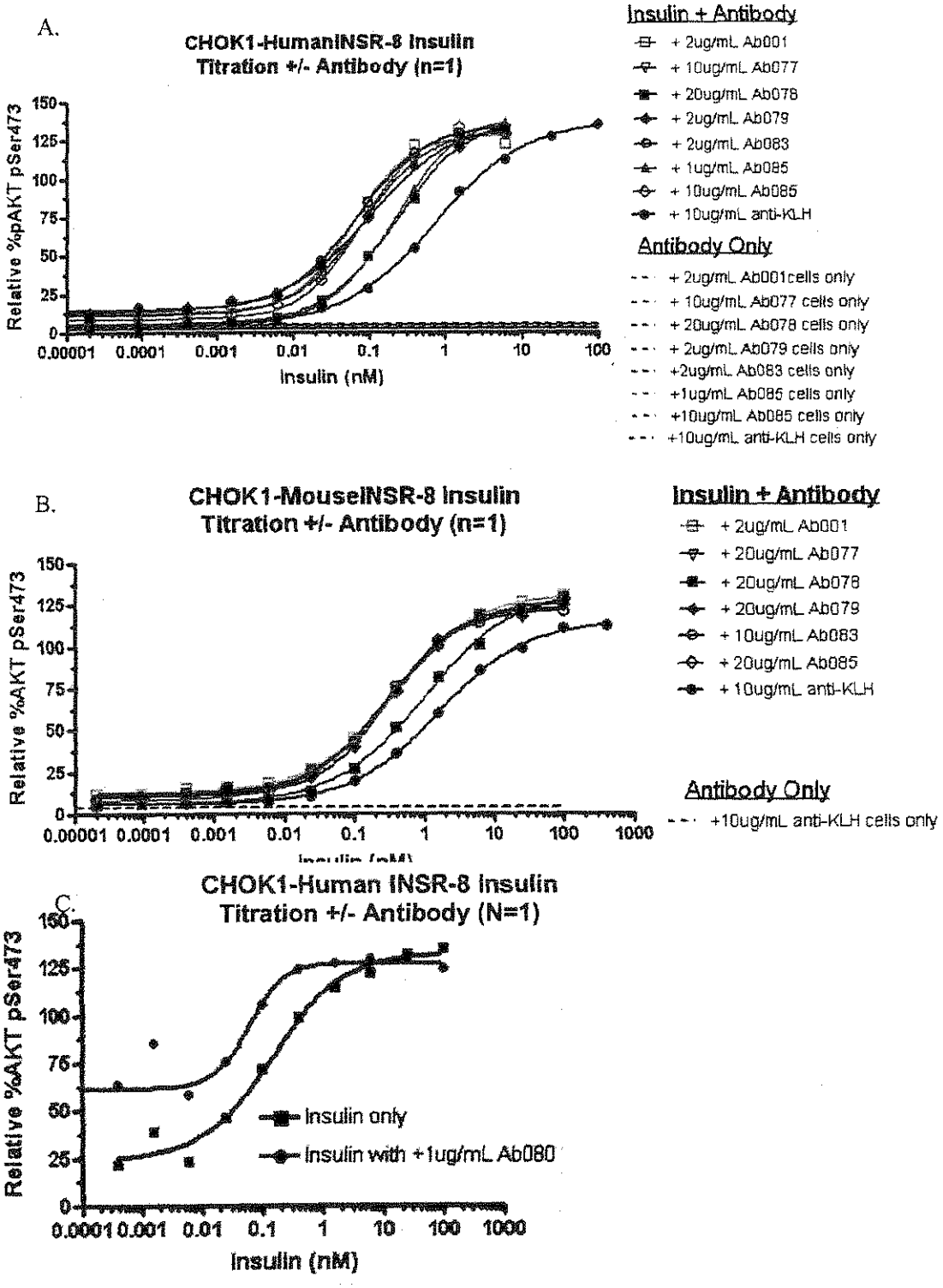
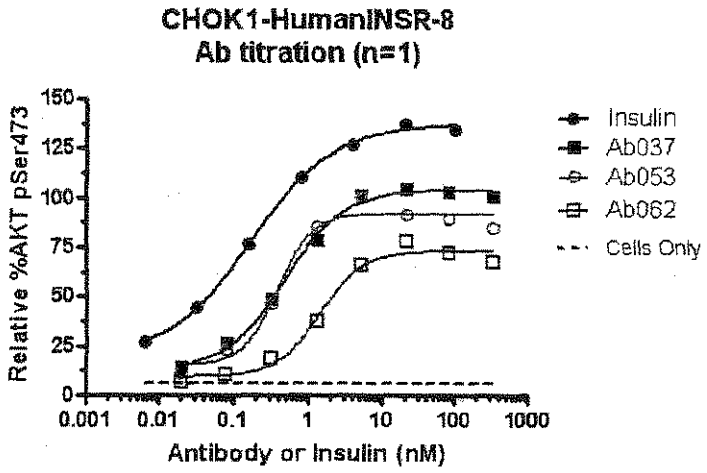

A.
CHOK1-HumanINSR-8 Insulin Titration +/- Antibody (n=1)
Relative %pAKT pSer473
Insulin (nM)
Insulin + Antibody
+ 2ug/mL Ab001
+ 10ug/mL Ab077
+ 20ug/mL Ab078
+ 2ug/mL Ab079
+ 2ug/mL Ab083
+ 1ug/mL Ab085
+ 10ug/mL Ab085
+ 10ug/mL anti-KLH
Antibody Only
+ 2ug/mL Ab001cells only
+ 10ug/mL Ab077 cells only
+ 20ug/mL Ab078 cells only
+ 2ug/mL Ab079 cells only
+2ug/mL Ab083 cells only
+1ug/mL Ab085 cells only
+10ug/mL Ab085 cells only
+10ug/mL anti-KLH cells only
B.
CHOK1-MouseINSR-8 Insulin Titration +/- Antibody (n=1)
Relative %AKT pSer473
Insulin + Antibody
+ 2ug/mL Ab001
+ 20ug/mL Ab077
+ 20ug/mL Ab078
+ 20ug/mL Ab079
+ 10ug/mL Ab083
+ 20ug/mL Ab085
+ 10ug/mL anti-KLH
Antibody Only
+10ug/mL anti-KLH cells only
C.
CHOK1-Human INSR-8 Insulin Titration +/- Antibody (N=1)
Relative %AKT pSer473
Insulin only
Insulin with +1ug/mL Ab080
Insulin (nM)

Figure 42

A..



B..

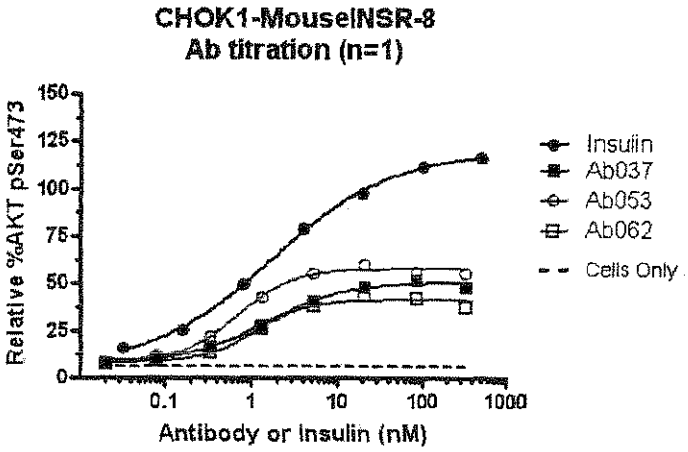


Figure 43

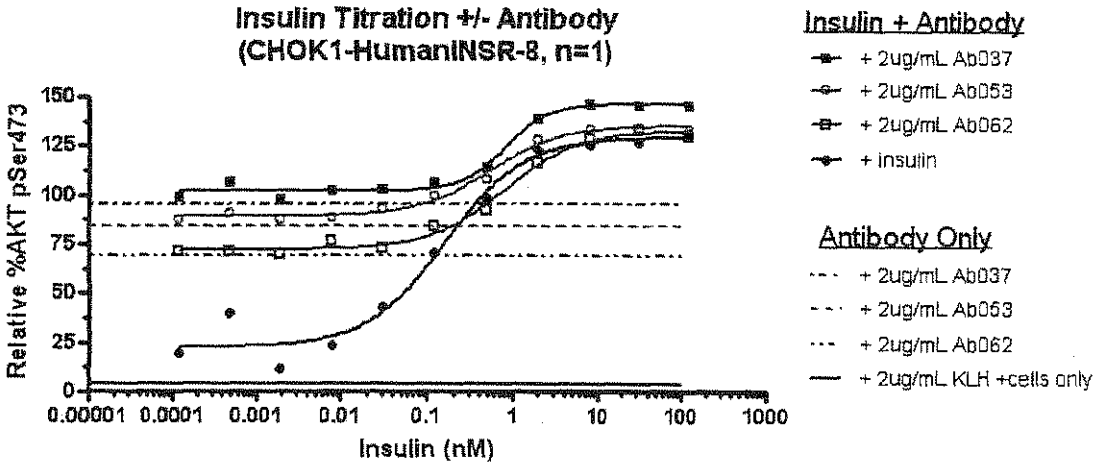
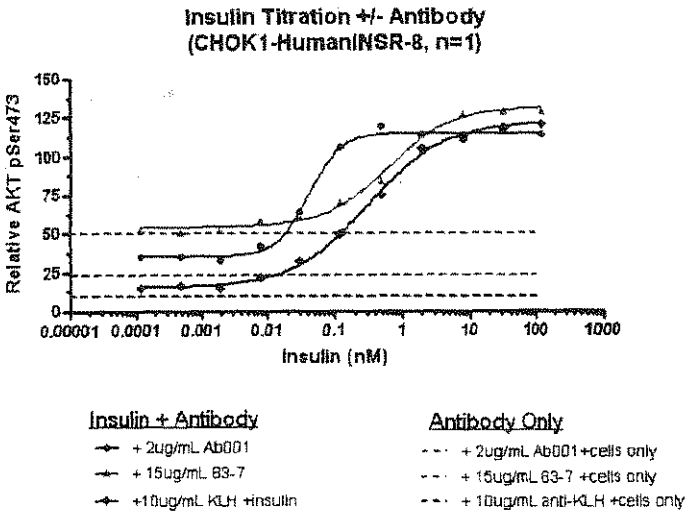


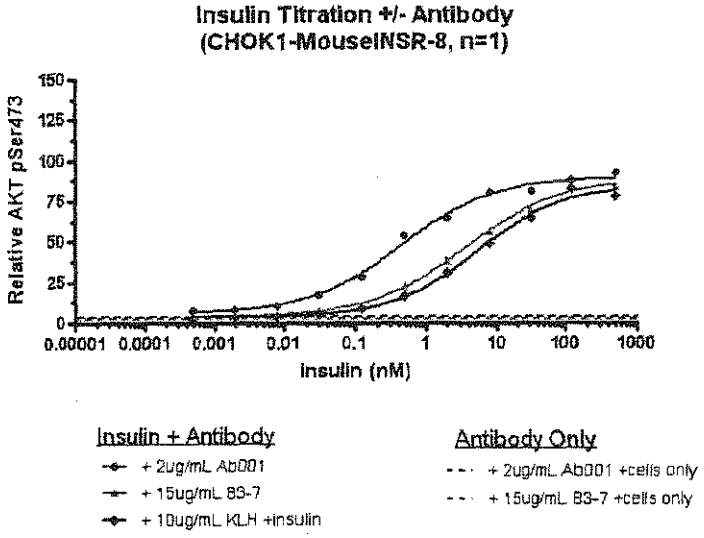
Figure 44

A.



	+2ug/mL Ab001	+15ug/mL 83-7	+2ug/mL anti-KLH
EC50	0.04093	0.6235	0.3129
EC50 (95% Confidence Interval)	0.03330 to 0.05030	0.4215 to 0.9225	0.2483 to 0.3942

B.



	+2ug/mL Ab001	+15ug/mL 83-7	+10ug/mL anti-KLH
EC50	0.4418	3.622	5.293
EC50(95% Confidence Interval)	0.2741 to 0.7121	2.681 to 4.893	3.294 to 8.505

Figure 45

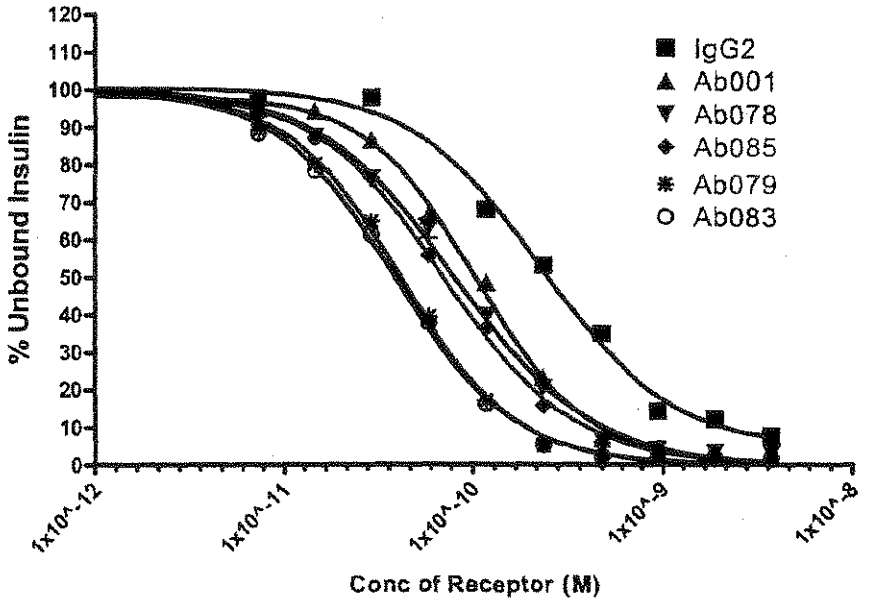


Figure 46

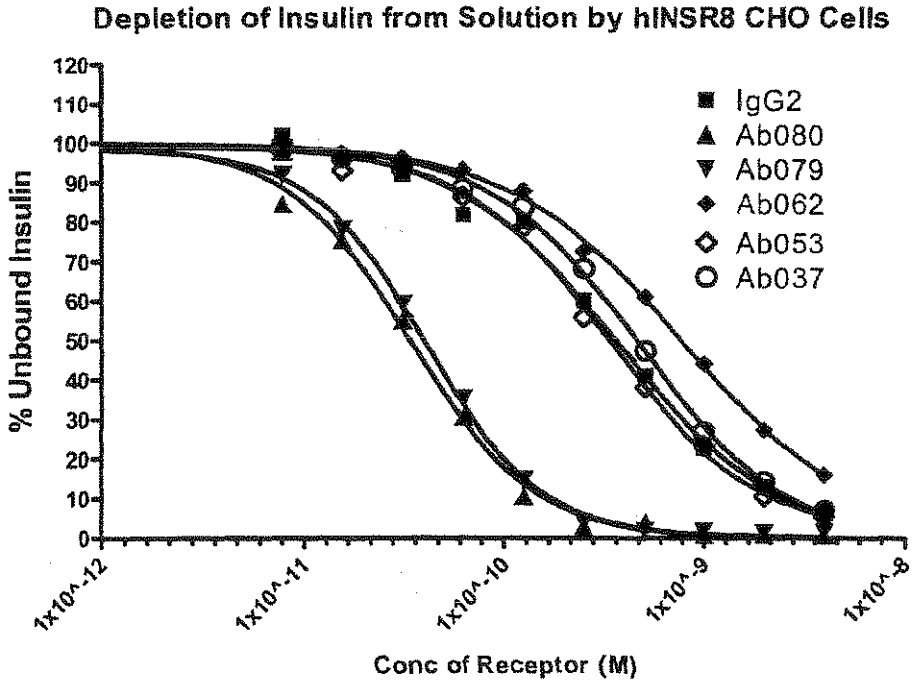


Figure 47

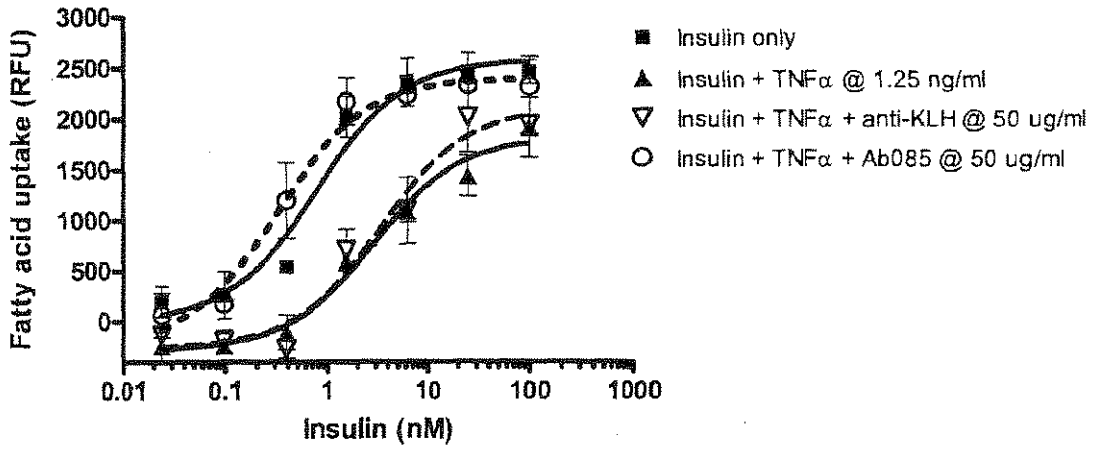

Fatty acid uptake (RFU)
3000
2500
2000
1500
1000
500
0
0.01
0.1
1
10
100
1000
Insulin (nM)
Insulin only
Insulin + TNFα @ 1.25 ng/ml
Insulin + TNFα + anti-KLH @ 50 ug/ml
Insulin + TNFα + Ab085 @ 50 ug/ml

Figure 48

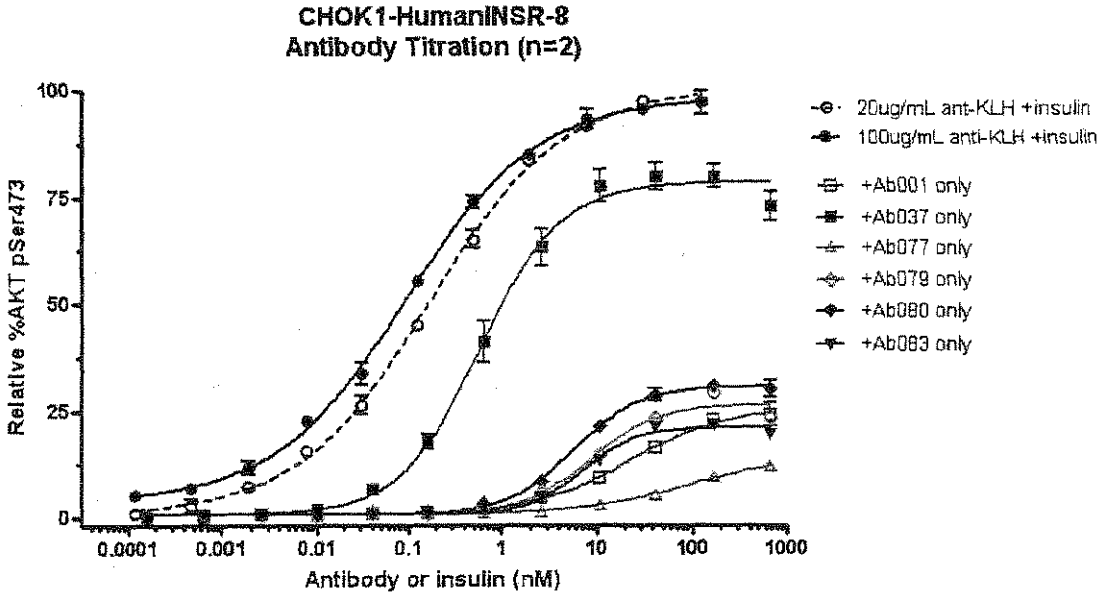

CHOK1-HumanINSR-8
Antibody Titration (n=2)
Relative %AKT pSer473
100
75
50
25
0
0.0001
0.001
0.01
0.1
1
10
100
1000
Antibody or insulin (nM)
20ug/mL anti-KLH +insulin
100ug/mL anti-KLH +insulin
+Ab001 only
+Ab037 only
+Ab077 only
+Ab079 only
+Ab080 only
+Ab083 only

Figure 49

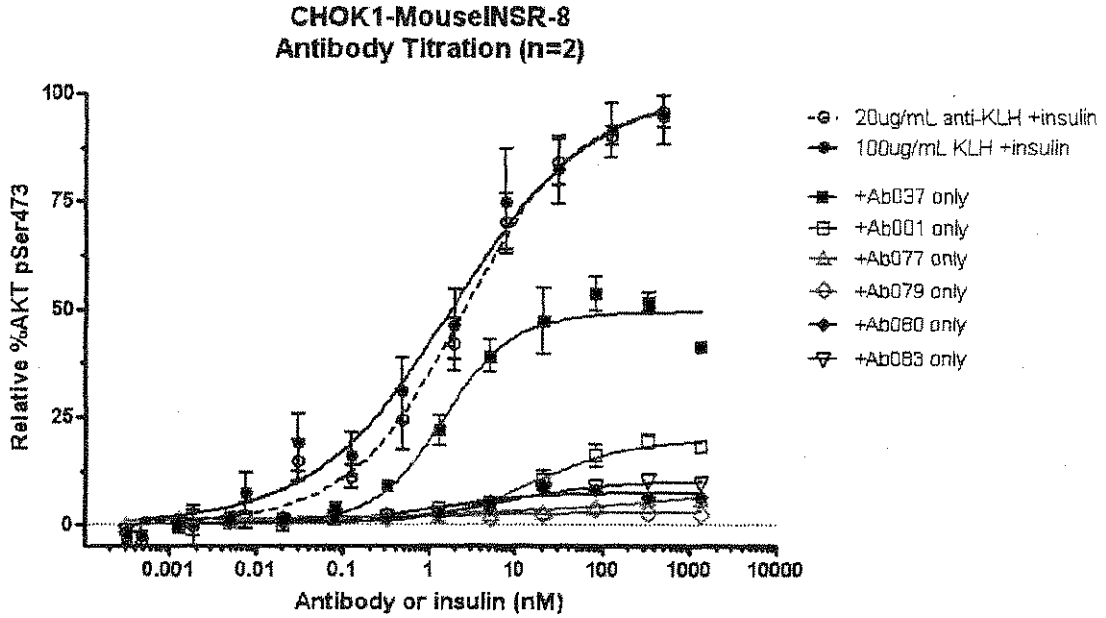


Figure 50

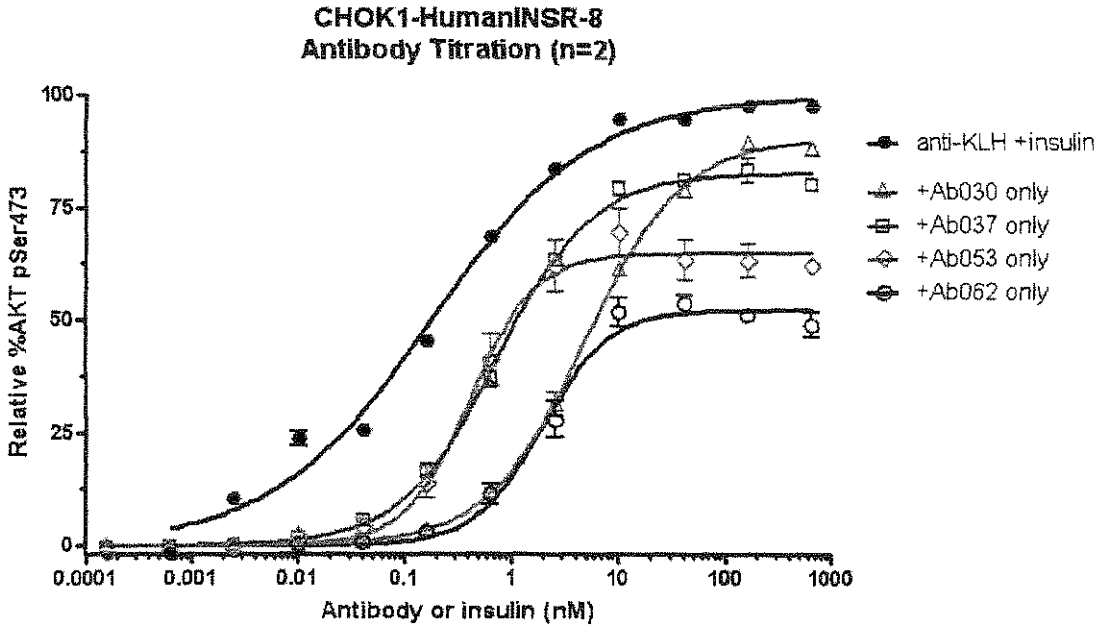


Figure 51

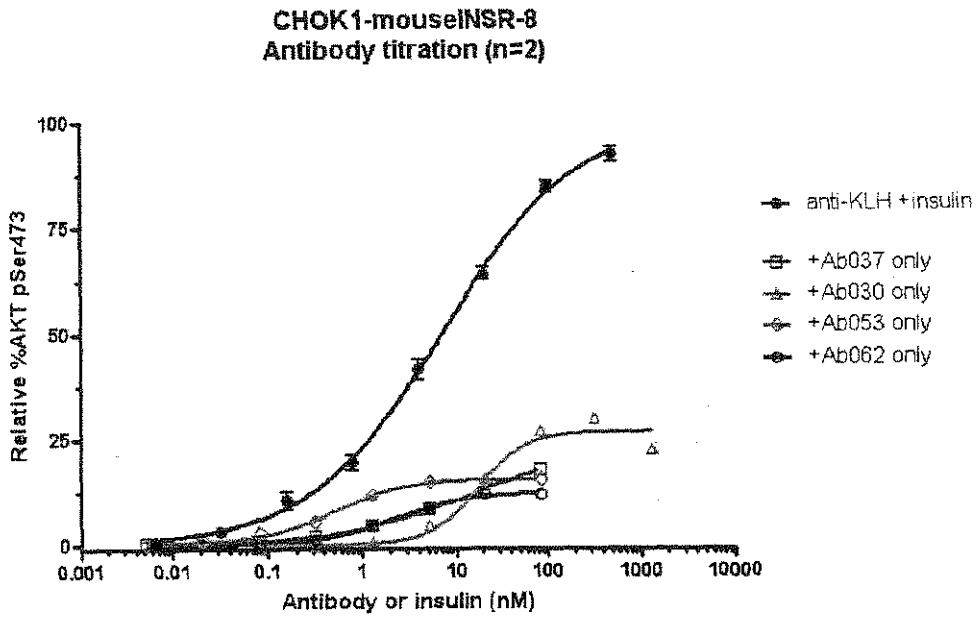


Figure 52

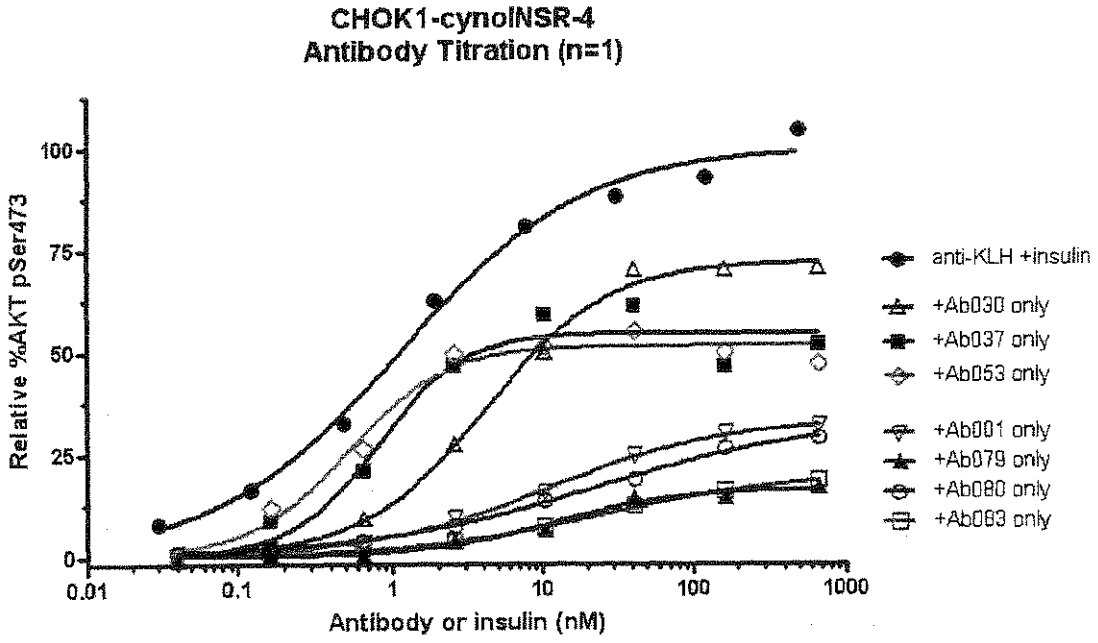


Figure 53

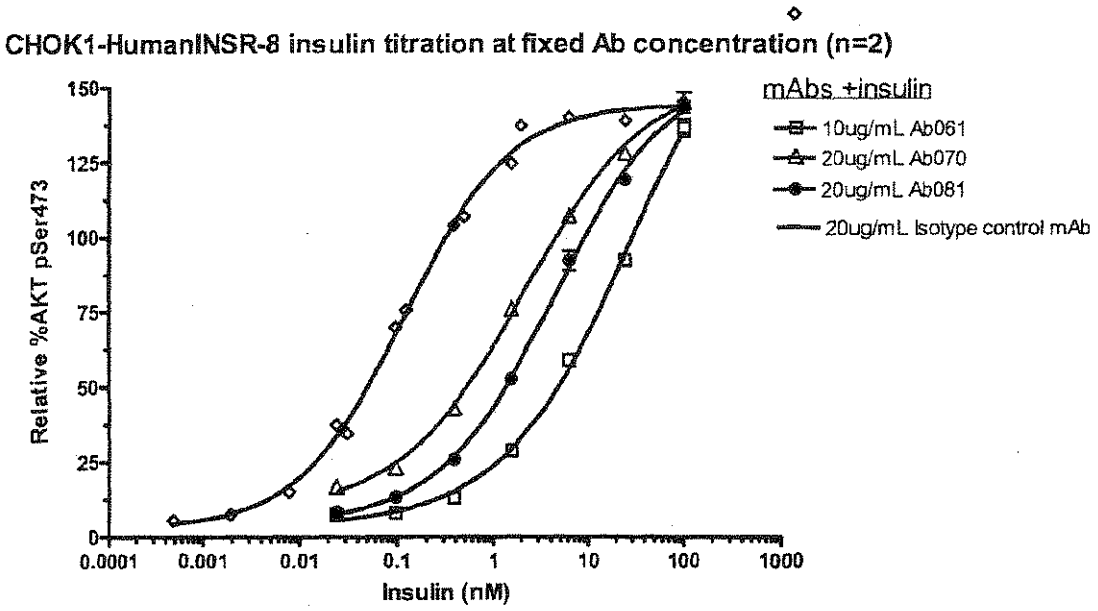

CHOK1-HumanINSR-8 insulin titration at fixed Ab concentration (n=2)
Relative %AKT pSer473
150
125
100
75
50
25
0
0.0001
0.001
0.01
0.1
1
10
100
1000
Insulin (nM)
mAbs +insulin
10ug/mL Ab061
20ug/mL Ab070
20ug/mL Ab081
20ug/mL Isotype control mAb

Table 1
Light Chain Sequences
Figure 54

Clone	Human PBMC		CHO Hu InsR		Cyno PBMC		CHO Cyno InsR		Rabbit PBMC		CHO Rabbit InsR	
	(-) insulin	*(+) insulin*	*(-) insulin*	*(+) insulin*	*(-) insulin*	*(+) insulin*	*(-) insulin*	*(+) insulin*	*(-) insulin*	*(+) insulin*	*(-) insulin*	*(+) insulin*
Ab001	+	++	+	++	+	++	+	++	+	++	++	+
Ab010	+	++			-	-						
Ab018					+	++						
Ab030	+	++			+	+						
Ab037	+	+	+	++	+	++	+	++	+	+	++	+
Ab040	+	+			+	++						
Ab050			++	+			++	+			+	+
Ab052			+	+			+	+			++	+
Ab053			++	+	+	+	++	+	+	+	++	+
Ab054			++	+			++	+			++	+
Ab058			+	+			+	+			++	+
Ab062			+	+			+	+	+	+	++	+
Ab077					+	++			-	-		
Ab078			-	++	+	++	-	++	-	++	-	++
Ab079					+	++			+	++		
Ab080			+	++	+	+	+	++	+	+	+	++
Ab083					+	++			+	++		
Ab085			-	++	+	++	-	++	+	++	-	++

Table 1
Light Chain Sequences

Name	Ab #	L-FR1	L-CDR1	L-FR2	L-CDR2	L-FR3	L-CDR3	L-FR4	SEQ ID NO:
XPA-15-093_VL	Ab023	QSVLT---QPP-SASGTPGQRVTISCSGS	ISNIGSNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSPHV	VFGGGTKLTVLG	21
XPA-15-096_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	FSNIGSNY-	VYWYQQLPGTARKLLIY	ADT	FRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGV-	VFGGGTKLTVLG	22
XPA-15-094_VL	Ab043	QSVLT---QPP-SASGTPGQRVTISCSGS	ISNIGSNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPGRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSPHV	VFGGGTKLTVLG	23
XPA-15-106_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VTWYQQLPGTAPKLLIY	SNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ATWDDS-LSGW-	VFGGGTKLTVLG	24
XPA-15-105_VL		QSVLT---QPP-SASGTPGQRVTISCSGG	PSNIGSNI-	VNWYQQLPGTAPKLLIY	SNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ETWDSN--TQ--	VFGGGTKLTVLG	25
XPA-15-100_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	ASNLGMHF-	VSWYQQLPGTAPKLLIY	DND	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	QSYDSS-LSGPV	LFGGGTKLTVLG	26
XPA-15-124_VL		QSVLT---QPP-SASGTPGQRVTISCSGG	SSNIGAGYD	VHWYQQLPGTAPKLLIY	GNN	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGP-	VFGGGTKLTVLG	27
XPA-15-121_VL	Ab047	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VNWYQQLPGTAPKLLIY	DNN	KRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	QSYDSS-LSGWE	VFGGGTKLTVLG	28
XPA-15-122_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGRNP-	VNWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGQ-	VFGGGTKLTVLG	29
XPA-15-127_VL		QSVLT---QPP-SASGTPGQRVTISCSGN	SSNIGNNY-	VAWYQQLPGTAPKLLIY	SDH	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGHV	IFGGGTKLTVLG	30
XPA-15-125_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	NSNIGSRT-	VNWYQQLPGTAPKLLIY	ENN	KRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	SSYAGS--NNLG	VFGGGTKLTVLG	31
XPA-15-133_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	FSNIGGNT-	VNWYQQLPGTAPKLLIY	SYD	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ASWDVS-LSGV-	VFGGGTKLTVLG	32
XPA-15-135_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGNNA-	VNWYQQLPGTAPKLLIY	TDS	RRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	VSRDDS-LNGW-	VFGGGTKLTVLG	33
XPA-15-139_VL	Ab018	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VNWYQQLPGTAPKLLIY	DNN	KRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ATWDDS-LNGP-	IFGGGTKLTVLG	34
XPA-15-138_VL	Ab001	QSVLT---QPP-SASGTPGQRVTISCSGS	TSNIGSNT-	VNWYQQLPGTAPKLLIY	RNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGFV	VFGGGTKLTVLG	35
XPA-15-143_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VNWYQQLPGTAPKLLIY	GNT	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGV-	VFGGGTKLTVLG	36
XPA-15-141_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGNNY-	VFWYQQLPGTAPKLLIY	RNY	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ATWDDS-LTGW-	VFGGGTKLTVLG	37
XPA-15-145_VL	Ab012	QSVLT---QPP-SASGTPGQRVTISCSGS	RSNIGANT-	VNWYQQLPGTAPKLLIY	GVN	HRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGW-	VFGGGTKLTVLG	38
XPA-15-140_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VNWYQQLPGTAPKLLIY	GAT	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	SSWDDS-LSGP-	VFGGGTKLTVLG	39

Table 1
Light Chain Sequences

Name	Ab #	L-FR1	L-CDR1	L-FR2	L-CDR2	L-FR3	L-CDR3	L-FR4	SEQ ID NO:
XPA-15-159_VL	Ab015	QSVLT---QPP-SASGTPGQRVTISCSGS	TSNIGNNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	SAWDDT-LNGP-	VFGGGTKLTVLG	40
XPA-15-167_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGNNY-	VSWYQQLPGTAPKLLIY	GDI	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDR-LNGP-	VFGGGTKLTVLG	41
XPA-15-169_VL	Ab034	QSVLT---QPP-SASGTPGQRVTISCSGG	SSNIGSNT-	VYWYQQLPGTAPKLLIY	DNN	KRPAGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGP-	VFGGGTKLTVLG	42
XPA-15-013_VL	Ab006	QSVLT---QPP-SASGTPGQRVTISCSGS	ISNIGSNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSPHV	VFGGGTKLTVLG	43
XPA-15-020_VL		QSVLT---QPF-SASGTPGQRVTISCSGS	SSNIGNNY-	VSWYQQLPGTAPKLLIY	SNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGL-	VFGGGTKLTVLG	44
XPA-15-017_VL	Ab017	QSVLT---QPP-SASGTPGQRVTISCTGS	SSNIGAGYD	VHWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGW-	VFGGGTKLTVLG	45
XPA-15-009_VL	Ab022	QSVLT---QPP-SASGTPGQRVTISCTGS	SSNIGAGYD	VHWYQQLPGTAPKLLIY	RND	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDHS-LSAHV	VFGGGTKLTVLG	46
XPA-15-033_VL		QSVLT---QPP-SASGTPGQRVTISCSGT	SSNFGRRT-	VNWYQQLPGTAPKLLIY	SNN	LRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGW-	VFGGGTKLTVLG	47
XPA-15-037_VL	Ab031	QSVLT---QPP-SASGTPGQRVTISCSGR	SSNIGYNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGP-	VFGGGTKLTVLG	48
XPA-15-042_VL	Ab027	QSVLT---QPP-SASGTPGQRVTISCSGR	SSNIENNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGV-	VFGGGTKLTVLG	49
XPA-15-036_VL	Ab030	QSVLT---QPP-SASGTPGQRVTISCTGS	SSNIGAGYD	VHWYQQLPGTAPKLLIY	DNN	KRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ASWDDS HLHV--	LFGGGTKLTVLG	50
XPA-15-047_VL	Ab036	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGGNS-	VHWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSPHV	VFGGGTKLTVLG	51
XPA-15-007_VL	Ab029	QSVLT---QPP-SASGTPGQRVTISCSGN	SSNIGNSY-	VSWYQQLPGTAPKLLIY	SND	IRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGP-	VFGGGTKLTVLG	52
XPA-15-074_VL	Ab039	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VNWYQQLPGTAPKLLIY	RNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGP-	VFGGGTKLTVLG	53
XPA-15-085_VL	Ab011	QSVLT---QPP-SASGTPGQRVTISCSGS	ISNIGSNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSPHV	VFGGGTKLTVLG	54
XPA-15-075_VL	Ab009	QSVLT---QPP-SASGTPGQRVTISCSGS	ISNIGSNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSPHV	VFGGGTKLTVLG	55
XPA-15-082_VL	Ab041	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VTWYQQLPGTAPKLLIY	SNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ATWDDS-LSGW-	VFGGGTKLTVLG	56
XPA-15-066_VL	Ab004	QSVLT---QPP-SASGTPGQRVTISCSGG	NSNIGSNY-	VSWYQQLPGTAPKLLIY	RNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGR-	VFGGGTKLTVLG	57
XPA-15-080_VL		QSVLT---QPP-SASGTPGQRVTISCTGS	SSNIGAGYV	VHWYQQLPGTAPKLLIY	TND	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	QSVDRS-LSGS-	VFGGGTKLTVLG	58
XPA-15-099_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	ISNIGSNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSPHV	VFGGGTKLTVLG	59

Table 1
Light Chain Sequences

Name	Ab #	L-FR1	L-CDR1	L-FR2	L-CDR2	L-FR3	L-CDR3	L-FR4	SEQ ID NO:
XPA-15-102_VL	Ab044	QSVLT---QPP-SASGTPGQRVTISCSGS	TSNIGNNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	SAWDDT-LNGP-	VFGGGTKLTVLG	60
XPA-15-115_VL	Ab046	QSVLT---QPP-SASGTPGQRVTISCSGS	ISNIGSNY-	VSWYQXLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSPHV	VFGGGTKLTVLG	61
XPA-15-111_VL	Ab045	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VNWYQQLPGTAPKLLIY	GNS	NRSSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDR-LNGP-	VFGGGTKLTVLG	62
XPA-15-142_VL		QSVLT---QPP-SASGTPGQRVTISCSGR	NSNIGSNY-	VSWYQQLPGTAPKLLIY	RNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDVADYYC	SSYAGS--NNFV	VFGGGTKLTVLG	63
XPA-15-146_VL		QSVLT---QPP-SASGTPGQRVTISCSGI	DSNFGSNS-	VNWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGW-	VFGGGTKLTVLG	64
XPA-15-144_VL		QSVLT---QPP-SASGTPGQRVTISCTGS	SSNIGAGYD	VHWYQQLPGTAPKPLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	TSYTGN--NQFV	IFGGGTKLTVLG	65
XPA-15-154_VL	Ab033	QSVLT---QPP-SASGTPGQRVTISCSGI	SSNIGNNF-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-PRGP-	VFGGGTKLTVLG	66
XPA-15-158_VL	Ab014	QSVLT---QPP-SASGTPGQRVTISCSGC	SSNIGNNA-	VNWYQQLPGTAPKLLIY	RSD	QRLAGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	QSYDSS-LIGHW	VFGGGTKLTVLG	67
XPA-15-155_VL	Ab048	QSVLT---QPP-SASGTPGQRVTISCSGI	SSNIGNNF-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-PRGP-	VFGGGTKLTVLG	68
XPA-15-165_VL	Ab049	QSVLT---QPP-SASGTPGQRVTISCSGR	SSNIGYNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGP-	VFGGGTKLTVLG	69
XPA-15-023_VL	Ab025	QSVLT---QPP-SASGTPGQRVTISCSGS	TSNIGNNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	SAWDDT-LNGP-	VFGGGTKLTVLG	70
XPA-15-022_VL	Ab024	QSVLT---QPP-SASGTPGQRVTISCSGT	SSNLGSHT-	VSWYQQLPGTAPKLLIY	DNN	ERPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSAW-	VFGGGTKLTVLG	71
XPA-15-019_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGNNA-	VNWYQQLPGTAPKLLIY	SNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	GTWDDS-LSVW-	VFGGGTKLTVLG	72
XPA-15-021_VL	Ab023	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNP-	VNWYQQLPGTAPKLLIY	DNS	KRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	GTWDDS-LSVW-	VFGGGTKLTVLG	73
XPA-15-006_VL	Ab021	QSVLT---QPP-SASGTPGQRVTISCTGT	SSNIGAGFD	VHWYQQLPGTAPKLLIY	SNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGL-	VFGGGTKLTVLG	74
XPA-15-026_VL	Ab026	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGNNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGP-	VFGGGTKLTVLG	75
XPA-15-043_VL		QSVLT---QPP-SASGTPGQRVTISCTGS	SSNIGAGYD	VHWYQQLPGTAPKLLIY	KNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LGG--	VFGGGTKLTVLG	76
XPA-15-048_VL	Ab037	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGNSA-	VNWYQQLPGTAPKLLIY	DNN	KRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	QVWDSG--TA--	VFGGGTKLTVLG	77
XPA-15-062_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGNNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGP-	VFGGGTKLTVLG	78
XPA-15-059_VL	Ab028	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGNNY-	VSWYQQLPGTAPKLLIY	SNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LNGL-	VFGGGTKLTVLG	79

Table 1
Light Chain Sequences

Name	Ab #	L-FR1	L-CDR1	L-FR2	L-CDR2	L-FR3	L-CDR3	L-FR4	SEQ ID NO:
XPA-15-064_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGRRT-	VNWYQQLPGTAPKLLIY	DNN	KRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ATWDDS-LNGW-	VFGGGTKLTVLG	80
XPA-15-068_VL	Ab013	QSVLT---QPP-SASGTPGQRVTISCSGS	TSNIGNNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	SAWDDT-LNGP-	VFGGGTKLTVLG	81
XPA-15-081_VL	Ab007	QSVLT---QPP-SASGTPGQRVTISCSGS	TSNIGNNY-	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	SAWDDT-LNGP-	VFGGGTKLTVLG	82
XPA-15-065_VL	Ab038	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VTWYQQLPGTAPKLLIY	SNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ATWDDS-LSGW-	VFGGGTKLTVLG	83
XPA-15-077_VL	Ab040	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNS-	VNWYQQLPGTAPKLLIY	DNN	KRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDS-LSGP-	VFGGGTKLTVLG	84
XPA-15-086_VL	Ab042	QSVLT---QPP-SASGTPGQRVTISCSGS	SSNIGSNT-	VTWYQQLPGTAPKPLIY	SNN	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	ATWDDS-LSGW-	VFGGGTKLTVLG	85
XPA-15-088_VL		QSVLT---QPP-SASGTPGQRVTISCSGS	ASNLGMHF-	VSWYQQLPGTAPKLLIY	DND	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	QSYDSS-LSGPV	LFGGGTKLTVLG	86
XPA.015.175_VL	Ab019	DLVLTQSPASLAVSLGQRATISCRAS	KSVSTSGYSY	IHWYQQKPGQPPKLLIY	LAS	NLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYC	-QHNREP	RTFGGGTNLEIKR	1
XPA.015.176_VL	Ab088	DLVLTQSPASLAVSLGQRATISCRAS	KSVTTSGYSY	IHWYQQKPGQPPKLLIY	LAS	NLESGAPARFSGSGSGTDFTLNIHPVEEEDAGNYYC	-QHNREP	RTFGGGTKLEIKR	2
XPA.015.177_VL		DIVMTQSPASLAVSLGQRATISCRAS	KSVSTSGYSY	IHWYQQKPGQPPKLLIY	LAS	NLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYC	-QHNREP	RTFGGGTNLEIKR	3
XPA.015.178_VL	Ab089	DLVLTQSPASLAVSLGQRATISCRAS	KSVSTSGYSY	IHWYQQKPGQPPKLLIY	LAS	NLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYC	-QHNREL	RTFGGGTKLEIKR	4
XPA.015.179_VL		DLVLTQSPASVAVSLGQRATISCRAS	KSVSTSGYSY	MHWYQQKPGQPPKLLIY	LAS	NLESGVPARFSGSGSGTDFTLNIHPVEEEDVATYYC	-QHNRDP	RTFGGGTKLEIKR	5
XPA.015.181_VL	Ab010*	DVQIIQSPSYLAASPGETITINCRAS	KSIS----KY	LAWYQEKPGKTNKLLIY	SGS	TLQSGIPSRFSGSGSGTDFTLTISSLEPEDFAMYYC	QQHNEYP	LTFGAGTKLELKR	6
XPA.015.182_VL	Ab020	DVQITQSPSYLAASPGETITINCRAS	KSIS----KY	LAWYQEKPGKTNKLLIY	SGS	TLQSGIPSRFSGSGSGTDFTLTISSLEPEDFAMYYC	QQHNEYP	LTFGAGTKLELKR	7
XPA.015.183_VL		DLVLTQSPASLAVSLGQRATISCRAS	KSVSTSGYSY	IHWYQQKPGQPPKLLIY	LAS	NLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYC	-QHNREL	RTFGGGTKLEIKR	8
XPA.015.184_VL		DIVMTQSPTSLAVSLGQRATISCRAS	ESVSISGYSY	IHWYQQRPGQPPKLLIY	LAS	NLESGVPARFSGSGSGTDFTLNIHPVEEEDVATYYC	-QHNRDP	RTFGGGTKLEIKR	9
XPA.015.185_VL	Ab003	DIQMTQSPSYLAASPGETITINCRAS	KSIS----KY	LAWYQEKPGKTNKLLIY	SGS	TLQSGIPSRFSGSGSGTDFTLTISSLEPEDFAMYYC	QQHNEYP	LTFGAGTKLELKR	10
XPA.015.186_VL		DIQMTQSPSSLSASLGDTITITCHAS	QNIN----VW	LTWYQQKPGNIPKLLIS	KAS	NLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYC	QQGQSYP	WTFGGGTKLEIKR	11
XPA.015.187_VL		DLVLTQSPASLAVSLGQRATISCRAS	KSVSTSGYSY	IHWYQQKPGQPPKLLIY	LAS	NLESGVPARFSGSGSGTDFTLNIHPVEEEDAGNYYC	-QHNREP	RTFGGGTKLEIKR	12
XPA.015.188_VL	Ab008	DVQITQSPSYLTASPGETITINCRAS	KSIS----NY	LAWYQEKPGKTNKLLIY	SGS	TLQSGIPSRFSGSGSGTDFTFTISSLEPEDFAMYYC	QQHNEYP	LTFGAGTKLELKR	13

Table 1
Light Chain Sequences

Name	Ab #	L-FR1	L-CDR1	L-FR2	L-CDR2	L-FR3	L-CDR3	L-FR4	SEQ ID NO:
XPA.015.189_VL		DIVMTQSPASLAVSLGQR ATISCRAS	KSVSISGYS Y	IHWYQQKPGQPPKLLIY	LAS	NLESGVPARFSGSGSGTDFTLNIHPVEEEDAGNYYC	- QHNREP	RTFGGGTKLEIKR	14
XPA.015.190_VL	Ab002	DIQMTQTTSSLSASLGDR VTISCRAS	QDIS---- NY	LNWYQQKPDGTVKLLIY	YTS	RLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATFYC	QQYSDL P	YTFGGGTKLEIKR	15
XPA.015.191_VL		DVQITQSPSSLSASLGER VSLTCRAS	QDIG---- SS	LNWLQQEPDGTIKRLIS	ATS	TLDSGVPKRFSGSRSGSDYSLTISSLEPEDFVDYYC	LQYASY P	FTFGSGTKVEIKR	16
XPA.015.192_VL	Ab005	DIQMTQSPSYLAASPGET ITINCRAS	KSIS---- KY	LAWYQEKPGKTNKLLIY	SGS	TLQSGIPSRFSGSGSGTDFTLTISSLEPEDFAMYYC	QQHNEY P	LTFGAGTKLELKR	17
XPA.015.173_VL	Ab087	DIQMTQSPSSLSASLGGK VTITCKAS	QHIN---- KY	IAWYQHKPGKGPRLLIH	YTS	TLQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYC	LQYDNL -	YTFGGGTKLEIKR	18
XPA.015.174_VL		DIVMTQSPSSLFASLGER VSLTCRAS	QDIG---- DR	LYWLQQEPDGAIKRLIF	ATS	SLDSGVPKRFSGSRSGSEYSLTISSLESEDFVDYYC	LQYASS P	WTFGGGTKLEIKR	19
XPA.015.172_VL		DIVMTQSPTSLAVSLGQR ATISCRAS	KSVSTSGYS Y	IHWYQQKPGQPPKLLIY	LAS	NLESGVPARFSGSGSGTDFILNIHPVEEEDAATYYC	- QHNRDP	RTFGGGTKLELKR	20
XPA.15.193	Ab050	NFMLTQPHSVSESPGKTV SISCTGS	SGSIGSNY	VQWYQQRPGSAPTTVIY	EDN	QRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYC	QSYYNS NV	VFGGGTKLTVL	87
XPA.15.194	Ab051	SSELTQDPAVSVALGQTV RITCQGN	SLRSFY	AIWYQQKPGQAPVLVIY	GKN	IRPSGIPDRFSGSNSGDTASLTITGTQAEDEADYYC	NSRDNN RNHL	LFAGGTKVTVL	88
XPA.15.195	Ab052	QAMLTQPASLSASPGASA SLTCTLR	SGINVVAYN	IYWYRQKSGSPPQSVLR	YKSD SDS	ERDSGVPSRFSGSKDVSANAGILLISGLQSEDEADYYC	LIWHNS AW	VFGGGTQLTVL	89
XPA.15.196	Ab053	QSALTQPRSVSESPGKTV TISCTGS	GGSIGSNY	VQWYQQRPGSAPTTVIF	EDN	RRPSGVPDRFSGSIHSSSNSASLTISGLKTEDEADYYC	QSYVGT IV	VFGGGTKVTVL	90
XPA.15.197	Ab054	QSALTQPRSVSESPGKTV TISCTGS	GGSIGSNY	VQWYQQRPGSAPTTVIF	EDN	RRPSGVPDRFSGSIHSSSNSASLTISGLKTEDEADYYC	QSYVGT IV	VFGGGTKVTVL	91
XPA.15.198	Ab055	SYELTQLPSVSVSPGQTA RITCSGD	ALPNKY	AYWYQQKSGQAPVLVIY	EDT	RRPSEIPERFSASSSGIMATLTISGAQVEDEAEYYC	YSTDSS GNER	VFGGGTKLTVL	92
XPA.15.199	Ab056	QSALTQPASVSESPGQSI TISCTGT	GSDIGTYNL	VSWYQHHPGKAPKLMIY	EVT	KRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYC	SSYTSS STLY	VFGTGTKLTVL	93
XPA.15.200	Ab057	QTVVTQEPSFSVSPGGTV TLTCGLI	SGSVSTSYY	PSWYQQTPGQAPRMLVH	STS	TRYSGVPDRFSGSILGNKAALTITGAQADDESDYYC	ALYMGG GIY	VFGGGTQLTVL	94
XPA.15.201		QAVLTQPSSSSASPGESA RLTCTLP	SDINVRYHN	IYWYQEKPGSPPRYLLY	YYSD SSK	GQGSGVPSRFSGSKDVSTNTGILVISGLQSEDEAEYYC	MTWSSN GSG	VFGGGTQLTVL	95
XPA.15.202	Ab058	QSVLTQPPSVSGAPGQRV TISCTGS	RSNIGADHD	VHWYQQIPGRAPKLLIY	GNS	NRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYC	QSYDNS LSGS	VFGGGTKLTVL	96
XPA.15.203		QTVVTQEPSFSVSPGGTV TLTCGLN	SASVSTYSY	PSWYQQTPGQAPRMLIY	STN	TRSSGVPDRFSGSILGNKAALTITGAQADDESDYYC	ALYMGS GIW	VFGGGTKLTVL	97
XPA.15.204	Ab059	QAVLTQPASLSASPGASA SLTCTLR	SDISVGVYR	ISWYQQKPGSPPQYLLS	YNSD SNN	HQGSGVPSRFSGSKDASANAGILLISGLQSEDEADYYC	MIWHIN AW	VFGGGTKVTVL	98
XPA.15.205		QSVLTQPFSVSGAPGQRV TISCIGS	RSDIGYYA	VHWYRQLPGTAPKLVIY	AND	NRPSGVPDRFSGSKSGTSAFLAISGLQADDEADYYC	QSYDTV TGKG	VFGGGTKVTVL	99

Table 1
Light Chain Sequences

Name	Ab #	L-FR1	L-CDR1	L-FR2	L-CDR2	L-FR3	L-CDR3	L-FR4	SEQ ID NO:
XPA.15.206		QSVLTQPPSVSGAPGQRVTISCTGS	SSNIGAGYY	AHWYQQLPGTAPRLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYC	QSYDSSLSGPNY	VFGTGTKVTVL	100
XPA.15.207	Ab060	QAVLTQPASLSASPGESARLTCTLP	SDINVRYYN	IYWYQQKPGSPPRYLLY	YYSDSNK	DQGSGVPSRFSGSKDVSTNTGILVISGLQSEDEAEYYC	MTWSSNGSG	VFGGGTQLTVL	101
XPA.15.208		QAVLTQPASLSASPGESARLTCTLP	SDINVRYHN	IYWYQEKPGSPPRYLLY	YYSDSSK	GQGSGVPSRFSGSKDVSTNTGILVISGLQSEDEAEYYC	MTWSSNGSG	VFGGGTKLTVL	102
XPA.15.209	Ab061	QTVVTQEPSFSVSPGGTVTLTCGLS	SGSVSTGYS	PGWYQQTPGQAPRTLVY	NTN	TRSSGVPDRFSGSILGNKAALTITGAQADDESDYYC	ALYMGSGTY	VFGGGTKLTVL	103
XPA.15.211	Ab062	QSVLTQPPSVSGAPGQRVTISCTGS	SSNIGAGYD	VHWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYC	QSYDSSLSGSG	VFGGGTKVTVL	104
XPA.15.212	Ab063	SSELTQPPSVSVAPGKTATITCGGD	NIASKS	VHWYQQKPGQAPVLVLY	DDS	VRPSDIPERFSGSNSANTATLTLTRVEAGDEGEYYC	QVWDVRSDHP	FFGPGTKVTVL	105
XPA.15.213	Ab064	QAVVTQEPSLTVSPGGTVTLTCASS	TGAVTSGYY	PNWFQQKPGQAPRALIY	STS	NKHSWTPARFSGSLLGGKAALTLSGVQPEDEAEYYC	LLYYGGAQPW	VFGGGTQLTVL	106
XPA.15.214	Ab065	QAGLTQPPSVSKGLRQTATLTCTGD	NNIVGDQG	AAWLQQHQGHPPKLLSF	RNN	SRPSGISERFSASRSRNTASLTITRLQPEDAADYYC	SAWDSFLSAW	VFGGGTKLTVL	107
XPA.15.215	Ab066	SSELTQDPAVSVAVGQSVRITCQGD	SLKNFY	ATWYQQRPGQAPLLVIF	GKN	NRPSGIPDRFSGSSSGNTASLTVTGAQADDEADYYC	NSPDSSNKLV	VFGGGTKLTVL	108
XPA.15.216	Ab067	EIVLTQSPGTLSLSPGERATLSCRAS	QSVSSSY	LAWYQQKPGQAPRLLIY	GAS	SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSL	GTFGQGTKLEIK	109
XPA.15.217	Ab068	DVVMTQTPLSLSVTPGQPASISCKAS	QSLLYTNGDTY	VSWYVQKPGQAPQLLFS	DVS	SRFFGVPDRFSASGSGTDFTLKISRVEAEDVGVYYC	VQAMYLP	LVFGQGTKVEIK	110
XPA.15.218		SSELTQDPAVSVALGQTVRITCQGD	SLRSYY	ASWYQQKPGQAPVLVIY	GKN	NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC	NSRDSSGNHL	MFGGGTQLTVL	111
XPA.15.219	Ab086	QSALTQPASVSGSLGQSITISCTGT	SSDIGLYKF	VSWYQQHPGKAPKLMIY	DVS	YRPSGVSNRFSGSSSGNTASLTISGLQAEDEADYYC	NSYTSSSTLV	VFGGGTKLTVL	112
XPA.15.220		SSELTQDPAVSVALGQTVRITCQGD	SLRNYY	ASWYQQKPGQAPLLVMY	DRN	SRPSGIPDRFSGSRSGNTASLTITGAQAEDEADYYC	NSRDSSGNHA	VFGGGTQLTVL	113
XPA.15.221		SYELMQPPSVSVAPGQTATITCGGN	NIGTKS	VHWYQQKTGQAPVLVVY	DDS	DRPSGIPERFSGSNSGNTATLTISRLEAGDEADYYC	QVWDRSSEHH	VFGGGTQLTVL	114
XPA.15.222	Ab069	SSELTQDPAVSVALGQTVRITCQGD	SLRSYY	ASWYQQKPGQAPVLVIY	GKN	NRPSGIPDRFSGSRSGNTASLTITGAQAEDEADYYC	NSRDSSGNHV	VFGGGTKVTVL	115
XPA.15.223		SSELTQDPAVSVALGQTVRITCQGD	SLRSYS	VAWYQQKPGQAPLLVIY	GNT	NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC	NSRASSGFSW	VFGGGTKVTVL	116
XPA.15.224		SSELTQDPAVSVALGQTVRITCQGD	SLRSYY	ASWYQQKPGQAPVLVIY	GKN	NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC	NSRDSSGNHA	VFGGGTQLTVLG	117
XPA.15.225		SYELMQPPSVSVAPGQTATITCGGN	NIGTKS	VHWYQQKTGQAPVLVVY	DDS	DRPSGIPERFSGSNSGNTATLTISRLEAGDEADYYC	QVWDRSSEHH	VFGGGTQLTVL	118
XPA.15.226	Ab070	SSELTQDPAVSVALGQTVRITCQGD	SLRSYY	TSWYQQKPGQAPVLVIF	GKN	NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC	NSRDSSGNYA	VFGGGTQLTVL	119

Table 1
Light Chain Sequences

Name	Ab #	L-FR1	L-CDR1	L-FR2	L-CDR2	L-FR3	L-CDR3	L-FR4	SEQ ID NO:
XPA.15.227	Ab071	SSELTQDPAVSVALGQTVRITCQGD	SLRSYY	ASWYQQKPGQAPVLVFY	GKN	NRPSGIPGRFSGSKSGNTASLTITGAQAEDEADYYC	NSRDSSGNHW	VFGGGTKLTVL	120
XPA.15.228	Ab072	SYVLTQPPSASGTPGQRVTISCSGS	NSNIGSNF	VTWYQQLPGAAPKLLIY	TNS	QRPSGVPDRFSGSRSGTSASLAISGLQSEDEADYFC	AAWDDSLNGP	VFGGGTQLTVL	121
XPA.15.229	Ab073	QSVLTQPPSVSAAAGQKVTISCSGS	SSNIGNNY	VTWYQHVPGTAPKLLIF	DND	KRPSGIPDRFSGSKSGTSATLAITGLQTGDEADYYC	GTWDSSLNP	LFGGSTQLTVL	122
XPA.15.230	Ab074	SSELTQDPAVSVALGQTVRITCQGD	SLRSYY	ASWYQQKPGQAPVLVIY	GKN	NRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYC	SSRDSSGDQW	VFGGGTKLTVL	123
XPA.15.231		SSELTQNPAVSVALGQTVRITCQGD	SLRNYY	ASWYQQKPGQAPLLVMY	DRN	SRPSGIPDRFSGSRSGNTASLTITGAQAEDEADYYC	NSRDSSGNHA	VFGGGTQLTVL	124
XPA.15.232	Ab075	QSVLTQPPSVSAAPGQKVTISCSGS	SSNIGNNY	VTWYQHVPGTAPKLLIF	DND	KRPSGIPDRFSGSKSGTSATLAITGLQTGDEADYYC	GTWDSSLNP	LFGGGTQLTVL	125
XPA.15.233		QSVLTQPPSVSAAAGQKVTISCSGS	SSNIGNNY	VTWYQHVPGTAPKLLIF	DND	KRPSGIPDRFSGSKSGTSATLAITGLQTGDEADYYC	GTWDSSLNP	LFGGGTQLTVL	126
XPA.15.234		QSVLTQPPSVSAAAGQKVTISCSGS	SSNIGNNY	VTWYQHVPGTAPKLLIF	DND	KRPSGIPDRFSGSKSGTSATLAITGLQTGDEADYYC	GTWDSSLNP	LFGGGTQLTVL	127
XPA.15.235		DVVMTQSPLSLPVTLGQPASISCRSS	QSLVYSDGNTY	LNWFQQRPGQSPRRLIY	KVS	NRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	MQGTH	WSFGQGTRLEIK	128
XPA.15.236		EIVLTQSPDFQSVTPKEKVTITCRAS	QSIGSS	LHWYQQKPDQSPKLLIK	YAS	QSISGVPSRFSGSGSGTDFTLTTNSLEAEDAATYYC	HQSSSLP	WTFGQGTKVEIK	129
XPA.15.237		DIQLTQSPSSLSASVGDRVTITCRAS	QGISNS	LAWYQQKPGKAPKLLLY	AAS	RLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYC	QQYYSTL	LTFGGGTKVDIK	130
XPA.15.238		EIVLTQSPGTLSLSPGERATLSCRAS	QSVSSSY	LAWYQRKPGRAPRLLIY	GAS	SRATGIPNRFSGSGSGTDFTLTISRLEPEDFAVYYC	QQYGSSP	PTFGQGTKLEIK	131
XPA.15.239		DIVMTQSPLSLPVTPGEPASISCRSS	QSLLHSNGYNY	LDWYLQKPGQSPQLLIY	LGS	NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	MQALQTP	HTFGQGTKLEIK	132
XPA.15.241	Ab076	EIVMTQSPATLSVSPGERATLSCRAS	QSISTN	LAWYQQKPGQTPRLLIY	GAS	TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	QQYNSE	ISFGQGTRLEIK	133
XPA.15.242		DIQMTQSPSSLSASVGDRVTITCRAS	QGISNS	LAWYQQKPGKAPKLLLY	ATS	RLETGVPSRFSGSGSGTDYTLTISSLQPEDFASYYC	QQFYSN	PSFGQGTKVEIK	134
XPA.15.243	Ab077	DIQMTQSPSSLSASVGDRVTITCRAS	QGISSW	LAWYQQKPGKAPKLLIY	AAS	SLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQANSFP	ITFGQGTRLEIK	135
XPA.15.244	Ab078	DIQLTQSPSSLSASVGDRVTITCRAS	QGISSA	LAWYQQKPGKAPKVLIY	DAS	SLERGVPSRFSGSGTGTDFTLTISSLQPEDFASYYC	HQFNSYP	DTFGQGTRLEIK	136
XPA.15.245	Ab079	AIRMTQSPSTLSASVGDRVTITCRAS	QSISTW	LAWYQQKPGKAPKLLIY	TTS	TLESGVPSRFSGSRSGTEFTLTISSLQPDDFATYYC	QQYNSYP	LTFGGGTKVEIK	137
XPA.15.246	Ab080	EIVLTQSPGTLSLSPGERATLSCRAS	QSLSSSF	LAWYQQKPGQAPRLLIY	GAG	SRATGVPDRFSGSGYGTDFSLTISRLELEDFAVYYC	QQYDRSQ	ITFGQGTRLEIK	138
XPA.15.247	Ab081	DVVMTQSPLSLSVTLGQPASISCRSS	LSLVYGDENTY	LNWFQQRPGQSPRRLLY	KVS	DRDSGVPDRFSGSGSGTDFTLKISRVEADDVGVYYC	MQGTHWP	YTFGQGTKLEIK	139

Table 1
Light Chain Sequences

Name	Ab #	L-FR1	L-CDR1	L-FR2	L-CDR2	L-FR3	L-CDR3	L-FR4	SEQ ID NO:
XPA.15.248	Ab082	EIVLTQSPDFQSVTPKET VTISCRAS	QNIGVS	LHWYQQKPDQSPKVLIK	YAS	QSLSGVPSRFSGTGSGTDFTLTIKSLEAEDAATYYC	LQTSSLP	WTFGQGTKVEIK	140
XPA.15.249	Ab083	AIQLTQSPSSLSASVGDR VTISCRAS	QSITSY	LNWYQQKPGKAPNLLIY	AAS	SLQSGVPSRFSGSGSGTDFTLTIAGLQPEDFATYYC	QQFDSYP	FTFGGGTKLEIK	141
XPA.15.250	Ab084	AIRMTQSPSTLSASVGDR VTITCRAS	QSISSW	LAWYQQTPGKAPKLLIY	AAS	NLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	QQSYNTP	LTFGGGTKVEIK	142
XPA.15.272		QSALTQPASVSGSPGQSI TISCLGT	INDVGLYNL	VSWYQQHPGKAPKLMIY	EVS	KRPSGVSNRFSGSKSGNTASLTISGLQAEDEAVYYC	NSYTSSNFW	VFGGGTQLTVLG	143
XPA.15.275	Ab085	QTVVTQEPSFSVSPGGTV TLTCGLT	SGSVSTRNF	PGWYQQTPGQTLRTLIY	NTN	TRSSGVPDRFSGSILGNKAALTITGAQADDESDYYC	VLYMTGDIW	VFGGGTKVTVLG	144
XPA.15.282		QSVLTQPPSVSAAAGQKV TISCSGS	SSNIGNNY	VTWYQHVPGTAPKLLIF	DND	KRPSGIPDRFSGSKSGTSATLAITGLQTGDEADYYC	GTWDSSLNP	LFGGGTQLTVLG	145
XPA.15.284		QSVLTQPPSVSAAAGQKV TISCSGS	SSNIGNNY	VTWYQHVPGTAPKLLIF	DND	KRPSGIPDRFSGSKSGTSATLAITGLQTGDEADYYC	GTWDSSLNP	LFGGGTQLTVLG	146
XPA.15.293		DIVMTQTPLSLPVTPGEP ASISCRSS	QSLLDSDDG NTY	LDWYVQKPGQSPQLLMY	SLS	YRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	MQRIEFP	YTFGQGTKLEIKR	147
XPA.15.110		QSVLTQPPSASGTPGQRV TISCSGS	SSNIGRNP	ISWYQQLPGTAPKLLIY	NND	QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDSLNGPVW	VFGGGTKLTVLG	148
XPA.15.120		QSVLTQPPSASGTPGQRV TISCSGS	SSNIGNNY	VSWYQQLPGTAPKLLIY	GNS	NRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	AAWDDSLSAV	VFGGGTKLTVLG	149
XPA.15.163		QSVLTQPPSASGTPGLRV IISCAGS	SSNIGAGYD	VHWYHQLPGTAPKLLIY	GNS	NQPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYC	TSYTGNNQFV	IFGGGTKLTVLG	150

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
XPA.015 .172_VH		QVQLQQSEAELVK PGASVKISCKAS	GYTFSSYW	MSWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNGKFKGKATLTADKSSGTAYMQLSSLTSEDSAVYFC	ARGVS- GYGAMDY	WGQGTSVTVSS	151
XPA.015 .173_VH	Ab087	EVQLVESGGGLVK PGGSLKLSCAAS	GFTFSNYA	MSWVRQTPEKRLEWVAT	IS-- DGGHYI	DYPDNVKGRFTISRDNAKNNLYLQMSHLRSEDSAMYYC	ARA----- TNFAY	WGQGTLVTVSA	169
XPA.015 .174_VH		QVQLQQSGPELVK PGASVKLSCKAS	GYTFTSYD	INWVKQRPGQGLEWIGW	IYPRDGS T--	KSNEKFKGKATLTVDTSSSTAYMELHSLTSEDSAVYFC	AR------- EFDY	WGQGTLVTVSA	170
XPA.015 .175_VH	Ab019	QVQLQQSEAELVK PGASVKISCKAS	GYTFSNYW	MNWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNGKFKGKATLIADKSSSTAYMQLSSLTSEDSAVYFC	ARGVS- GYGAMDY	WGQGTSVTVSS	160
XPA.015 .176_VH	Ab088	QVQLQQSEAELVK PGASVKISCKAS	GYTFSSYW	MSWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNGKFKGKATLTADKSSGTAYMQLSSLTSEDSAVYFC	ARGVS- GYGAMDY	WGQGTSVTVSS	153
XPA.015 .177_VH		QVQLQQSEAELVK PGASVKISCKAS	GYTFSNYW	MNWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNGKFKGEATLIADKSSSTAYMQLSSLTSEDSAVYFC	ARGVS- GYGAMDY	WGQGTSVTVSS	159
XPA.015 .178_VH	Ab089	QVQLQQSEAELVK PGASVKISCKAS	GYTFSSYW	MNWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNVKFKGKATLTADKSSGTAYMQLSSLTSEDSAVYFC	ARGVS- GYGAMDY	WGQGTSVTVSS	154
XPA.015 .179_VH		EVQLQQSVAELVK PGASVKISCKAS	GYTFSNYW	MNWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNGRFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFC	ARGVS- GYGAMDY	WGQGTSVTVSS	161
XPA.015 .181_VH	Ab010*	EVQLQQSGPVLVK PGASVKMSCKAA	GYTFTDSY	MNWVKQSHGKSLEWIGD	INPYNGG T--	SYNQHFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYC	AR----- RRGAMDY	WGQGTSVTVSS	163
XPA.015 .182_VH		EIQLQQSGPVLVK PGASVKMSCKAA	GYTFTDSY	MNWVKQSHGKSLEWIGD	INPYNGG T--	SYNQHFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYC	AR----- RRGAMDY	WGQGTSVTVSS	164
XPA.015 .183_VH	Ab020	QVQLQQSEAELVK PGASVKISCKAS	GYTFSSYW	MNWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNVKFKGKATLTADKSSGTAYMQLSSLTSEDSAVYFC	ARGVS- GYGAMDY	WGQGTSVTVSS	155
XPA.015 .184_VH		EVQLQQSVAELVK PGASVKISCKAS	GYTFSNYW	MNWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNGRFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFC	ARGVS- GYGAMDY	WGQGTSVTVSS	162
XPA.015 .185_VH	Ab003	EVQLQQSGPELVK PGASVKISCKAS	GYTFTDSY	MNWVKQSHGKSLKWIGD	INPNNGG S--	NYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYC	AR----- RRGAMDY	WGQGTSVTVSS	157
XPA.015 .186_VH		QVQLQQSRAELVK PGASVKLSCKAS	GYTFTRYW	MHWVKQRPGQGLEWIGM	IHPNSGG T--	NYNEKFRSKATLTGDKSSSTAYMQLNSLTSDDSAVYYC	ARWDYGSAS YFDF	WGQGTTLIVSS	165
XPA.015 .187_VH		EVQLQQSGAELVK PGASVKISCKAS	GYTFSNYW	MNWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNGKFKGKATLTADKSSGTAYMQLSSLTSEDSADYFC	ARGVS- GYGAVDH	WGQGTSVTVSS	166
XPA.015 .188_VH	Ab008	EVQLQQSGPELVK PGASVKISCKAS	GYTFTDSY	MNWVKQSHGKSLEWIGD	INPNNGG T--	NYNQKFKDKATLTVDKSSSSAFMELRSLTSEDSAVYYC	AR----- RRGAMDY	WGQGTSVTVSS	156
XPA.015 .189_VH		EVQLQQSVAELVK PGASVKISCKAS	GYAFSSYW	MNWVKQRPGKGLEWIGQ	IYPGDGD T--	NYNGKFKGKATLTADKSSGTAYMQLSSLTSEDSAVYFC	ARGVS- GYGAMDY	WGQGTSVTVSS	152
XPA.015 .190_VH	Ab002	EVKLVESEEGLVK PGGSLKLSCAAS	GFTFSNYA	MSWVRQTPEKRLEWVAT	IS-- DGGHYT	YYSDTIKGRFTISRDNAKNNLFLQLSHLKSEDTAIYYC	ARG----- TVFDY	WGQGTTLTVSS	167
XPA.015 .191_VH		QVQLQQPGAELVK PGASVKLSCKAS	GYIFTNYW	MHGVKQRPGQGLEWIGM	IHPNSGS T--	SYNEKFKTKATLTVDKSSSTAYMQLSSLTSEDSAVYYC	ARGYGSTYW YFDV	WGTGTTVTVSS	168
XPA.015 .192_VH		EVQLQQSGPELVK PGASVKISCKAS	GYTFTDSY	MNWVKQSHGKSLEWIGD	INPNNGD T--	NYNQKFKDKATLTVDKSSSSAFMELRSLTSEDSAVYYC	AR---- RRGAMDY	WGQGTSVTVSS	158

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
XPA.15.006	Ab021	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYE	MNWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARATGIGGYHFDY	WGQGTLVTVSQ	288
XPA.15.009	Ab022	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSYW	MHWVRQAPGKGLEWVSG	INNSGGTT	FYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARDRRFLEWTFDY	WGQGTLVTVSQ	289
XPA.15.019		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSNAW	MSWVRQAPGKGLEWVSA	IGTGGGT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	AKSRWLPYFDY	WGQGTLVTVSQ	290
XPA.15.043		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSDHY	MDWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	AKEIPGRWLQLGGFDY	WGQGTLVTVRL	291
XPA.15.062		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSNYV	ISWVRQAPGKGLEWVSA	ISGSGGST	FYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTANYYC	ARVGLSGWYYFDY	WGQGTLVTVSS	292
XPA.15.085	Ab011	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSNYA	MGWVRQAPGKGLEWVSS	ISGSGGTT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARHKGLQPLDY	WGQGTLVTVSF	293
XPA.15.099		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSNYA	MGWVRQAPGKGLEWVSS	ISGSGGTT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARHKGLQPLDY	WGQGTLVTVSQ	294
XPA.15.141		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFDDYG	MNWVRQAPGKGLEWVSG	VSWNGSRT	HYAYSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARRSPLKDGFDI	WGLGTLVTVTQ	295
XPA.15.142		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFNKFA	VHWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ASDVEGGYFHNSGPDY	WGQGTLVTVSS	296
XPA.15.144	Ab033	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFTNYN	MIWVRQAPGKGLEWVSG	VSWNGSRT	HYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARERGSWDTTGYYNYYYYGMDV	WGQGTLVTVSS	297
XPA.15.146		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSNYW	MSWVRQAPGKGLEWVST	VSATGPHT	YYADSAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARQVGGGPFDI	WGQGTLVTVSS	298
XPA.15.154		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSNY	MSWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARVGSSGWYYFDY	WGQGTLVTVSS	299
XPA.15.155		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSNY	MSWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARVGSSGWYYFDY	WGQGTLVTVSS	300
XPA.15.158	Ab014	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSNAW	MSWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	AAPTVPYYYYGMDV	WGQGTLVTVSS	301
XPA.15.165	Ab049	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSNY	MSWVRQAPGKGLEWVSS	ISGGST	YYADSRKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARLDWSSGAFDI	WGQGTLVTVSS	302
XPA.15.193	Ab050	QVQLVQSGAELKKPGATVKISCKVS	GYTFGDYH	MHWVKQAPGKGLEWMGL	VDPENGET	EYGEKFQDRITMAADTSTDTAYMELSSLRSEDTAVYYC	ARSPSSSGYFRVDGFDI	WGQGTMVTVSS	226
XPA.15.194	Ab051	QVQLVQSGAEVKKPGSSVKVSCKAS	GGTFSSYA	ISWVRQAPGQGLEWMGG	IIPIFGTA	NYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC	AGKLYSRDYWYFDL	WGRGTLVTVSS	227
XPA.15.195	Ab052	EVQLVQSGAEVKKPGESLKISCKGS	GYRFTSYW	IGWVRQMPGRGLEWMGI	IYPGDSDT	RYSPSFQGQVTISVDKSISTAYLQWSSLKASDTAMYYC	ATHHASGRGLDP	WGQGTLVTVSS	228
XPA.15.196	Ab053	QVQVVQSGAEVKKPGASVKVSCKAS	GYTFTGHY	MHWVRQAPGQGLEWMGW	INPNSGGT	NYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYC	ARGSSSSWPVYFYYMDV	WGKGSTVTVSS	229
XPA.15.	Ab054	QVQLVQSGAEVKK	GYTFTGHY	MHWVRQAPGQGLEWMGW	INPNSGG	NYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYC	ARGSSSSWP	WGKGTTVTVSS	230

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
197		PGASVKVSCKAS			T		VYFYYMDV		
XPA.15.198	Ab055	QVQLVQSGAEVKKPGSSVKVSCKAS	GGTFSSYA	ISWVRQAPGQGLEWMGG	IIPIFGTA	NYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC	ARGQGWLRFYGMDV	WGQGTTVTVSS	231
XPA.15.199	Ab056	QVQLVQSGSEVKKPGASVKVSCKAS	GYTFTNSY	MHWVRQAPGQGLEWMGI	INPSAGT	SYAQKFQGRVTMTRDTSTSTVYMELSSLKSEDTAVYYC	ARDVGWLPGDY	WGQGTLVTVSS	232
XPA.15.200	Ab057	QMQLVQSGAEVKKPGESLKISCKGY	GYRFSDNW	IGWVRQMPGRGLEWMGI	IYPGDSET	RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC	ARHAPLAVAGMALGD	WGQGTLVTVSS	233
XPA.15.202	Ab058	QLQLQQWGAGLLKPSETLSLTCAVY	SGSFSGYY	YSWIRQSPGRGLEWIGD	ISHTGST	DYNPSLKTRVTISVDTSKNQFSLNLNSVTAADTAVYYC	ARDAPKGGSGLYLFDY	WGQGILVTVSS	234
XPA.15.203		QVQLVQSGAEVKKPGSSVKVSCKAS	GGTFSSYA	ISWVRQAPGQGLEWMGR	IIPILGIA	WYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYC	ARDSYSSGWYSHGPEYFQH	WGQGTLVTVSS	235
XPA.15.204	Ab059	EVQLVQSGAEVKKPGSSVKVSCKAS	GGTFSSYA	ISWVRQAPGQGLEWMGR	IIPIFGIA	NYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYC	AREPDYDFWNDAFDI	WGQGTMVTVSS	236
XPA.15.205		QVQLVQSGAEVKKPGSSVKVSCKAS	GYTFSSYA	ISWVRQAPGQGLEWMGG	IIPIFGTA	NYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC	ASHYYDFWSGYQYYYGMDV	WGQGTTVTVSS	237
XPA.15.206		QMQLVQSGAEVKKPGASVKVSCKAS	GYTFTSYA	MHWVRQAPGQRLEWMGW	INAGNGNT	RYSQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYC	ARYTSGSFDY	WGQGTLVTVSS	238
XPA.15.207	Ab060	QMQLVQSGAEVKKPGSSVKVSCKAS	GGTFSSYA	ISWVRQAPGQGLEWMGI	INPSGGST	SYAQKFQGRVTMTRDRSTSTVYMELSSLTSEDTAVYYC	VRDNHGWSFDY	WGQGTLVTVSS	239
XPA.15.208		QMQLVQSGAEVKKPGSSVKVSCKAS	GGTFSSYA	ISWVRQAPGQGLEWMGG	IIPIFGTA	NYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC	ATKGSDFWSGYYYYYYMDV	WGKGTTVTVSS	240
XPA.15.209	Ab061	QMQLVQSGAEVKKTGESLKISCQGY	GYRFTDNW	IGWVRQMPGRGLEWMGI	IYPGDSET	RYSPSFQGQVTISADKSISTAYLEWSSLKASDTAMYYC	ARHAPLAVAGMALGD	WGQGTLVTVSS	241
XPA.15.210		QVQLVQSGAEVKKPGSSVKVSCKAS	GGTFSSYA	ISWVRQAPGQGLEWMGG	IIPIFGTA	NYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC	ARGLPPKPYYDFWSGYWGYYYYGMDV	WGQGTTVTVSS	242
XPA.15.211	Ab062	QVQLQQWGAGLLKPSETLSLTCAVY	GGSFSGYY	WSWIRQPPGKGLEWIGE	INHSGST	NYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYC	ARGPSGWYIREFDY	WGQGTLVTVSS	243
XPA.15.212	Ab063	QVQLQQSGPGLVKPSQTLSLTCAIS	GDSVSSNSAA	WNWIRQSPSRGLEWLGR	TYYRSKWYT	DYALSVKSRITINPDTSKNQFSLHLNSVTPEDTAVYYC	AREGWLGYFDF	WGQGTLVTVSS	244
XPA.15.213	Ab064	QVQLVQSGAEVKKPGESLKISCKGS	GFSFPSYW	IGWVRQMPGKGLELVGI	IYPGDSDI	RYSPSFQGQVTISADTSISTVYLQWSSLQTTDTATYYC	ARGGFNWFDP	WGQGTLVTVSS	245
XPA.15.214	Ab065	QVQLVQSGAEVKKPGESLKISCKGS	GYSFTSYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC	ARHELGIDY	WGQGTLVTVSS	246
XPA.15.215	Ab066	EVQLVQSGAEVKKPGSSVKVSCKAS	GGTFSSYA	ISWVRQAPGQGLEWMGG	IIPIFGTA	NYAQKFQGRVTITADKSTSTAYMELSRLRSDDTAVYYC	ARDASYGGNSEGFDY	WGQGTLVTVSS	247

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
XPA.15.216	Ab067	EVQLVQSGAEVKKPGSSVKVSCKAS	GGTFSSYA	ISWVRQAPGQGLEWMGG	IIPIFGTA	NYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYC	ARASGDYDFWSGYYGAEYFQH	WGQGTLVTVSS	248
XPA.15.217	Ab068	EVQLVQSGAEVKQPGSSVKVSCKAS	GGSFNSYT	FSWVRQAPGQGLEWMGW	ISAYNGGTNYFA	NYALKFQGRVTMTTDTSTGTAYMELRSLRSDDTAVYYC	ARVRDSWSHEDYSYYYYMDV	WGKGTTVTVSS	249
XPA.15.218		QVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYA	MSWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNSLYLQMNSLRAEDTAVYYC	ARERVFPDYYDSIASNYPLDDI	WGQGTMVTVSS	250
XPA.15.219	Ab086	EVQLVETGGGVVRPGGSLRLSCAAS	GFTFGDYG	MSWVRQAPGKGLEWVSG	INWNGGST	GYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYC	ARDILGVEFDY	WGQGTLVTVSS	251
XPA.15.220		EVQLVQSGAEVKKPGESLKISCKGS	GYSFTSYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC	ARLGSGSYSFDY	WGQGTLVTVSS	252
XPA.15.221		EVQLVESGGGVVQPGMSLRLSCAAS	GFTFDDYA	MHWVRQAPGKGLEWVSS	ISWNSANI	VYADSVRGRFTISRDNAKNSLYLQMNSLRADDMALYYC	VKGDTTMIYYAMAV	WGQGTTVTVSS	253
XPA.15.222	Ab069	EVQLVQSGAEVKKPGESLKISCKGS	GYSFTSYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC	ARLGRGYYGMDV	WGQGTTVTVSS	254
XPA.15.223		QMQLVQSGAEVKKPGESLKISCKGS	GYSFTSYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC	ARWGPDAFDI	WGQGTMVTVSS	255
XPA.15.224		EVQLVESGGSVVQPGGSLRLSCAAS	GFTFSDYY	MSWIRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSENTLYLQMNSLRAEDTAVYYC	AKDDYDFWSGYYDPYYYGMDV	WGQGTTVTVSS	256
XPA.15.225		EVQLLESGGGLVQPGMSLRLSCAAS	GFTFDDYA	MHWVRQAPGKGLEWVSS	ISWNSANI	VYADSVRGRFTISRDNAKNSLYLQMNSLRADDMALYYC	VKGDTTMIYYAMAV	WGQGTTVTVSS	257
XPA.15.226	Ab070	EVQLVQSGAEVKKPGESLKISCKGS	GYSFTSYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTSYLQWSSLRASDTAMYYC	ARLGSGWYGNDY	WGQGTLVTVSS	258
XPA.15.227	Ab071	EVQLVQSGAEVKKPGESLKISCKGS	GYSFTSYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC	ARWDAGYSP	WGQGTLVTVSS	259
XPA.15.228	Ab072	QMQLVQSGAEVKKPGESLKISCKGS	GYSFTGYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTAYLQWSSLKVSDTAMYYC	GRISTPYAFDI	WGQGTMVTVSS	260
XPA.15.229	Ab073	QVQLQESGPGLVKPSGTLSLTCAVS	GGSISSSNW	WSWVRQPPGKGLEWIGE	IYHSGST	NYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYC	ARVGAAAAWFDP	WGQGTLVTVSS	261
XPA.15.230	Ab074	EVQLVQSGAEVKKPGESLKISCKGS	GYSFTSYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC	ARWDAGYSP	WGQGTLVTVSS	262
XPA.15.231		QMQLVQSGAEVKKPGESLKISCKGS	GYSFSSSW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADRSISTAYLQWSSLKASDTAMYYC	ARVGASGWTFDY	WGQGTLVTVSS	263
XPA.15.232	Ab075	EVQLVETGGGVVQPGRSLRLSCAAS	GFSFSSYD	MYWVRQAPGKGLEWVAV	ISYDGNDK	QYADSVKGRFTISRDNSKRTLYLQMDSLRTEDTATYYC	TREGNGREIDY	WGPGTLVTVSS	264
XPA.15.233		QVQLVQSGAEVRRPGASVKVSCEAS	GYTFHSYD	INWVRQATGQGLEWVGW	MNPNSGNI	DFAQKFQGRVTMTRNTSINTAYMELSSLRSDDTAVYYC	ARVNWNYGGTSDS	WGQGTLVTVSS	265

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
XPA.15.234		QVQLQESGPGLVKPSGTLSLTCAVS	GGSISSSNW	WSWVRQPPGKGLEWIGE	IYHSGST	NYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYC	ARVGVAAFDY	WGQGTLVTVSS	266
XPA.15.235		EVQLVESGGGVVQPGRSLRLSCAAS	GFTFSSYA	MHWVRQAPGKGLEWVAV	ISYDGSNK	YYADSVKGRFTISRDNSKNTLCLQMNSLRAEDTAVYYC	AREEAYGDAFDI	WGQGTMVTVSS	267
XPA.15.236		QMQLVQSGAEVKKPGESLKISCKGS	GYSFTSYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC	ARWGPDAFDI	WGQGTMVTVSS	268
XPA.15.237		EVQLVETGGGVVRPGRSLRLSCAAS	GFTFEDYA	MHWVRQGPGKGLEWVSS	ISWNGGFI	GYADSVKGRFTISRDNAKNSLYLQMNSLSAEDTALYYC	AKGASYDSYAAMDV	WGQGTTVTVSS	269
XPA.15.238		EVQLVESGGGVVQPGGSLRLSCAAS	GFTFSSYA	MSWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	AKDPRVVHRFDI	WGQGTMVTVSS	270
XPA.15.239		QLQLQESGPGLVKPSETLSLTCTVS	GGSFSTYY	WSWVRQAPGKGLEWIGN	IYYSGKT	NYNPSLESRVTISVDTSKNQFSLKLSSVTTADTAVYYC	ARDSFYFESSRSWNDLFDI	WGQGTMVTVSS	271
XPA.15.240		QLQLQESGPGLVKPSETLSLTCTVS	GGSFSTYY	WSWVRQAPGKGLEWIGN	IYYSGKT	NYNPSLGSRVTISVDTSKNQFSLKLSSVTAADTAVYYC	ARDSFYFESSRSWNDLFDI	WGQGTMVTVSS	272
XPA.15.241	Ab076	EVQLVESGGGVVQPGGSLRLSCAAS	GFTFDDYA	MHWVRQAPGKGLEWVSL	ISWDGGST	YYADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYC	AKARGVVIIDY	WGQGTLVTVSS	273
XPA.15.242		QLQLQESGPGLVKPSETLSLTCTVS	GGSFSTYY	WSWIRQAPGKGLEWIGN	IYYSGKT	NYNPSLESRVTISVDTSKNQFSLKLSSVTAADTAVYYC	ARDSFYFESSRSWNDLFDI	WGQGTMVTVSS	274
XPA.15.243	Ab077	EVQLVESGGGVVQPGGSLRLSCAAS	GFTFSSYW	MTWVRQAPGKGLEWVAN	INQDGSEK	HYVDSVKGRFTISRDNAKNSLYLQMNSLRGEDTAVYYC	ARGRGAWAFDY	WGQGTLVTVSS	275
XPA.15.244	Ab078	QVQLVQSGGGLVQPGGSLRLSCAAS	GFTFSSYS	MNWVRQAPGKGLEWVSS	ISSSSSYI	YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYC	ARDQGGELLGFTGYFDY	WGQGTLVTVSS	276
XPA.15.245	Ab079	QMQLVQSGAEMKKPGASVKVSCKAS	GYSFSDYG	ITWVRQAPGQGFEWMGW	ISGYNGNT	NYAQKFQDRVTMTTDTSTSTAYMELRSLKSDDTAVYFC	ARARGVWMFDN	WGQGTLVTVSS	277
XPA.15.246	Ab080	EVQLVESGGGVVQPGGSLRLSCAAS	GFTFDDYA	MHWVRQAPGKGLEWVSL	ISWDGGST	YYADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYC	AKARGVVIIDY	WGQGTLVTV88	278
XPA.15.247	Ab081	EVQLVETGGGVVQPGRSLRLSCAAS	GFTFSSYA	MHWVRQAPGKGLEWVAV	ISYDGSNK	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	ARHEWGFGMDV	WGQGTTVTVSS	279
XPA.15.248	Ab082	QMQLVQSGAEVKKPGESLKISCKGS	GYSFTSYW	IGWVRQMPGKGLEWMGI	IYPGDSDT	RYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYC	ARWGPDAFDI	WGQGTMVTVSS	280
XPA.15.249	Ab083	QVQLVESGGGLVQPGGSLRLSCAAS	GFTFSSYA	MSWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	AKDRVGAANGWFDP	WGQGTLVTVSS	281
XPA.15.250	Ab084	QVQLVESGGGLVQPGGSLRLSCAAS	GFTFKNYW	MTWVRQAPGKGLEWVAD	IKGDGSRQ	HYADSVKGRFTISRDNARNSLFLQMNSLRVEDTALYYC	ATDPPWDRDAFDL	WGQGTMVTVSS	282
XPA.15.272		QVQLVESGGGLVQPGGSLRLSCAAS	GFTFGGYW	MSWVRQAPGKGLEWVSN	IKQDGSEQ	YYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAIYYC	ARDRMDYIFDI	WGRGTLVTVSS	283
XPA.15.	Ab085	EVQLVESGGGVVQ	GFIFSSYG	MHWVRQVPDKGLEWVAG	ISLRGSD	YYADSVKGRFTISRDNSKNTLYLQMNNLRPDDTAVYYC	ARGFRWPVT	WGQGTLVTVSS	284

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
275		PGRSLRLSCAAS			N		PFDH		
XPA.15.282		QVQLQESGPGLVKPSGTLSLTCAVS	GGSISSSNW	WSWVRQPPGKGLEWIGE	IYHSGST	NYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYC	ARPDYSNYGGAFDY	WGQGTLVTVSS	285
XPA.15.284		QVQLQESGPGLVKPSGTLSLTCAVS	GGSISSSNW	WSWVRQPPGKGLEWIGE	IYHSGST	NYNPSLKSRVTISVDKSKNQFSLKLSSVTAADTAVYYC	ARVGAAAAWFDP	WGQGTLVTVSS	286
XPA.15.293		QLQLQESGPGLVKPSETLSLTCTVS	GGSFSTYY	WSWVRQAPGKGLEWIGN	IYYSGKT	NYNPSLESRVTISVDTSKNQFSLKLSSVTAADTAVYYC	ARDSFYFESSRSWNDLFDI	WGQGTMVTVSS	287
XPA-15-007_VH	Ab029	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSS-YG	MHWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARDRYSSGWYW-----SDY------	WGQGTLVTVSS	221
XPA-15-013_VH	Ab006	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-YA	MGWVRQAPGKGLEWVSS	ISGSGGTT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AR---HKGLQ---PLDY--------	WGQGTLVTVSS	179
XPA-15-017_VH	Ab017	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSS-YS	MNWVRQAPGKGLEWVSV	IY-SGDST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARQV-RDGDY--GDWFDP------	WGQGTLVTVSS	216
XPA-15-020_VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSS-YS	MNWVRQAPGKGLEWVSL	IYRDGST-	TYADSVRGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARES-TR------LRGSYYYGMDV	WGQGTLVTVSS	215
XPA-15-021_VH	Ab023	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-AW	MSWVRQAPGKGLEWVSA	IGTGGGT-	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AK---SRWLP---YFDY--------	WGQGTLVTVSS	193
XPA-15-022_VH	Ab024	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSD-YY	MSWIRRAPGKGLEWVSR	ISWNSGSI	GYADSLKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARER-G---------YGYDY------	WGQGTLVTVSS	192
XPA-15-023_VH	Ab025	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSNY-	MSWVRQAPGKGLEWVSG	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARVG-SSGWYY------FDY--------	WGQGTLVTVSS	171
XPA-15-026_VH	Ab026	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-YV	ISWVRQAPGKGLEWVSA	ISGSGGST	EYPDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYC	----ARVG-LSGWYY------FDY--------	WGQGTLVTVSS	194

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
XPA-15-033 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSD-YY	MSWVRQAPGKGLEWVAV	ISYDGSNK	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	------AR--GS------SSFDY------	WGQGTLVTVSS	217
XPA-15-036 VH	Ab030	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YS	MNWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARD------SWELLGYDAFDI------	WGQGTLVTVSS	220
XPA-15-037 VH	Ab031	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSSNY-	MSWVRQAPGKGLEWVSS	I--SGGST	YYADSRKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARL------DWS------SGAFDI------	WGQGTLVTVSS	218
XPA-15-042 VH	Ab027	EVQLLESGGGLVQ PGGSLGLSCAAS	GFTFNN-YW	MSWVRQAPGKGLEWVSY	ISGSGRTI	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARVG-SSGWYY------FDY------	WGQGTLVTVSS	219
XPA-15-047 VH	Ab036	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSN-YA	MGWVRQAPGKGLEWVSS	ISGSGGTT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AR------HKGLQ------PLDY------	WGQGTLVTVSS	180
XPA-15-048 VH	Ab037	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YE	MNWVRQAPGKGLEWVSS	ISSSSRYA	DVANSVVGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AR------GEWLD------HFDY------	WGQGTLVTVSS	195
XPA-15-059 VH	Ab028	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFRN-YW	MTWVRQAPGKGLEWVAN	IKQDGSEK	YYVDSVKGRSTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARQV--G-------GGPFDI------	WGQGTLVTVSS	191
XPA-15-064 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSD-YY	MNWVRQAPGKGLEWVAL	ISYDGSNK	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTALYYC	----AS------QSTAFDI------	WGQGTLVTVSS	196
XPA-15-065 VH	Ab038	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSN-YA	MTWVRQAPGKGLEWVSY	IHAGGGT-	HYANSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AROL--HWEG------WGLGFDY---	WGQGTLVTVSS	183
XPA-15-066 VH	Ab004	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFRN-FA	MMWVRQAPGKGLEWVSG	ISWNSGSI	GYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARPS--GAYPT------PFDN------	WGQGTLVTVSS	223

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
XPA-15-068 VH	Ab013	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSSNY -	MSWVRQAPGKGLEWVSG	ISGSGGS T	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARVG-SSGWYY-----FDY--------	WGQGTLVTVSS	172
XPA-15-074 VH	Ab039	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YW	MSWVRQAPGKGLEWVSG	ISGSGGY T	SYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AKDS--SDWY-------TNS--------	WGQGTLVTVSS	222
XPA-15-075 VH	Ab009	EVQLLESGGGLVQ PWGSLRLSCAAS	GFTFSN-YA	MGWVRQAPGKGLEWVSS	ISGSGGT T	YYADSVKGRFTISRDNSKNTFYLQMNSLRAEDTAVYYC	----AR-----HKGLQ-----FLDY--------	WGQGTLVTVSS	181
XPA-15-077 VH	Ab040	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YW	MSWVRQAPGKGLEWVAV	ISKDGSS T	DYAHSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARDR--DWIP-------GDV--------	WGQGTLVTVSS	197
XPA-15-080 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YS	MNWVRQAPGKGLEWVSA	ISGSGGR T	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARDG--IWSA-------MDV--------	WGQGTLVTVSS	224
XPA-15-081 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSSNY -	MSWVRQAPGKGLEWVSG	ISGSGGS T	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARVG-SSGWYY-----FDY--------	WGQGTLVTVSS	173
XPA-15-082 VH	Ab041	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSN-YA	MTWVRQAPGKGLEWVSY	IHAGGGT -	HYANSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARDL--HWEG-------WGLGFDY--	WGQGTLVTVSS	186
XPA-15-086 VH	Ab042	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSN-YA	MTWVRQAPGKGLEWVSY	IHAGGGT -	HYANSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARDL--HWEG-------WGLGFDY--	WGQGTLVTVSS	184
XPA-15-088 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSN-YN	MQWVRQAPGKGLEWVSG	VSWNGSR T	HYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AREG-GSWDTT-GYYNYYYYG MDV	WGQGTLVTVSS	187
XPA-15-093 VH	Ab032	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSN-YA	MGWVRQAPGKGLEWVSS	ISGSGGT T	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AR-----HKGLQ-----PLDY--------	WGQGTLVTVSS	177

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
XPA-15-094_VH	Ab043	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-YA	MGWVRQAPGKGLEWVSS	ISGSGGTT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AR----HKGLQ----PLDY------	WGQGTLVTVSS	178
XPA-15-096_VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSS-YS	MNWVRQAPGKGLEWVAN	IKQDGRET	YYVDSVTGRFTISRDNSKNTLYLQMNSLRAEDTAMYYC	----TTDL-GRYYDILTGYYAPNY------	WGQGTLVTVSS	198
XPA-15-100_VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-YN	MQWVRQAPGKGLEWVSG	VSWNGSRT	HYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARER-GSWDTT-GYYNYYYYGMDV	WGQGTLVTVSS	188
XPA-15-102_VH	Ab044	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSNY-	MSWVRQAPGKGLEWVSG	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARVG-SSGWYY------FDY------	WGQGTLVTVSS	176
XPA-15-105_VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-YA	MGWVRQAPGKGLEWVSS	ISGSGGTT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARDH-SSSW------AFDY------	WGQGTLVTVSS	199
XPA-15-106_VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-YA	MTWVRQAPGKGLEWVSY	IHAGGGT-	HYANSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARDL-HWEG------WGLGFDY--	WGQGTLVTVSS	185
XPA-15-110_VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSS-YT	MDWVRQAPGKGLEWVSG	INWNGGST	GYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARVK-GYCSST-SCYFDYYYGMDV	WGQGTLVTVSS	200
XPA-15-111_VH	Ab045	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSS-YW	MSWVRQAPGKGLEWVSG	ISGSGGST	DYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AREL-PAFWS------AFDY------	WGQGTLVTVSF	225
XPA-15-115_VH	Ab046	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-YA	MGWVRQAPGKGLEWVSS	ISGSGGTT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AR----HKGLQ----PLDY------	WGQGTLVTVSS	182
XPA-15-120_VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSS-YW	MSWVRQAPGKGLEWVAN	IKQDGSEK	YYVDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARQV-G-------GGPFDI------	WGQGTLVTVSS	190

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
XPA-15-121 VH	Ab047	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YA	MSWVRQAPGKGLEWVSS	I--SGGST	YYADSRKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARH---ADQWP---GSWFDP------	WGQGTLVTVSS	202
XPA-15-122 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFRN-YA	MSWVRQAPGKGLEWVSS	I--SGGST	YYADSRKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AR------GGV---GDWFDP------	WGQGTLVTVSS	203
XPA-15-124 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFST-YV	MTWVRQAPGKGLEWVSV	IY-SGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARI---NWND---GGNFDY------	WGQGTLVTVSS	201
XPA-15-125 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSD-YY	MSWIRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARG---PVGI---SGNYDY------	WGQGTLVTVSS	205
XPA-15-127 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFNK-FA	VHWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ASDV-E-------GGYFHNSGPDH-	WGQGTLVTVSS	204
XPA-15-133 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YE	MNWVRQAPGKGLEWVAL	ISYDGSNK	DYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTALYYC	--AADLGI--GS-------GYFDY------	WGQGTLVTVSS	206
XPA-15-135 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSN-AW	MSWVRQAPGKGLEWVSA	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARD---PGGI---YDYFDY------	WGQGTLVTVSS	207
XPA-15-136 VH	Ab001	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YE	MNWVRQAPGKGLEWVSS	ISSSSSYI	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARV---RWYK-DSDAFDI------	WGQGTLVTVSS	209
XPA-15-139 VH	Ab018	EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YW	MSWVRQAPGKGLEWVSG	ISGSGGYI	HYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYC	----AREG--SGWL-------VDQ------	WGQGTLVTVSS	208
XPA-15-140 VH		EVQLLESGGGLVQ PGGSLRLSCAAS	GFTFSS-YT	MDWVRQAPGKGLEWVSS	ISSSSSYI	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	VREAWREN--NDWYE-------LDY------	WGQGTLVTVSS	212

Table 2
Heavy Chain Sequences

Name	Ab #	H-FR1	H-CDR1	H-FR2	H-CDR2	H-FR3	H-CDR3	H-FR4	SEQ ID NO:
XPA-15-143 VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-YA	MNWVRQAPGKGLEWVAH	INQDGSEK	YYVESVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----GKLR--GG------AYNDY---------	WGQGTLVTVSS	210
XPA-15-145 VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSN-YA	MTWVRQSPGKGLEWVSV	ISGSGGTT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AKAK--GS------QVFDY---------	WGQGTLVTVSS	211
XPA-15-159 VH	Ab015	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSSNY-	MSWVRQAPGKGLEWVSG	ISGSGGST	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARVG-SSGWYY------FDY---------	WGQGTLVTVSS	174
XPA-15-163 VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFTN-YN	MIWVRQAPGKGLEWVSG	VSWNGSRT	HYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARER--GSWDTT-GYYNYYYYGMDV	WGQGTLVTVSS	189
XPA-15-167 VH		EVQLLESGGGLVQPGGSLRLSCAAS	GFTFDD-YG	MSWVRQAPGKGLEWVSF	ISGSGGST	NYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARVG-SSGWYY------FDY---------	WGQGTLVTVSS	213
XPA-15-169 VH	Ab034	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSS-YW	MSWVRQAPGKGLEWVSS	I--SGGST	YYADSRKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----AREV--EYSS-SWGAFDI---------	WGQGTLVTVSS	214
XPA-15-171 VH	Ab016	EVQLLESGGGLVQPGGSLRLSCAAS	GFTFSD-YY	MSWIRQAPGKGLEWVSA	ISGSGGGT	YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC	----ARVG-SSGWYY------FDY---------	WGQGTLVTVSS	175
XPA.15.196	Ab053	QVQLVQSGAEVKKPGASVKVSCKAS	GYTFTGHY	MHWVRQAPGQGLEWMGW	INPNSGGT	NYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYC	ARGSSSSWPVYFYYMDV	WGKGSTVTVSS	303

Table 3

Clone No.	Antibody No.	Light Chain SEQ ID NO:	Heavy Chain SEQ ID NO:
XPA.015.172		20	151
XPA.015.173	Ab087	18	169
XPA.015.174		19	170
XPA.015.175	Ab019	1	160
XPA.015.176	Ab088	2	153
XPA.015.177		3	159
XPA.015.178	Ab089	4	154
XPA.015.179		5	161
XPA.015.181	Ab010*	6	163
XPA.015.182		7	164
XPA.015.183	Ab020	8	155
XPA.015.184		9	162
XPA.015.185	Ab003	10	157
XPA.015.186		11	165
XPA.015.187		12	166
XPA.015.188	Ab008	13	156
XPA.015.189		14	152
XPA.015.190	Ab002	15	167
XPA.015.191		16	168
XPA.015.192		17	158
XPA.015.006	Ab021	74	288
XPA.015.007	Ab029	52	221
XPA.015.009	Ab022	46	289
XPA.015.013	Ab006	43	179
XPA.015.017	Ab017	45	216
XPA.015.019		72	290
XPA.015.020		44	215
XPA.015.021	Ab023	73	193
XPA.015.022	Ab024	71	192
XPA.015.023	Ab025	70	171
XPA.015.026	Ab026	75	194
XPA.015.033		47	217
XPA.015.036	Ab030	50	220
XPA.015.037	Ab031	48	218
XPA.015.042	Ab027	49	219
XPA.015.043		76	291
XPA.015.047	Ab036	51	180
XPA.015.048	Ab037	77	195
XPA.015.059	Ab028	79	191
XPA.015.062		78	292
XPA.015.064		80	196
XPA.015.065	Ab038	83	183
XPA.015.066	Ab004	57	223
XPA.015.068	Ab013	81	172
XPA.015.074	Ab039	53	222
XPA.015.075	Ab009	55	181
XPA.015.077	Ab040	84	197

Table 3

XPA.015.080		58	224
XPA.015.081		82	173
XPA.015.082	Ab041	56	186
XPA.015.085	Ab011	54	293
XPA.015.086	Ab042	85	184
XPA.015.088		86	187
XPA.015.093	Ab032	21	177
XPA.015.094	Ab043	23	178
XPA.015.096		22	198
XPA.015.099		59	294
XPA.015.100		26	188
XPA.015.102	Ab044	60	176
XPA.015.105		97	199
XPA.015.106		24	185
XPA.015.110		148	200
XPA.015.111	Ab045	62	225
XPA.015.115	Ab046	61	182
XPA.015.120		149	190
XPA.015.121	Ab047	28	202
XPA.015.122		29	203
XPA.015.124		27	201
XPA.015.125		31	205
XPA.015.127		30	204
XPA.015.133		32	206
XPA.015.135		33	207
XPA.015.138	Ab001	35	209
XPA.015.139	Ab018	34	208
XPA.015.140		39	212
XPA.015.141		37	295
XPA.015.142		63	296
XPA.015.143		36	210
XPA.015.144	Ab033	65	297
XPA.015.145		38	211
XPA.015.146		64	298
XPA.015.154		66	299
XPA.015.155		68	300
XPA.015.158	Ab014	67	301
XPA.015.159	Ab015	40	174
XPA.015.163		150	189
XPA.015.165	Ab049	69	302
XPA.015.167		41	213
XPA.015.169	Ab034	42	214
XPA.015.171	Ab016	151	175
XPA.015.193	Ab050	87	226
XPA.015.194	Ab051	88	227
XPA.015.195	Ab052	89	228
XPA.015.196	Ab053	90	229 (303)
XPA.015.197	Ab054	91	230
XPA.015.198	Ab055	92	231
XPA.015.199	Ab056	93	232

Table 3

XPA.015.200	Ab057	94	233
XPA.015.201		95	---
XPA.015.202	Ab058	96	234
XPA.015.203		97	235
XPA.015.204	Ab059	98	236
XPA.015.205		99	237
XPA.015.206		100	238
XPA.015.207	Ab060	101	239
XPA.015.208		102	240
XPA.015.209	Ab061	103	241
XPA.015.210		---	242
XPA.015.211	Ab062	104	243
XPA.015.212	Ab063	105	244
XPA.015.213	Ab064	106	245
XPA.015.214	Ab065	107	246
XPA.015.215	Ab066	108	247
XPA.015.216	Ab067	109	248
XPA.015.217	Ab068	110	249
XPA.015.218		111	250
XPA.015.219	Ab086	112	251
XPA.015.220		113	252
XPA.015.221		114	253
XPA.015.222	Ab069	115	254
XPA.015.223		116	255
XPA.015.224		117	256
XPA.015.225		118	257
XPA.015.226	Ab070	119	258
XPA.015.227	Ab071	120	259
XPA.015.228	Ab072	121	260
XPA.015.229	Ab073	122	261
XPA.015.230	Ab074	123	262
XPA.015.231		124	263
XPA.015.232	Ab075	125	264
XPA.015.233		126	265
XPA.015.234		127	266
XPA.015.235		128	267
XPA.015.236		129	268
XPA.015.237		130	269
XPA.015.238		131	270
XPA.015.239		132	271
XPA.015.240		---	272
XPA.015.241	Ab076	133	273
XPA.015.242		134	274
XPA.015.243	Ab077	135	275
XPA.015.244	Ab078	136	276
XPA.015.245	Ab079	137	277
XPA.015.246	Ab080	138	278
XPA.015.247	Ab081	139	279
XPA.015.248	Ab082	140	280
XPA.015.249	Ab083	141	281

Table 3

XPA.015.250	Ab084	142	282
XPA.015.272		143	283
XPA.015.275	Ab085	144	284
XPA.015.282		145	285
XPA.015.284		146	286
XPA.015.293		147	287