

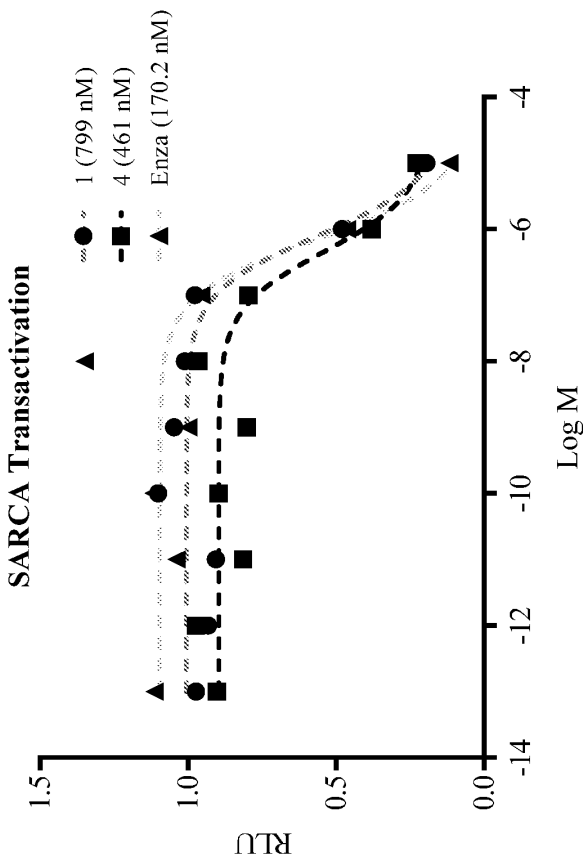


Figure 1

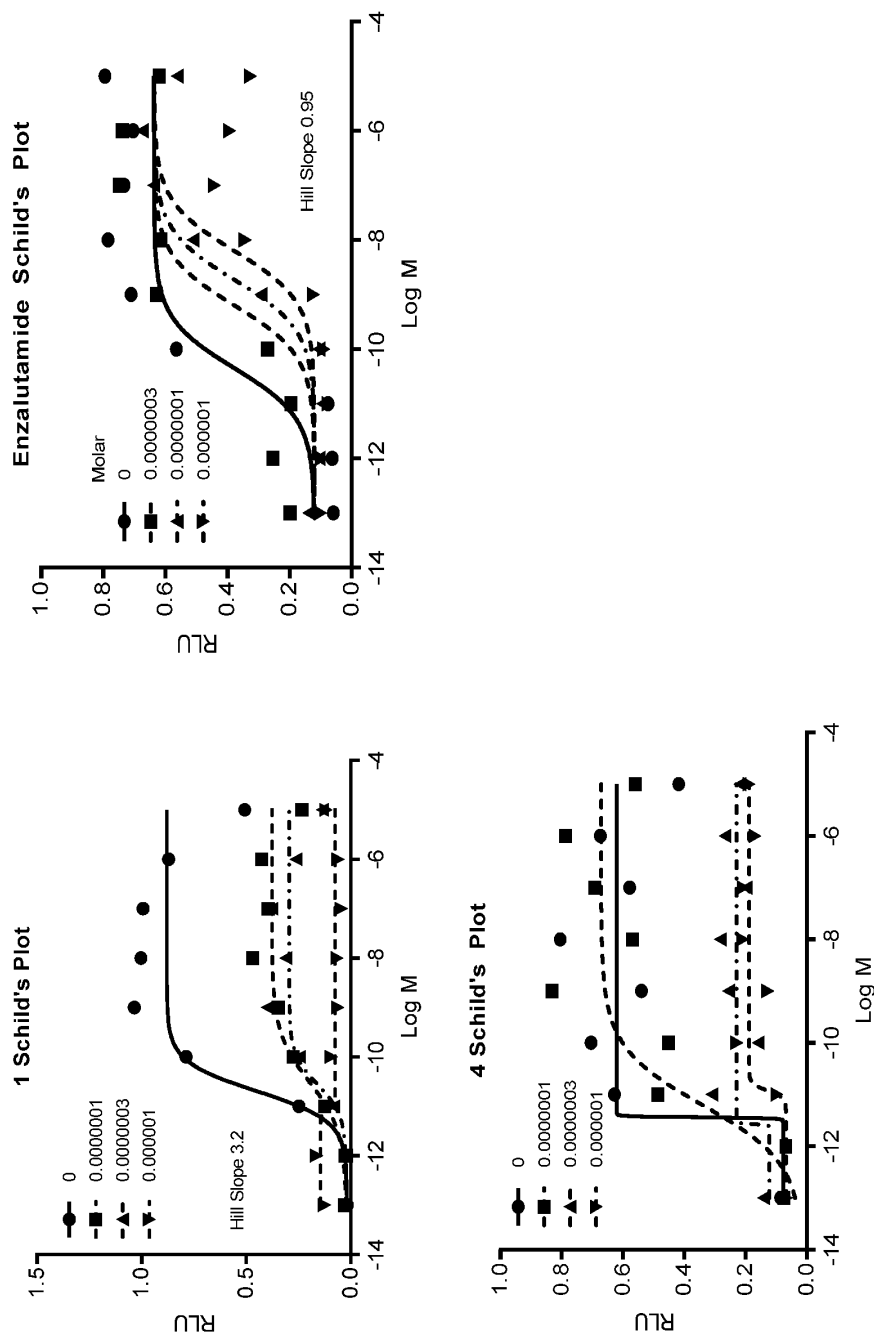
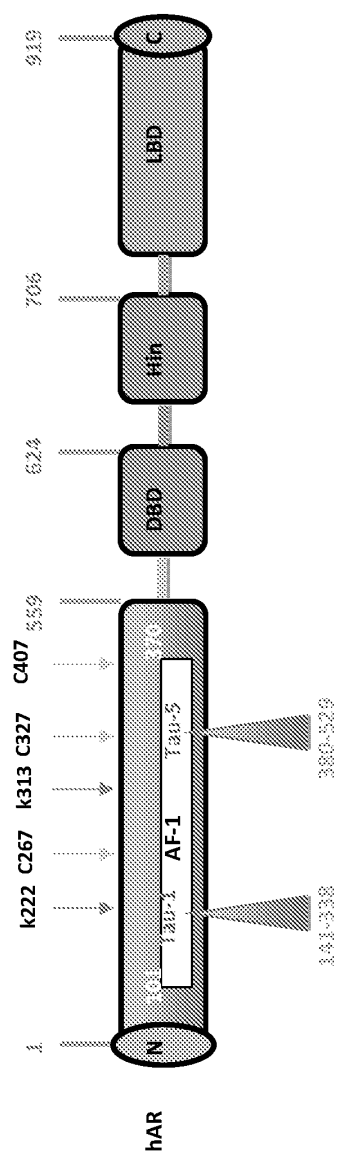


Figure 2



High	androgen receptor [OS=Homo sapiens]	0	3102.03
	Annotated Sequence	M.Wt	Positions in Protein
Vehicle	[K].STEDTAEYSPFKGGYTK.[G]	1880.85486	[302-318]
1	[K].STEDTAEYSPFKGGYTK.[G]	2218.93396	[302-318]
Vehicle	[R].GDCMYAPLLGVPPAVRPTPCAPLAECK.[G]	2785.3544	[265-291]
1	[R].GDCMYAPLLGVPPAVRPTPCAPLAECK.[G]	3783.59678	[265-291]

Figure 3

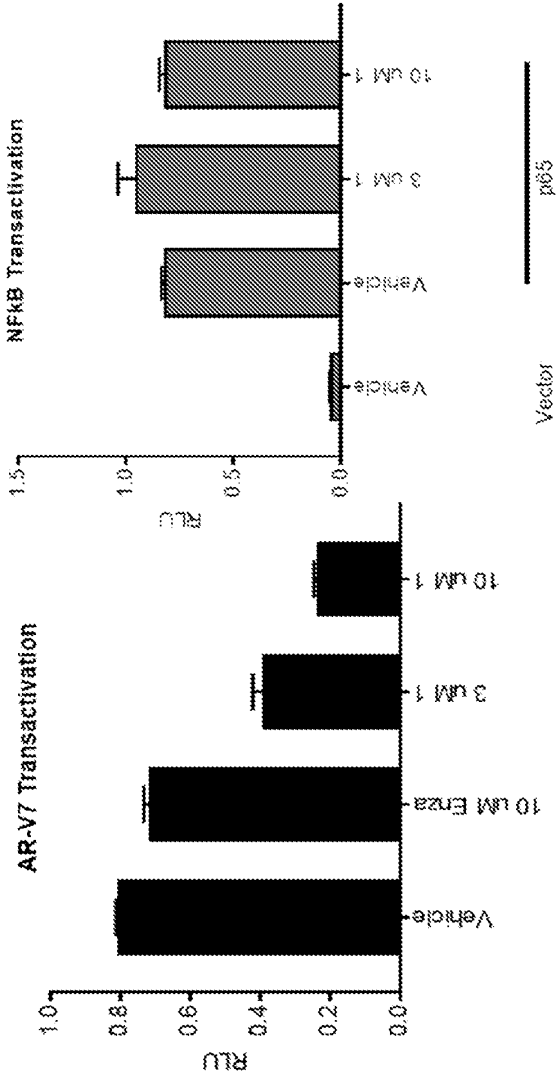


Figure 4

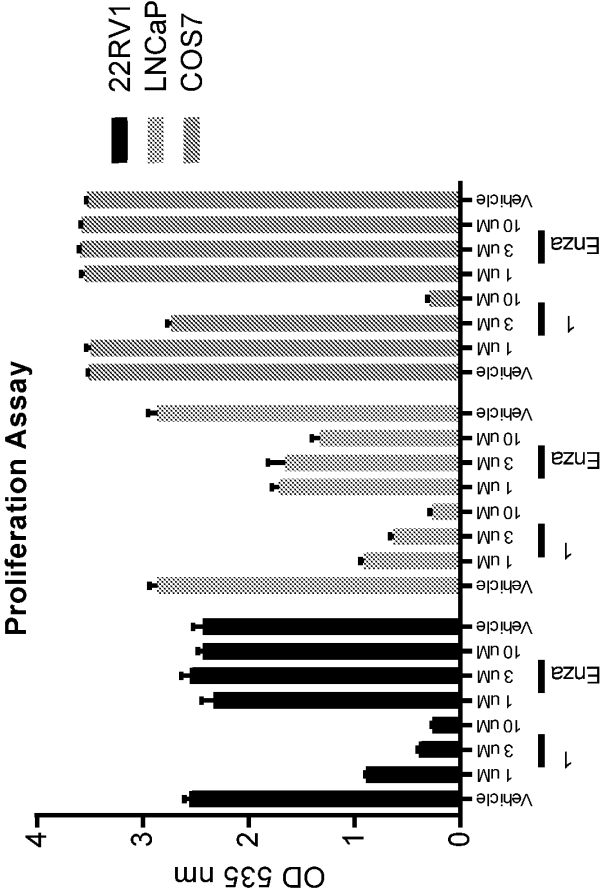


Figure 5

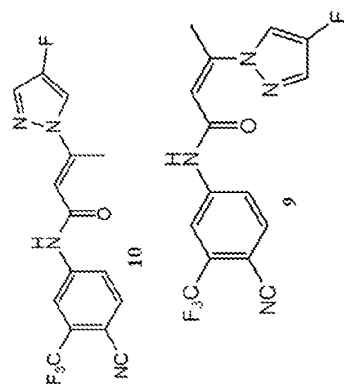
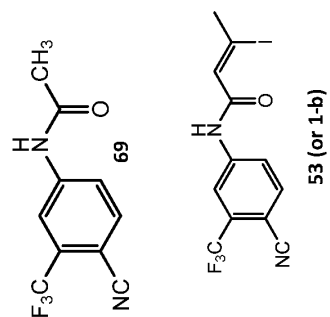
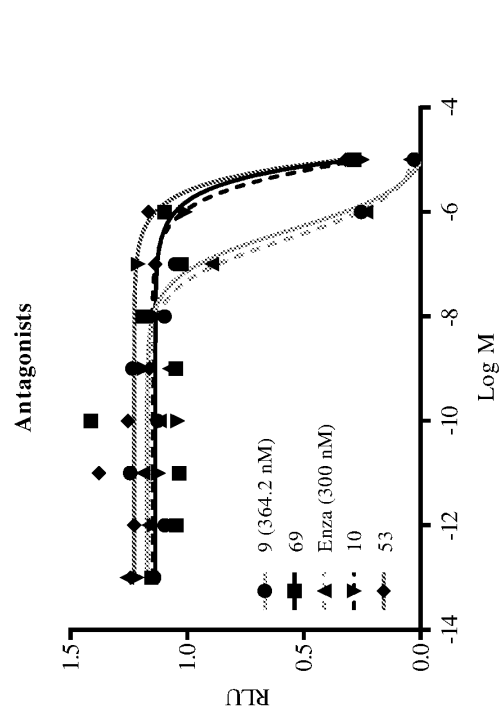


Figure 6

[illegible]

Figure 7

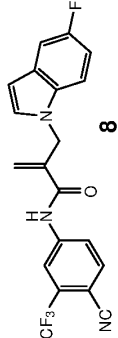
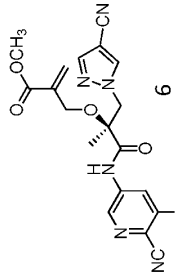
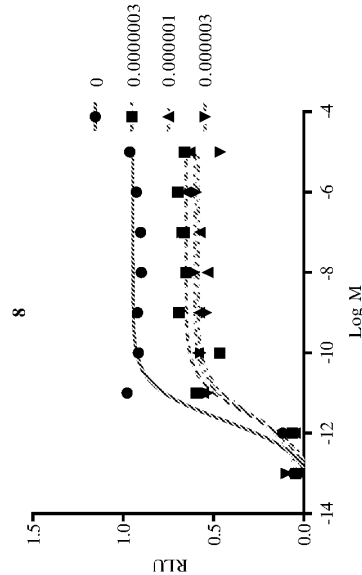
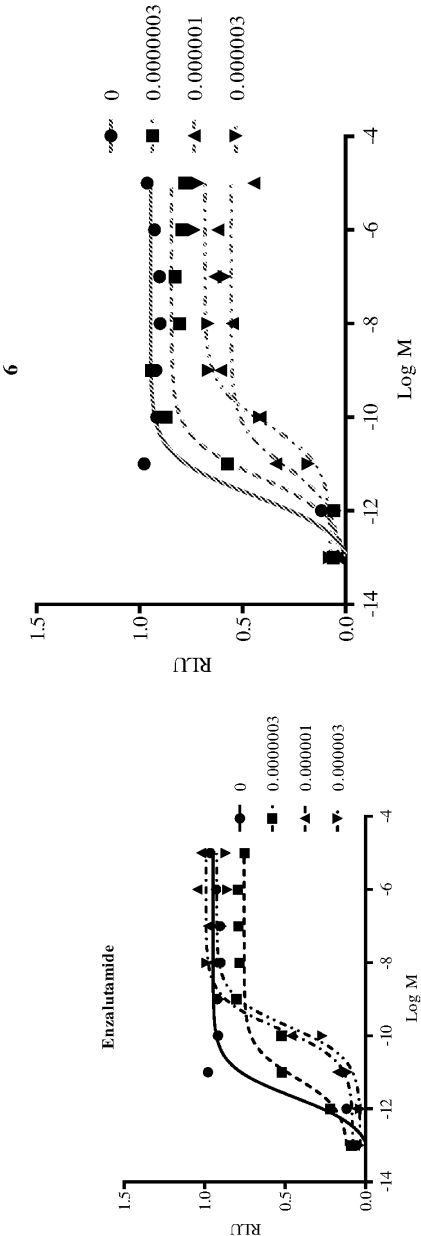


Figure 8

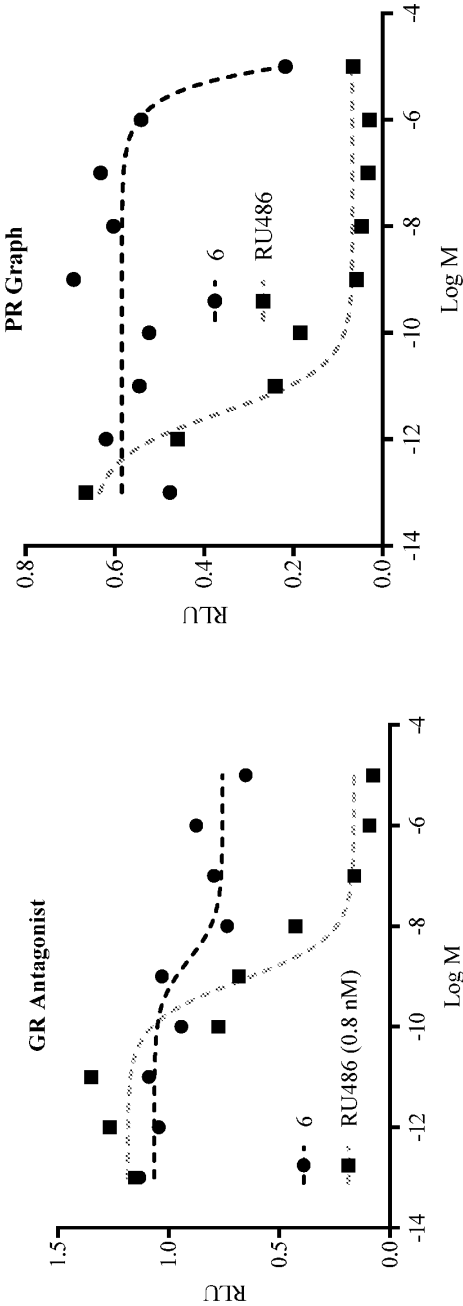
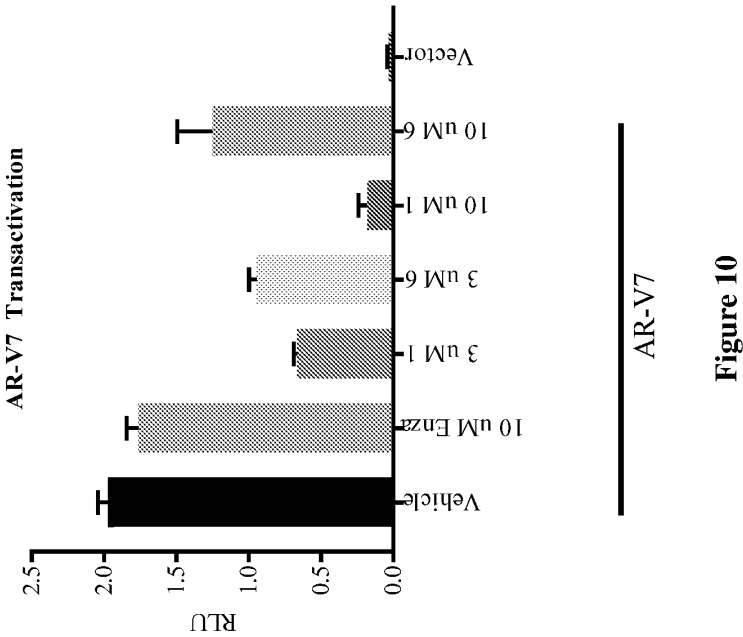


Figure 9



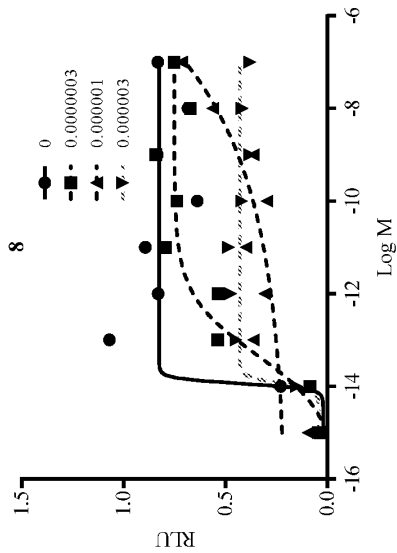
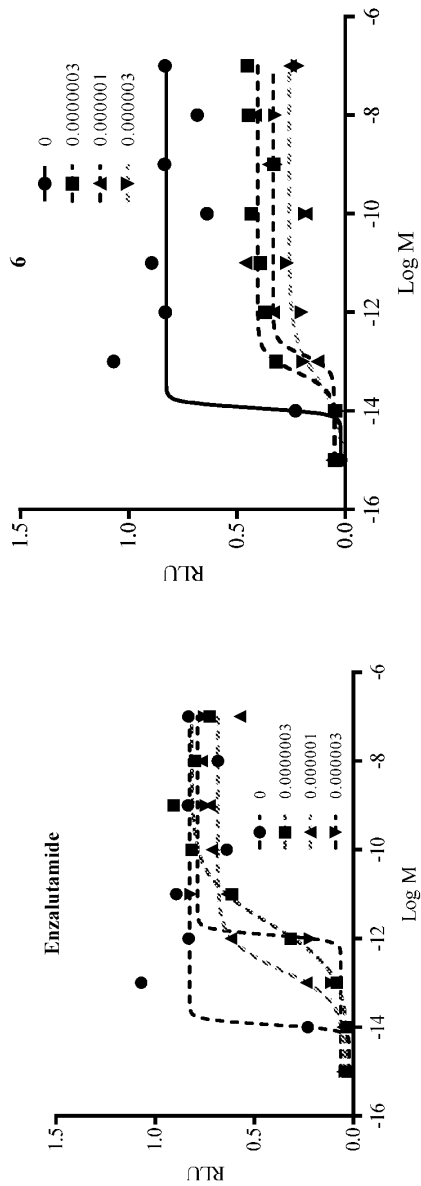


Figure 11

AR AF-1 + **1** (covalent antagonist)

FALSE	High	[K]: STD ^{TA} TS ^{SP} K ⁺ [G]			1374.606
FALSE	High	[K]: STD ^{TA} TS ^{SP} KGGV ^{TK} [G]			1880.855
FALSE	High	[K]: GSLLD ^S SAGK ST STD ^{TA} TS ^{SP} K ⁺ [G]			2318.067
FALSE	High	[K]: GSLLD ^S SAGK ⁺ [S]			962.4789
FALSE	High	[K]: GLEGLGCGSAAAGSSGTL ^{EP} SL ^{YK} [S]	1xNarayanan1 [C9]		3280.509
FALSE	High	[R]: AREASGAP ^{TS} KONYLG ^{GT} STIS ^{DN} AK ⁺ [E]			2698.291
FALSE	High	[K]: AV ^{SV} SMGLGV ^{EA} LEHLS ^{PG} QLR ⁺ [G]			2379.234
FALSE	High	[K]: AV ^{SV} SMGLGV ^{EA} LEHLS ^{PG} QLR ⁺ [G]	1xOxidation [M6]		2395.229
FALSE	High	[K]: DLSEASTM ^{LI} QQOQOQ ^{EA} VESS ^{SS} GR ⁺ [A]			3007.427
FALSE	High	[K]: DLSEASTM ^{LI} QQOQOQ ^{EA} VESS ^{SS} GR ⁺ [A]	1xOxidation [M9]		3023.422
FALSE	High	[K]: DNYLG ^{GT} STIS ^{DN} AKELCK ⁺ [A]			1555.723
FALSE	High	[K]: DNYLG ^{GT} STIS ^{DN} AKELCK ⁺ [A]			2028.954
FALSE	High	[R]: DYN ^{EP} ILALAGPPPP ^{PP} PPH ^{PH} AR ⁺ [I]			2618.33
FALSE	High	[R]: EASGAP ^{TS} SK ⁺ [D]			934.4476
FALSE	High	[R]: EASGAP ^{TS} SKONYLG ^{GT} STIS ^{DN} AK ⁺ [E]			2471.153
FALSE	High	[R]: EASGAP ^{TS} SKONYLG ^{GT} STIS ^{DN} AKELCK ⁺ [A]			2944.384
FALSE	High	[R]: EASGAP ^{TS} SKONYLG ^{GT} STIS ^{DN} AKELCK ⁺ [A]	1xNarayanan1 [C/K]		3282.463
FALSE	High	[R]: GDCM ^{AP} ILGV ^{PP} AV ^{VR} PT ^{CP} AC ^{IA} ELCK ⁺ [G]			2769.359
FALSE	High	[R]: GDCM ^{AP} ILGV ^{PP} AV ^{VR} PT ^{CP} AC ^{IA} ELCK ⁺ [G]	1xOxidation [M4]		2785.354
FALSE	High	[R]: GDCM ^{AP} ILGV ^{PP} AV ^{VR} PT ^{CP} AC ^{IA} ELCK ⁺ [G]	1xNarayanan1 [N-Term]; 1xNarayanan1 [C3]		3107.439
FALSE	High	[R]: GDCM ^{AP} ILGV ^{PP} AV ^{VR} PT ^{CP} AC ^{IA} ELCK ⁺ [G]	1xOxidation [M4]; 1xNarayanan1 [N-Term]; 1xNarayanan1 [C3]		3123.434
FALSE	High	[R]: GDCM ^{AP} ILGV ^{PP} AV ^{VR} PT ^{CP} AC ^{IA} ELCK ⁺ [G]	Narayanan1 [C]; 1xNarayanan1 [N-Term]		3445.518
FALSE	High	[K]: GLEGLGCGSAAAGSSGTL ^{EP} SL ^{YK} [S]			2942.433

Figure 12

AR AF-1 + 4 (covalent antagonist)

FALSE	High	[K].GSLDDDSAGK.[S]		962.4789
FALSE	High	[K].GSLDDDSAGKSTEDTAESYSPK.[G]		2318.067
FALSE	High	[K].LENPLDYGSAAWAAAAQCR.[Y]		2006.939
FALSE	High	[K].LENPLDYGSAAWAAAAQCR.[Y]	1xNarayanan4 [C18]	2352.023
FALSE	High	[R].IKLENPLDYGSAAWAAAAQCR.[Y]		2248.118
FALSE	High	[R].IKLENPLDYGSAAWAAAAQCR.[Y]	1xNarayanan4 [C20]	2593.202
FALSE	High	[K].SGALDEAAAYQSR.[D]		1338.628
FALSE	High	[K].STEDTAESYSPK.[G]		1374.606
FALSE	High	[K].STEDTAESYSPKGGYTK.[G]		1880.855
FALSE	High	[K].GGYTKGLESGSGSAAAGSSGTLELPSTLSLYK.[S]	1xNarayanan4 [K5]; 1xNarayanan4 [N-Term]	3793.763
FALSE	High	[R].GDCNWPALLGVPPAVRPTPCAPLAECK.[G]	1xNarayanan4 [C3]; 1xNarayanan4 [N-Term]	3114.443
FALSE	High	[K].AVSVSMGLGVEALEHLSPEQLR.[G]		2379.234
FALSE	High	[K].AVSVSMGLGVEALEHLSPEQLR.[G]	1xOxidation [M6]	2395.229
FALSE	High	[K].DILSEASTMQLLQQQQEAVSEGSSGR.[A]		3007.427
FALSE	High	[K].DILSEASTMQLLQQQQEAVSEGSSGR.[A]	1xOxidation [M9]	3023.422
FALSE	High	[K].DNYLGGTSTISDNALCK.[E]		1555.723
FALSE	High	[K].DNYLGGTSTISDNALCK.[A]		2028.954
FALSE	High	[R].DYNFPLALAGPPPPPPHPPHAR.[I]		2618.33
FALSE	High	[R].EASGAPTSSKONYLGGTSTISDNALCK.[E]		2471.153
FALSE	High	[R].EASGAPTSSKONYLGGTSTISDNALCK.[A]		2944.384
FALSE	High	[K].ELCKAVSVSMGLGVEALEHLSPEQLR.[G]		2852.464
FALSE	High	[R].GDCNWPALLGVPPAVRPTPCAPLAECK.[G]		2769.359
FALSE	High	[R].GDCNWPALLGVPPAVRPTPCAPLAECK.[G]	1xOxidation [M4]	2785.354

Figure 13

AR-LBD + 1

Master	Accession	Description	Coverage [%]	# Razor Pe
Master Pr	P10275	androgen receptor [OS=Homo sapiens]	18	0
Checked	Confidence	Annotated Sequence	Modifications	Theo. MH-
FALSE	High	[K].STEDTAEYSPFK.[G]		1374.606
FALSE	High	[K].LLDSVQPIAR.[E]		1111.647
FALSE	High	[K].LENPLDYGSAWAAAAAQC.[Y]		2006.939
FALSE	High	[K].GLEGESLGCSGSAAGSGTLELPSTLSLYK.[S]		2942.43
FALSE	High	[R].DYNNFPLALAGPPPPPPHPPHAR.[I]		2618.33
FALSE	High	[K].DNYLGGTSTISDNK.[E]		1555.723
FALSE	High	[K].DILSEASTMQLLQQQQEAVSEGSSSGR.[A]		3007.427
FALSE	High	[K].AVSVSMGLGVEALEHLSPGEQLR.[G]	1xOxidation [M6]	2395.229
FALSE	High	[K].AVSVSMGLGVEALEHLSPGEQLR.[G]		2379.234

AR-LBD + 4

Master	Accession	Description	Coverage [%]	# Razor Pe
Master Pr	P10275	androgen receptor [OS=Homo sapiens]	11	0
Checked	Confidence	Annotated Sequence	Modifications	Theo. MH-
FALSE	High	[K].LENPLDYGSAWAAAAAQC.[Y]		2006.939
FALSE	High	[K].GLEGESLGCSGSAAGSGTLELPSTLSLYK.[S]		2942.43
FALSE	High	[K].DNYLGGTSTISDNK.[E]		1555.723
FALSE	High	[K].AVSVSMGLGVEALEHLSPGEQLR.[G]	1xOxidation [M6]	2395.229
FALSE	High	[K].AVSVSMGLGVEALEHLSPGEQLR.[G]		2379.234
FALSE	High	[K].GSLDDDSAGK.[S]		962.4789

Figure 14

4 MLM

Phase I						
Time	analyte(x EG)		IS (x EG)	Anal/IS	Time	Anal/IS %
0	3940694	2755049	1.43		0	1.430 100%
5	2906450	2947249	0.99		5	0.986 69%
10	2632336	2337707	1.13		10	1.126 79%
30	2108648	1886563	1.12		30	1.118 78%
60	1046659	778271.1	1.34		60	1.345 94%

4 MLM

Phase I & II						
Time	analyte(x EG)		IS (x EG)	Anal/IS	Time	Anal/IS %
0	4711970	5035823	0.93569		0	0.936 100%
5	3497147	3450159	1.013619		5	1.014 108%
10	3696696	3152550	1.172605		10	1.173 125%
30	2041952	1932637	1.056562		30	1.057 113%
60	2202823	2000177	1.101314		60	1.101 118%

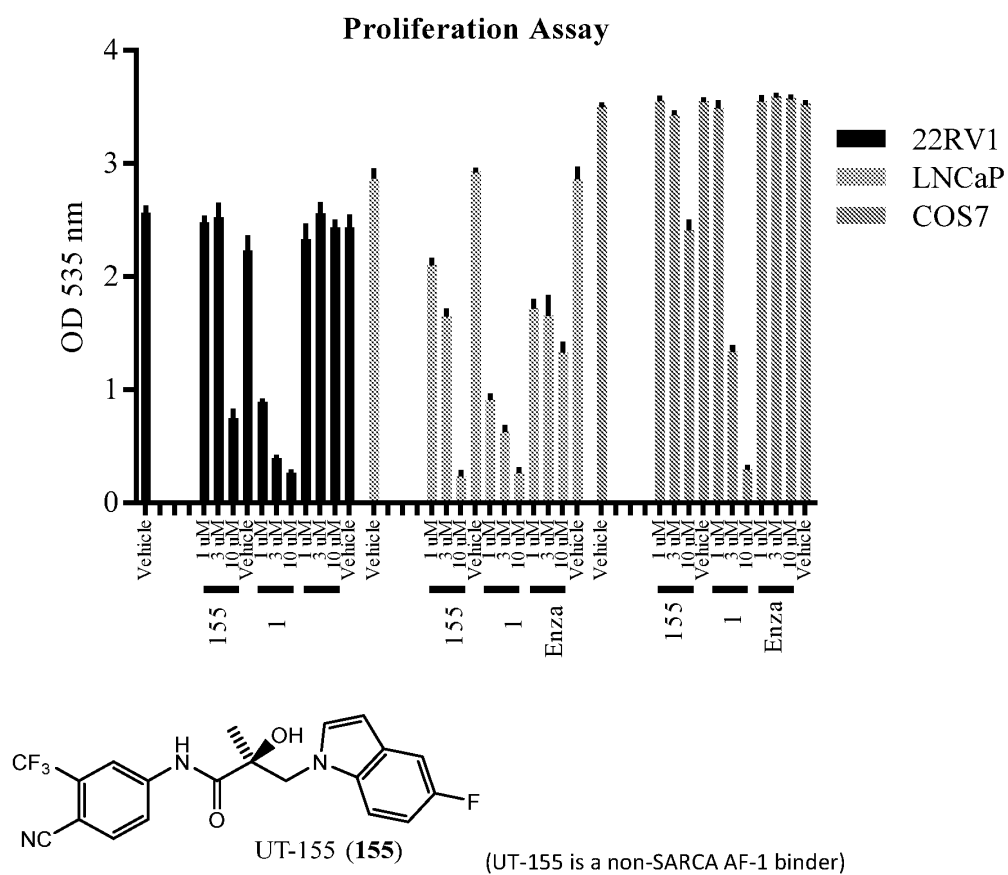
6 MLM

Phase I						
Time	analyte(x EG)		IS (x EG)	Anal/IS	Time	Anal/IS %
0	163845.8	566517.3	0.29		0	0.289 100%
5	588504.7	885265.5	0.66		5	0.665 230%
10	510986	606761	0.84		10	0.842 291%
30	36272.75	24022.66	1.51		30	1.510 522%
60	12995.89	176900.4	0.07		60	0.073 25%

6 MLM

Phase I & II						
Time	analyte(x EG)		IS (x EG)	Anal/IS	Time	Anal/IS %
0	4248167	3184143	1.334163		0	1.334 100%
5	1737176	2138713	0.812253		5	0.812 61%
10	1019967	753990.1	1.352759		10	1.353 101%
30	224536.5	74458.7	3.015585		30	3.016 226%
60	31116.22	11862.55	2.623064		60	2.623 197%

Figure 15

**Figure 16**

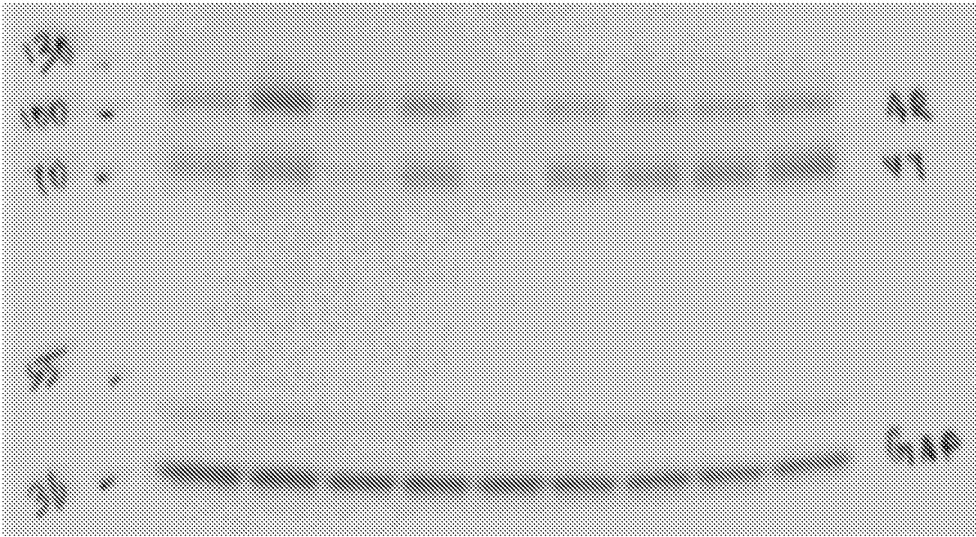


Figure 17

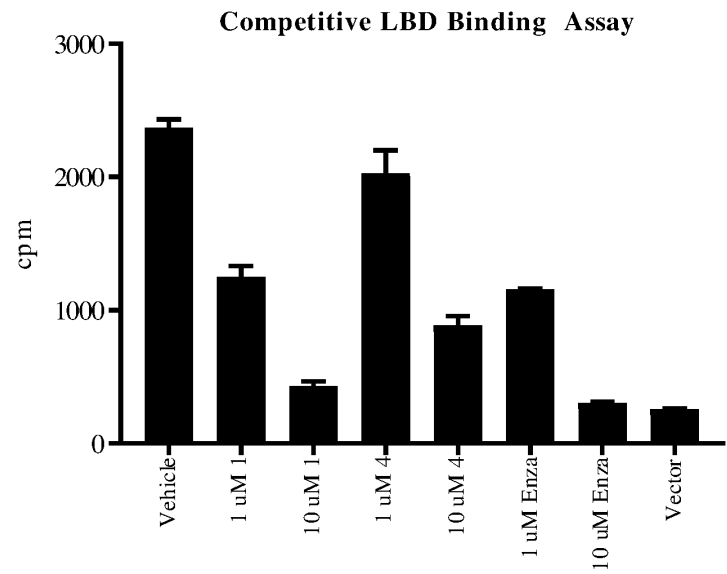


Figure 18

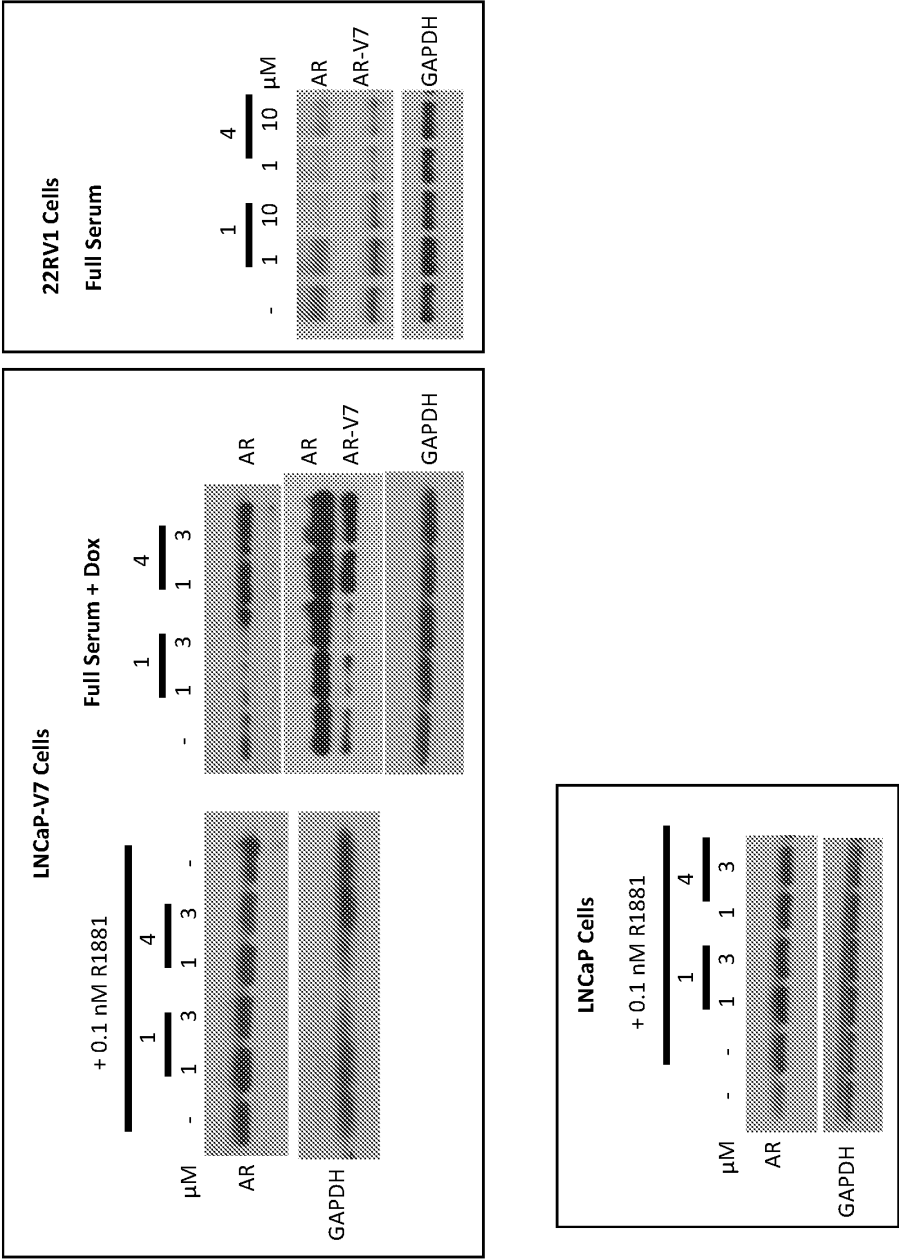
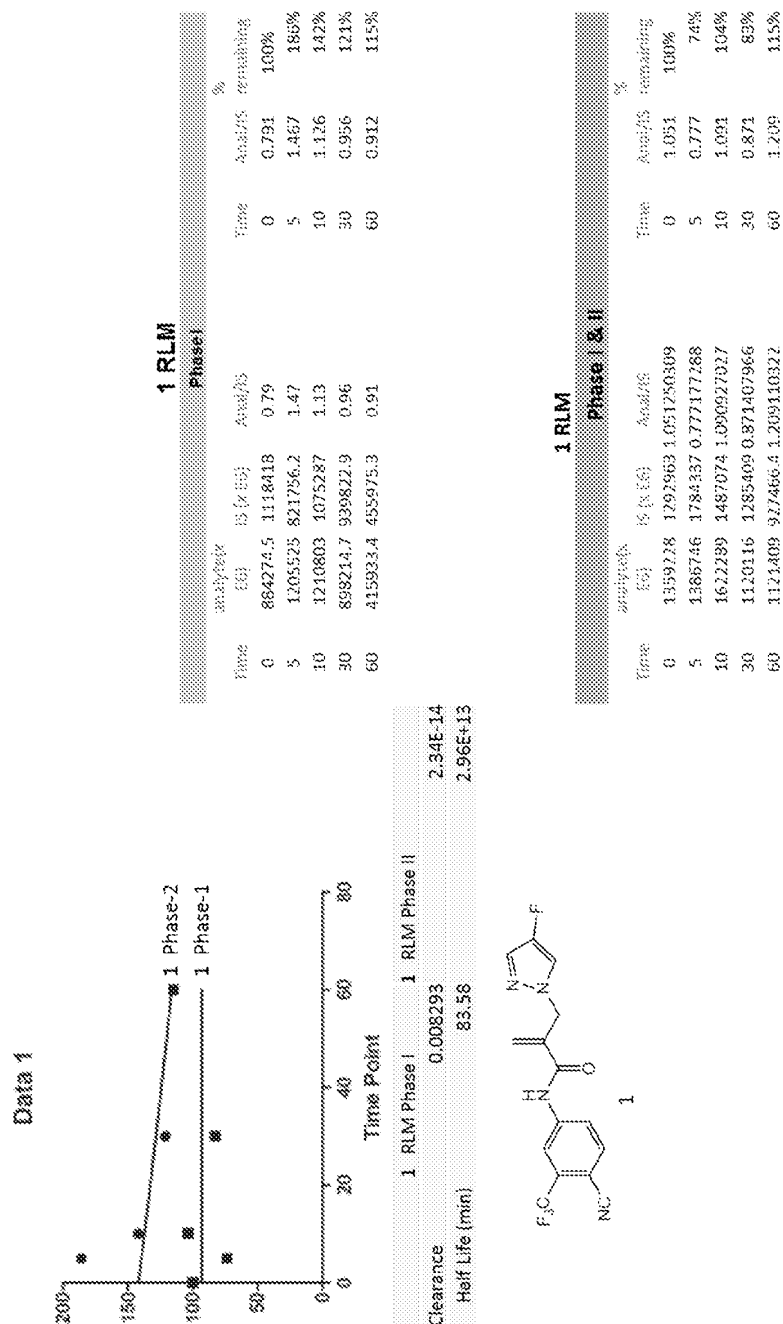


Figure 19



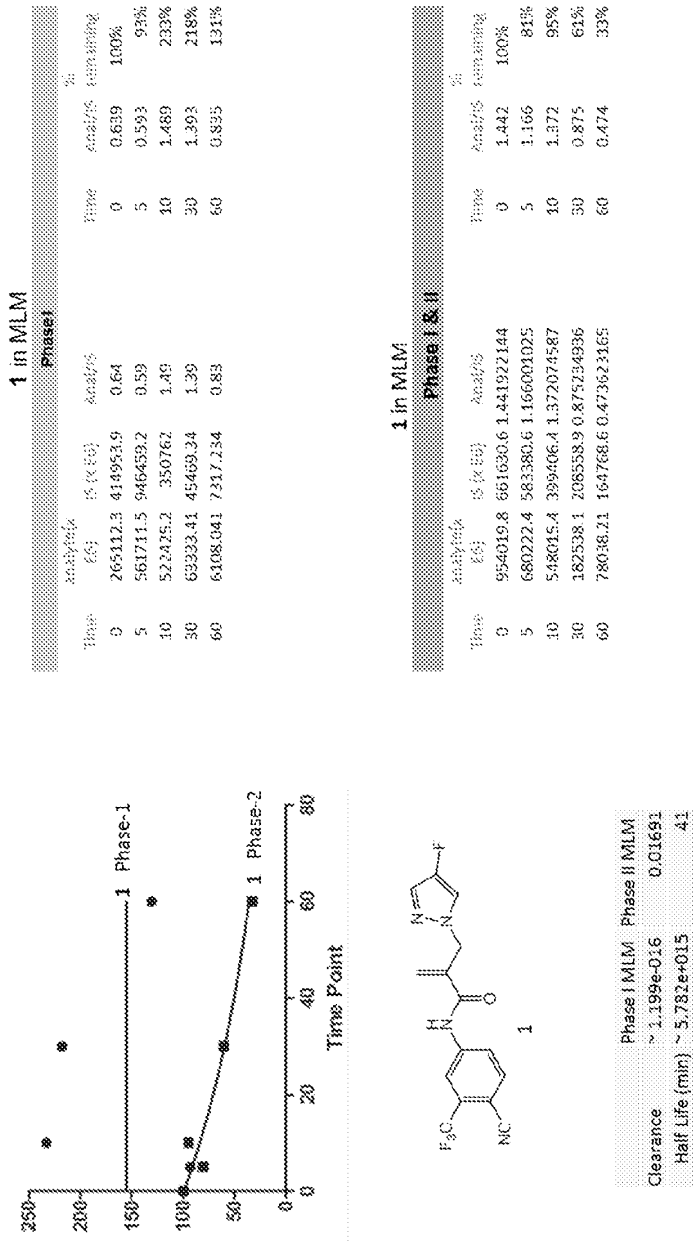


Figure 21

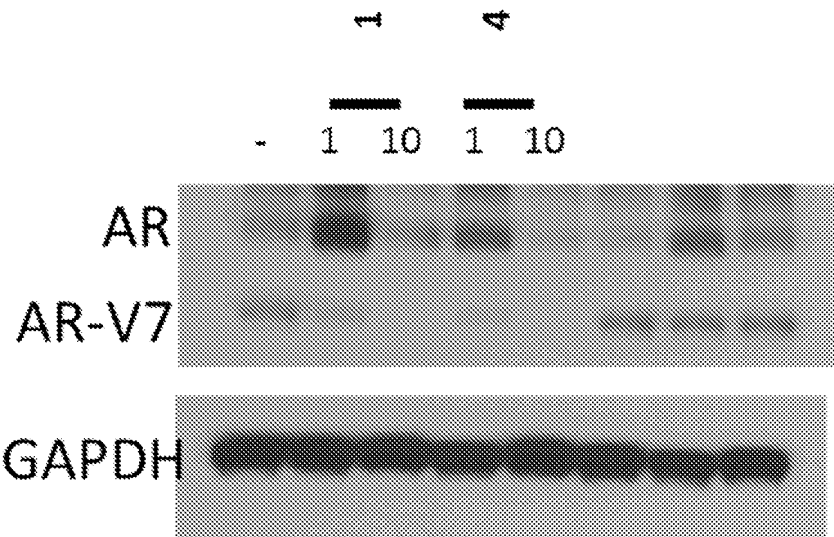


Figure 22

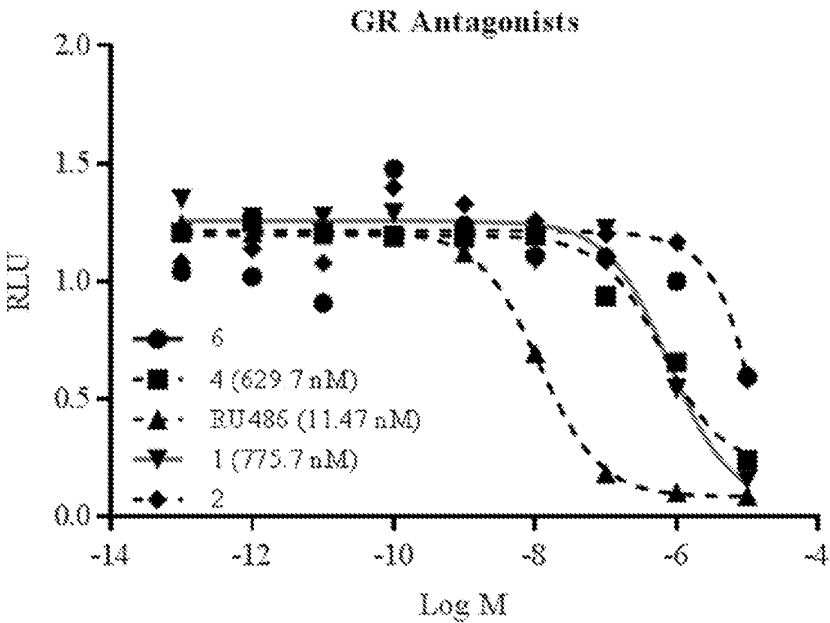


Figure 23

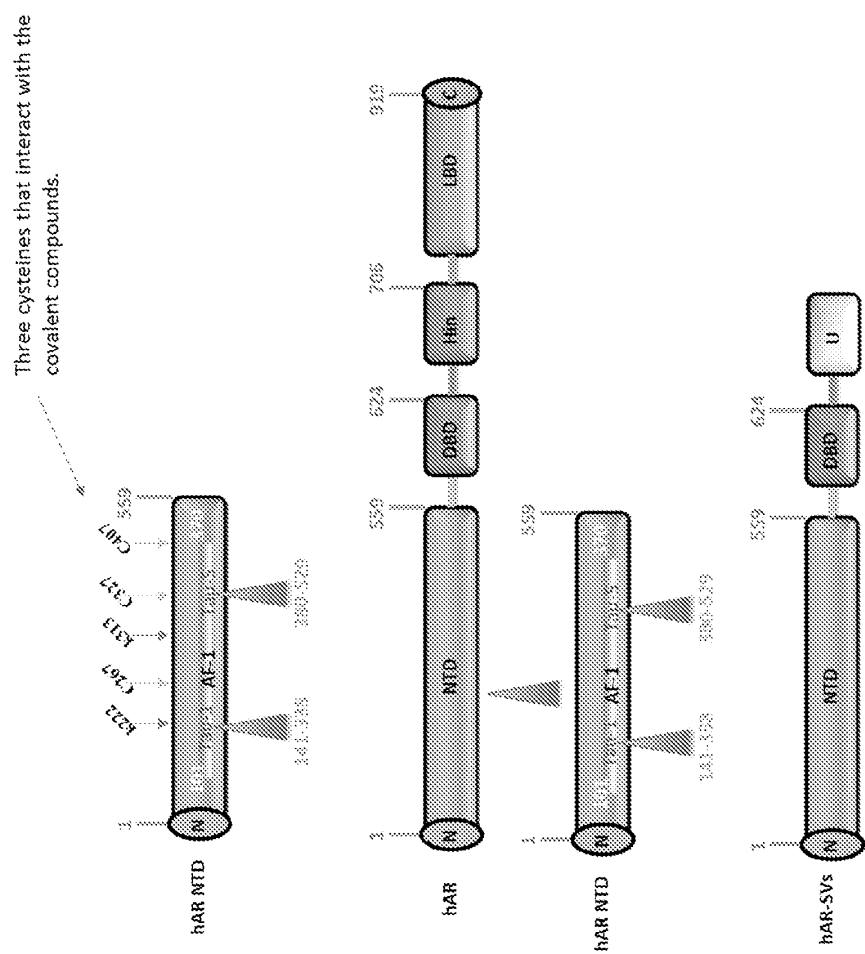


Figure 24

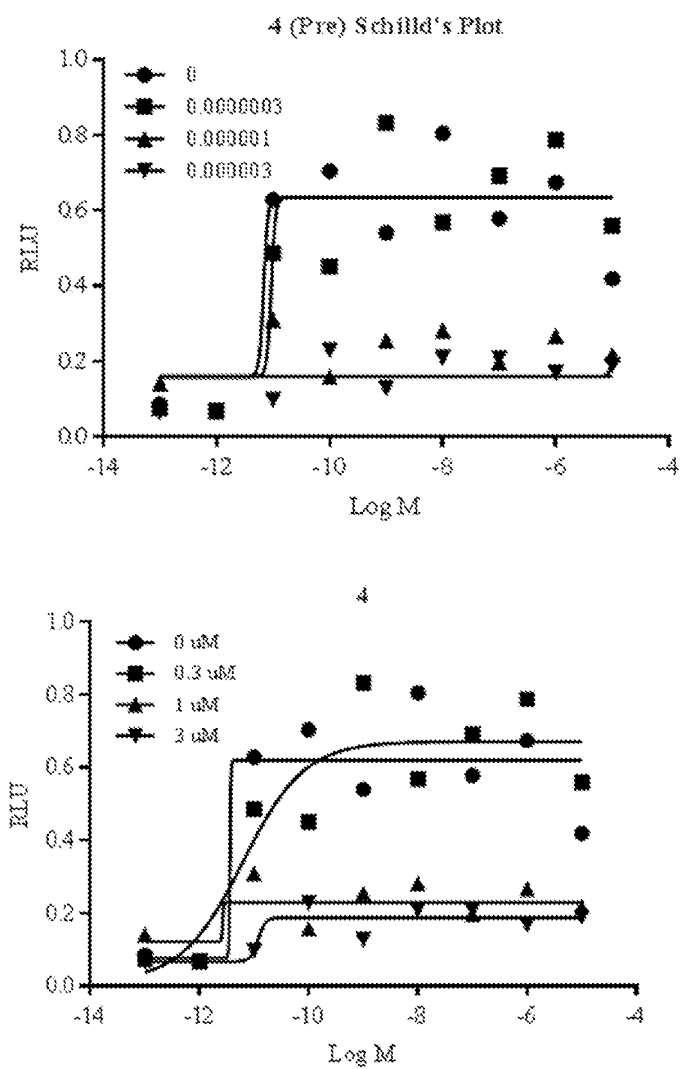


Figure 25A

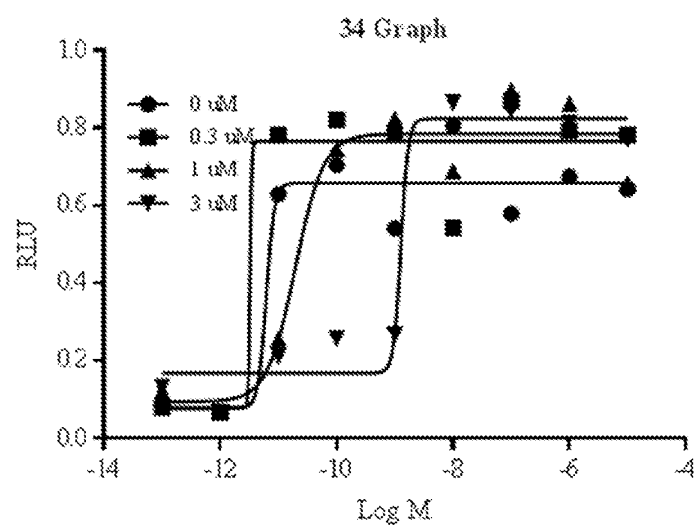
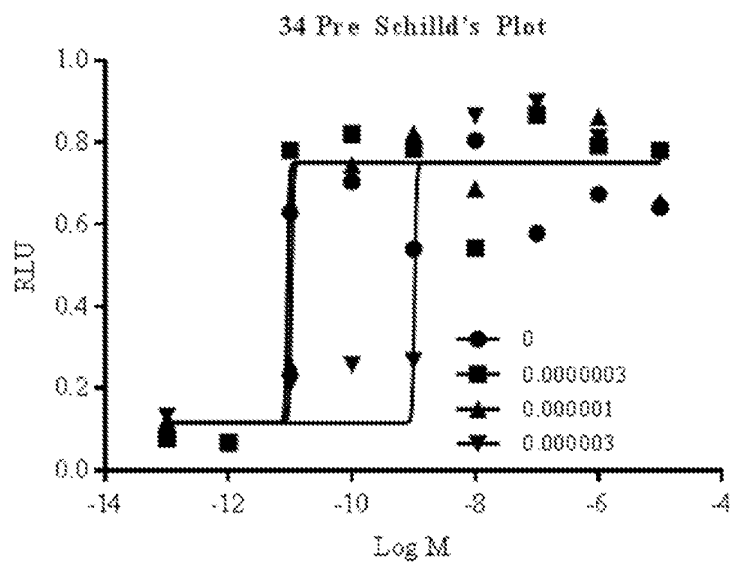


Figure 25B

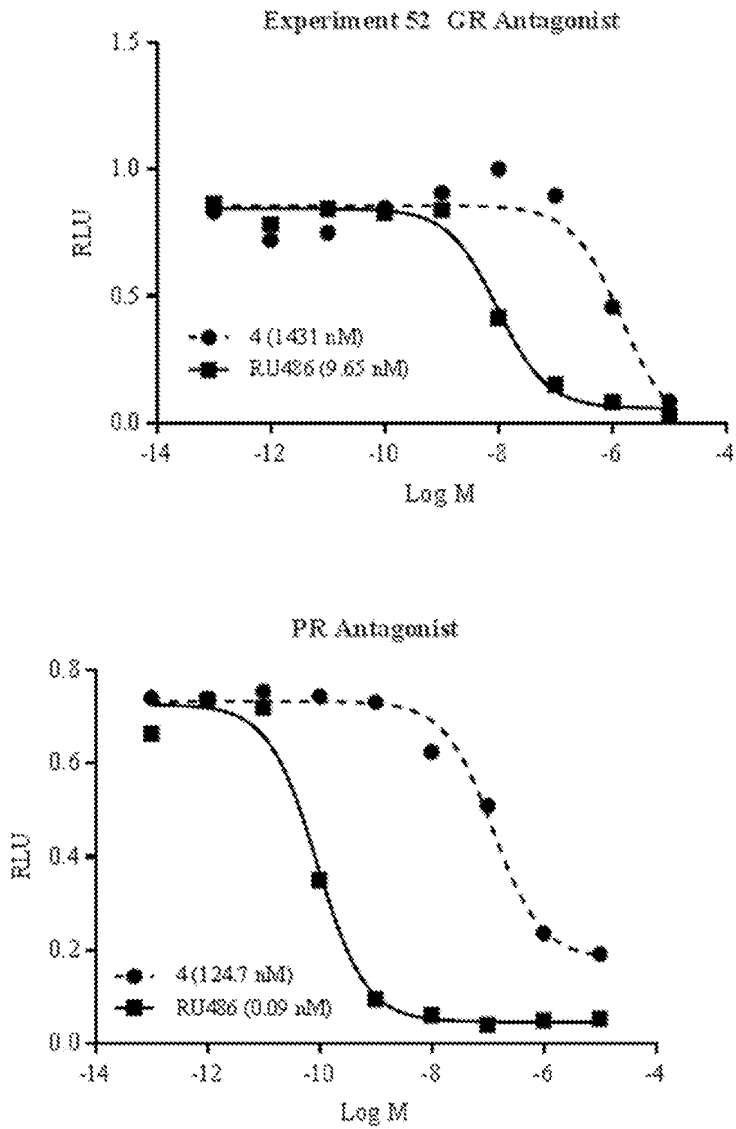


Figure 26

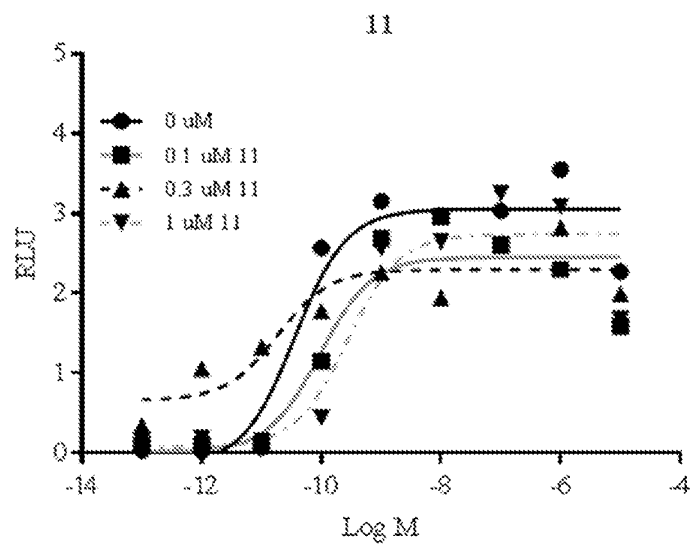


Figure 27

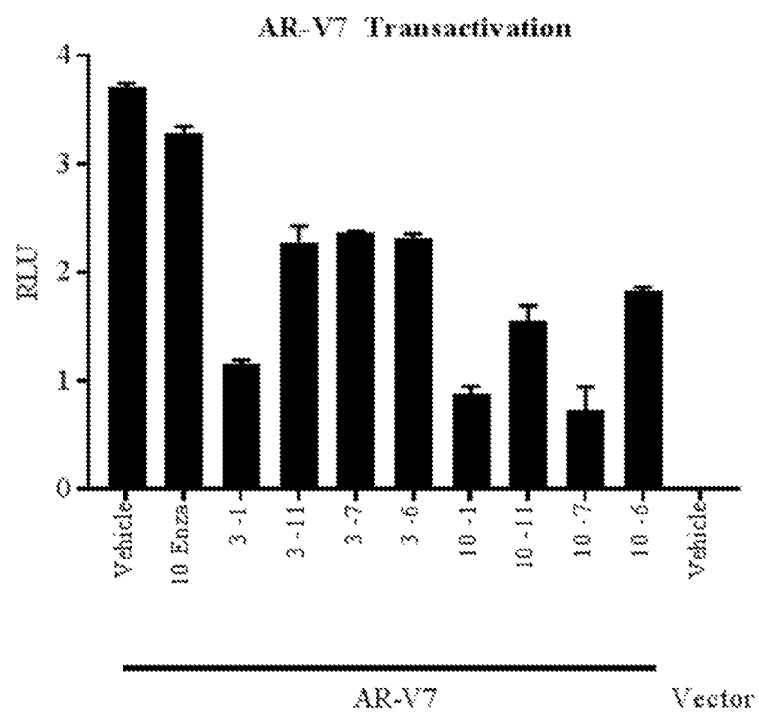


Figure 28

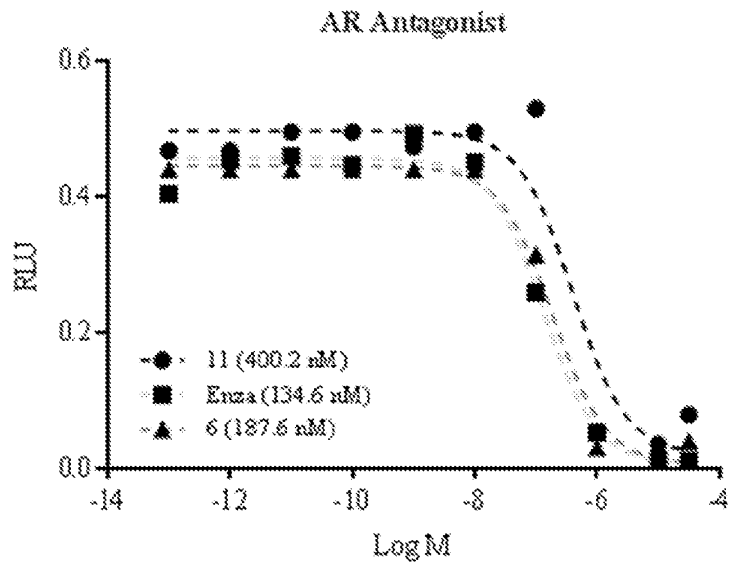


Figure 29

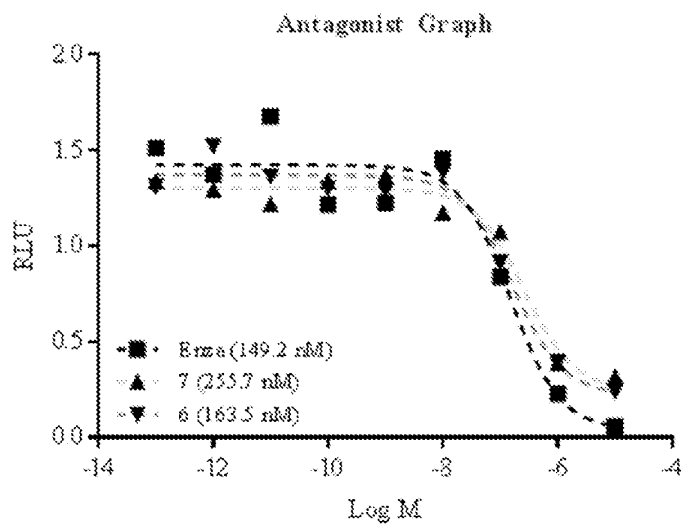


Figure 30

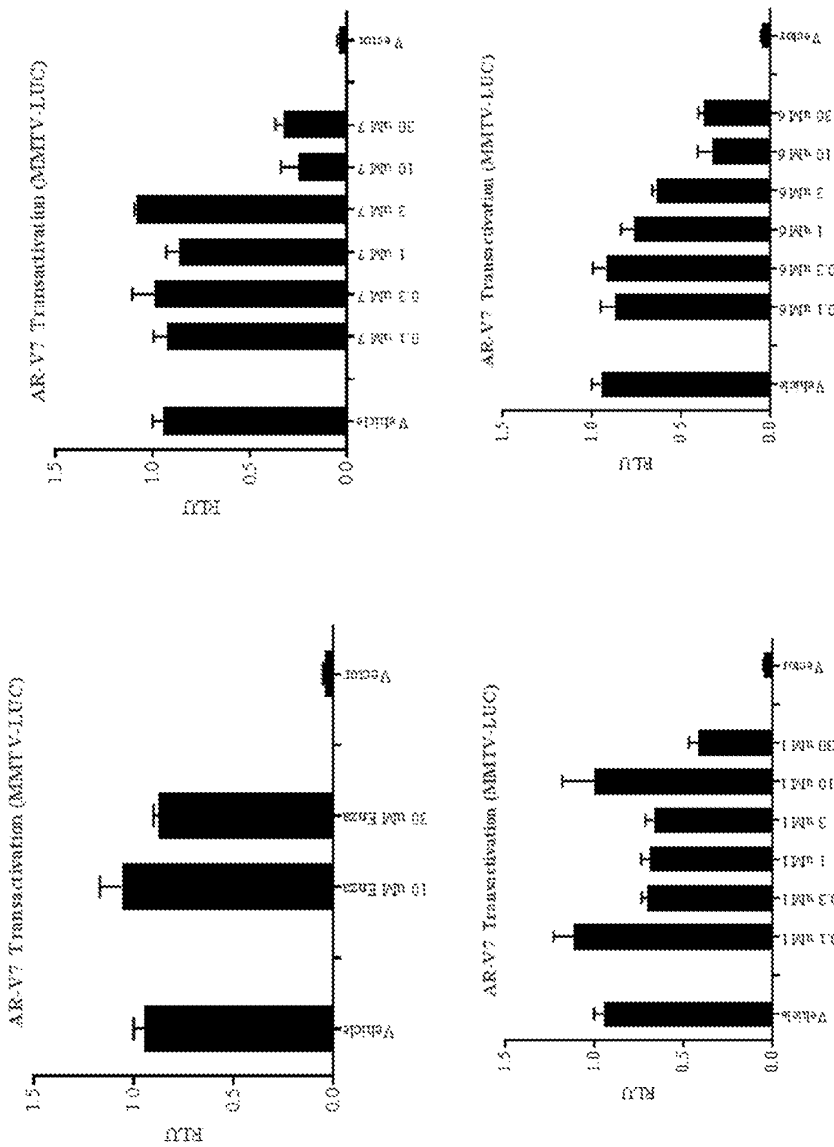
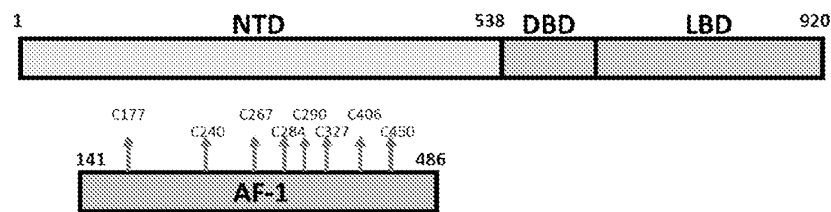


Figure 31

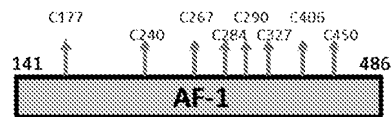


Experiment 05-28-2019 – Compound 1

Peptide	M.Wt.	Comp.	M.Wt. Add	C
[K].LENPLDYGSAAAAAQC.R.[Y]	2006.9	-		
[K].LENPLDYGSAAAAAQC.R.[Y]	2345.02	1	338	406
[K].GLEGESLGCSGSAAGSSGTLELPSTLS LYK.[S]	2942.43	-		
[K].GLEGESLGCSGSAAGSSGTLELPSTLS LYK.[S]	3280.51	1	338	327
[R].GDCMYAPLLGVPPAVRPTPCAPLAECK .[G]	3123.36	-		
[R].GDCMYAPLLGVPPAVRPTPCAPLAECK .[G]	2785.36	1	338	267

C240 was detected by M.S., but was not modified.

Figure 32

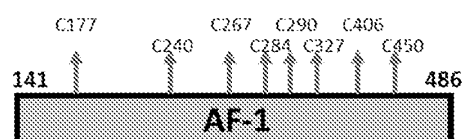


Experiment 06-05-2019 – Compound 1

Peptide	M.Wt.	Comp.	M.Wt. Add	C
[K].LENPLDYGSAAAAAQC.R.[Y]	2006.9	-		
[K].LENPLDYGSAAAAAQC.R.[Y]	2345.02	1	338	406
[K].GLEGESLGCSGSAAGSSGTLELPSTLS LYK.[S]	2942.43	-		
[K].GLEGESLGCSGSAAGSSGTLELPSTLS LYK.[S]	3280.51	1	338	327
[R].GDCMYAPLLGVPPAVRPTPCAPLAECK .[G]	3123.36	-		
[R].GDCMYAPLLGVPPAVRPTPCAPLAECK .[G]	2785.36	1	338	267

C240 was detected by M.S., but was not modified.

Figure 33

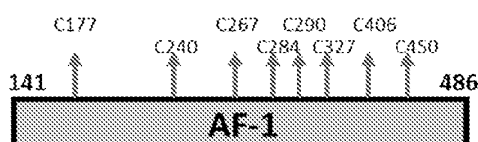


Experiment 06-05-2019 – Compound 4

Peptide	M.Wt.	Comp.	M.Wt. Add	C
[K].LENPLDYGSAWAAAAAQCR.[Y]	2006.9	-		
[K].LENPLDYGSAWAAAAAQCR.[Y]	2352.02	4	345	406
[K].GLEGESLGCSGSAAGSSGTLELP5TLS LYK.[S]	2942.43	-		
[K].GLEGESLGCSGSAAGSSGTLELP5TLS LYK.[S]	3287.51	4	345	327
[R].GDCMYAPLLGVPPAVRPTCAPLAECK .[G]	2769.36	-		
[R].GDCMYAPLLGVPPAVRPTCAPLAECK .[G]	3114.44	4	345	267

C240, C294, and C290 were detected by M.S., but was not modified.

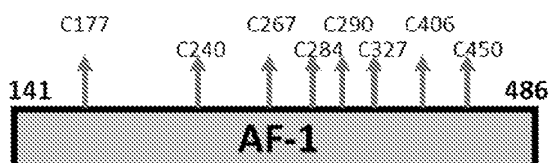
Figure 34



Experiment 07-19-2019

- 4 – C327, C406, C267 were modified. C240, C284, and C290 were not modified.
- 1 – C406, C327, C267 were modified. C240, C284, and C290 were not modified.
- UT-34 – No modifications at any C.
- 1 GST – GST has two C. 215 modified both the C.
- 4 GST – GST has two C. 239A modified both the C
- No other non-specific proteins in AF-1 protein batches were modified.

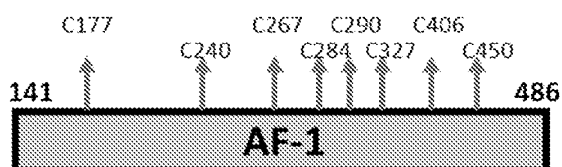
Figure 35



Experiment 08-02-2019

- 6 – C327, C406 were modified. C240, C284, and C290 were not modified.

Figure 36



Experiment 08-08-2019

- 6 – C327, C406 were modified. C240, C284, and C290 were not modified.
- 34+6 – C327 and C406 were modified. C240 was not modified.
- 6-GST – GST has two C. 143 modified both C.

Figure 37

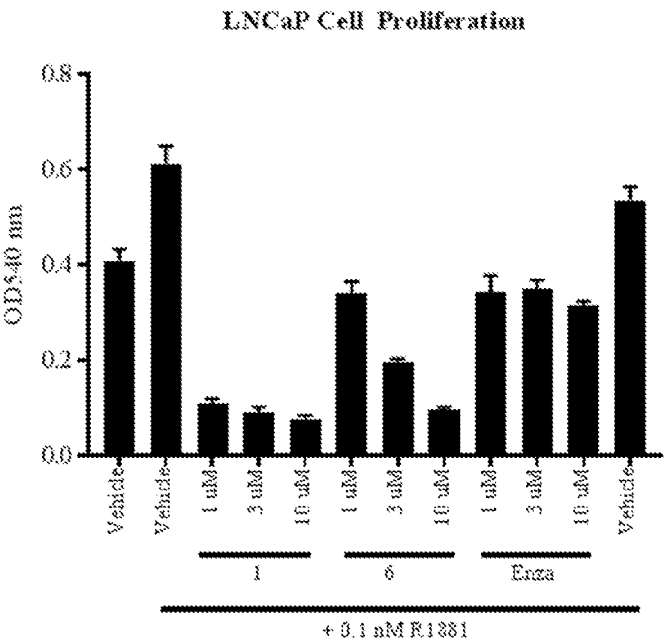


Figure 38

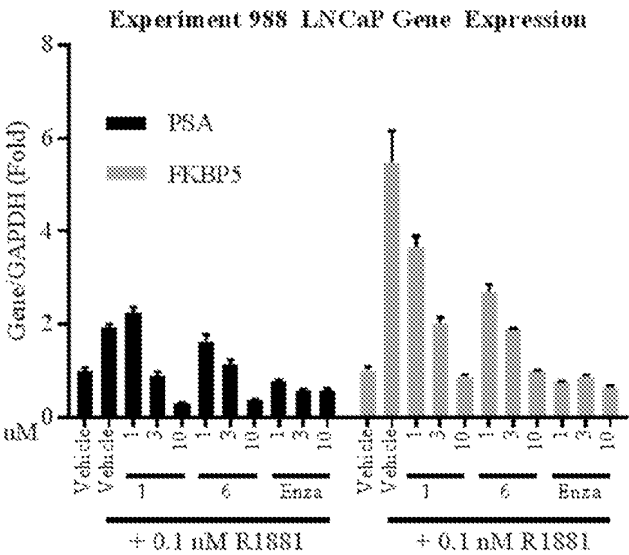


Figure 39

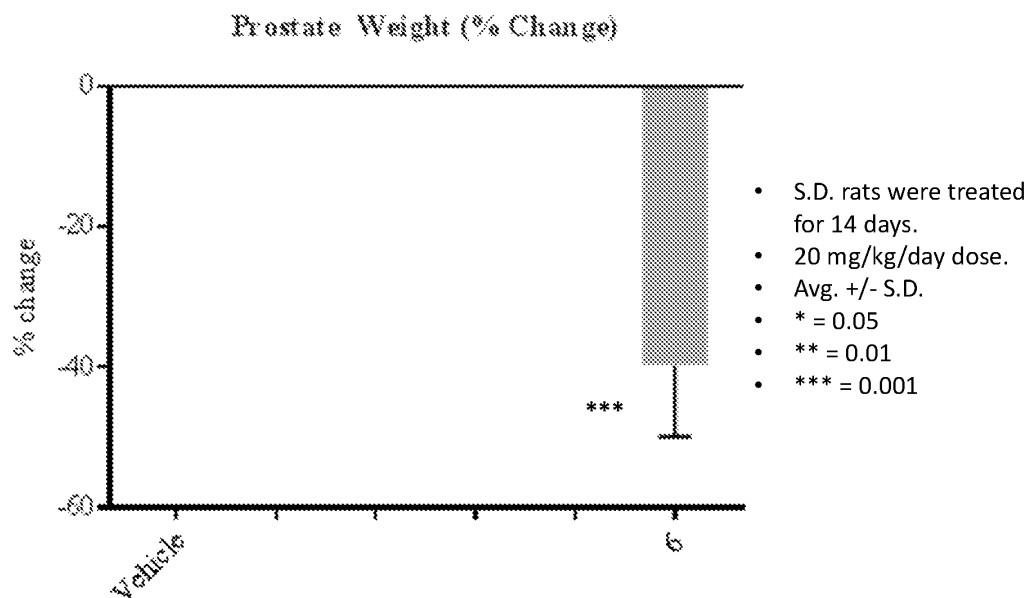


Figure 40A

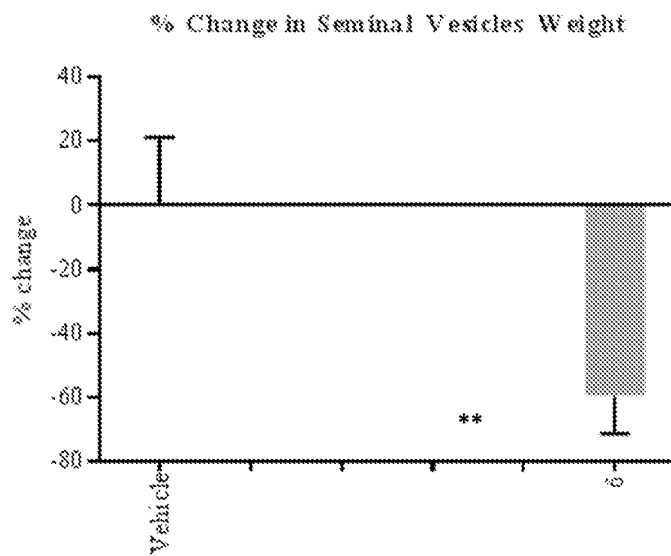


Figure 40B

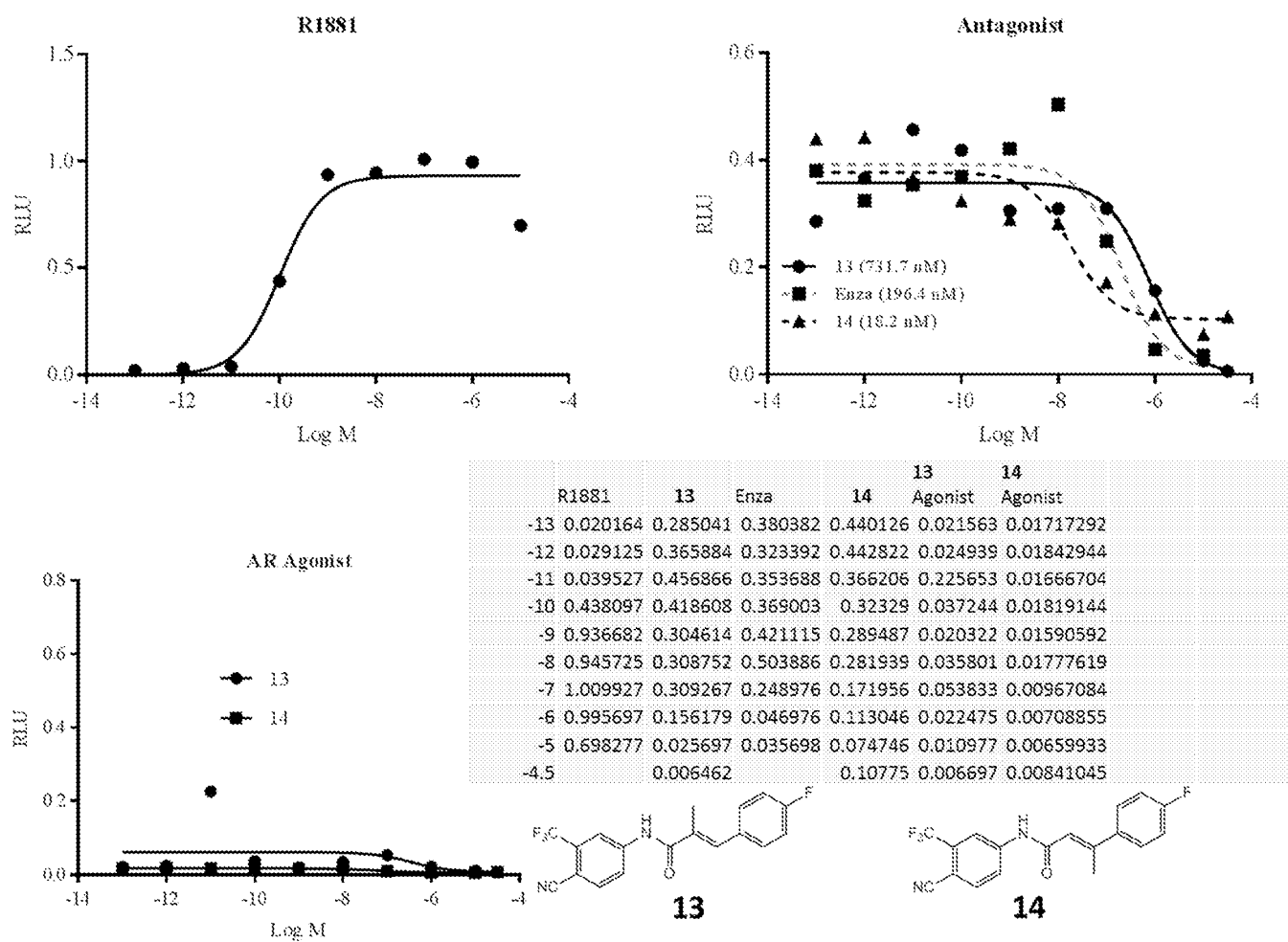


Figure 41

AR AF-1 + Compound 7 (covalent antagonist)

Top Apex	Confident	PSM Ambi	Annotated Sequence	Modifications
46.84	High	Unambigu	[K].GSLDDDSAGKSTEDTAEYSPFK.[G]	
	High	Unambigu	[K].GSLDDDSAGKSTEDTAEYSPFKGGYTK.[G]	
69.79	High	Unambigu	[K].LENPLDYGSAWAAAAAQCR.[Y]	
69.78	High	Unambigu	[K].LENPLDYGSAWAAAAAQCR.[Y]	1x Compound 7
	High	Unambigu	[R].IKLENPLDYGSAWAAAAAQCR.[Y]	
37.67	High	Unambigu	[K].SGALDEAAAYQSR.[D]	
57.43	High	Unambigu	[K].SGALDEAAAYQSRDYNNFPLALAGPPPPPPHAR.[I]	
43.34	High	Unambigu	[K].STEDTAEYSPFK.[G]	
40.32	High	Unambigu	[K].STEDTAEYSPFKGGYTK.[G]	
32.41	High	Unambigu	[K].GSLDDDSAGK.[S]	
69.81	High	Unambigu	[K].GLEGESLGCSGSAAGSSGTLELPSTLSLYK.[S]	1x Cmpd 7 [C9]; 1x Cmpd 7 [N-Terr
15.79	High	Unambigu	[R].AREASGAPTSSK.[D]	
67.49	High	Unambigu	[K].AVSVSMGLGVEALEHLSPEQLR.[G]	
64.06	High	Unambigu	[K].AVSVSMGLGVEALEHLSPEQLR.[G]	1xOxidation [M6]
68.61	High	Unambigu	[K].DILSEASTMQLLQQQQEAVSEGSSSGR.[A]	
64.92	High	Unambigu	[K].DILSEASTMQLLQQQQEAVSEGSSSGR.[A]	1xOxidation [M9]
42.09	High	Unambigu	[K].DNYLGGTSTISDNALCK.[E]	
51.08	High	Unambigu	[K].DNYLGGTSTISDNALCKELCK.[A]	
60.87	High	Unambigu	[R].DYNNFPLALAGPPPPPPHAR.[I]	
15.79	High	Unambigu	[R].EASGAPTSSK.[D]	
37.04	High	Unambigu	[R].EASGAPTSSKDNYLGGTSTISDNALCK.[E]	
66.86	High	Unambigu	[R].EASGAPTSSKDNYLGGTSTISDNALCKELCK.[A]	1x Cmpd 7 [C/K]
	High	Unambigu	[K].ELCKAVSVSMGLGVEALEHLSPEQLR.[G]	
81.05	High	Unambigu	[R].GDCMYAPLLGVPPAVRPTCAPLAECK.[G]	
68.13	High	Unambigu	[K].GLEGESLGCSGSAAGSSGTLELPSTLSLYK.[S]	

Figure 42

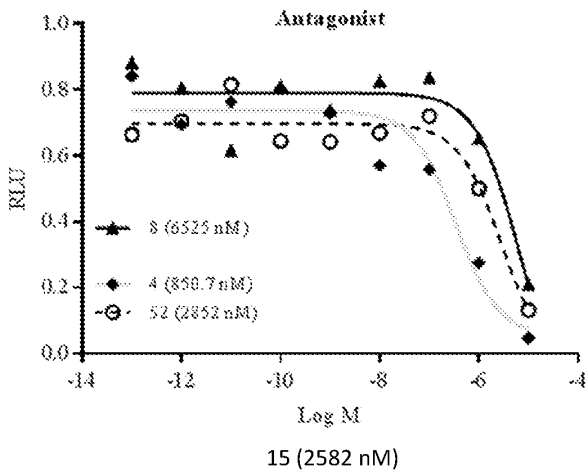


Figure 43

Compound 18

Androgen Receptor 24		15
Annotated Sequence	Modifications	
[K].LENPLDYGSAAAAAQC.[Y]	1xNarayanan77 [C18]	
[R].IKLENPLDYGSAAAAAQC.[Y]		
[R].IKLENPLDYGSAAAAAQC.[Y]	1xNarayanan77 [C20]	
[K].LLDSVQPIAR.[E]		
[R].MLYFAPDLVFNEYR.[M]	1xOxidation [M1]	
[K].SGALDEAAAYQSR.[D]		
[K].STEDTAEYSPFK.[G]		
[K].STEDTAEYSPFKGGYTK.[G]		
[K].LENPLDYGSAAAAAQC.[Y]		
[K].AVSVSMGLGVEALEHLSPEQLR.[G]		
[K].AVSVSMGLGVEALEHLSPEQLR.[G]	1xOxidation [M6]	
[K].DILSEASTMQLLQQQQEAVSEGSSSGR.[A]		
[K].DILSEASTMQLLQQQQEAVSEGSSSGR.[A]	1xOxidation [M9]	
[K].DNYLGGTSTISDPAK.[E]		
[R].DYNNFPLALAGPPPPPPHAR.[I]		
[R].EASGAPTSSKDNYLGGTSTISDPAK.[E]		
[K].ELCKAVSVSMGLGVEALEHLSPEQLR.[G]		
[K].GLEGESLGCSGSAAGSSGTLELPSTLSLYK.[S]		
[K].GLEGESLGCSGSAAGSSGTLELPSTLSLYK.[S]	1xNarayanan77 [C9]	
[K].GSLDDSAAG.[S]		

Figure 44

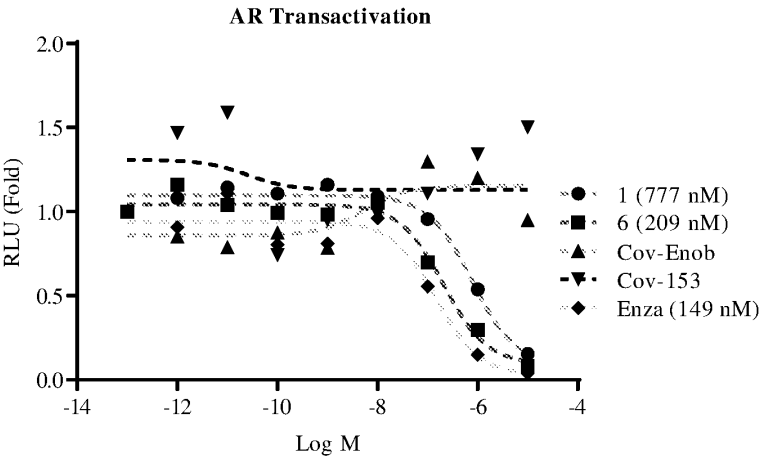


Figure 45

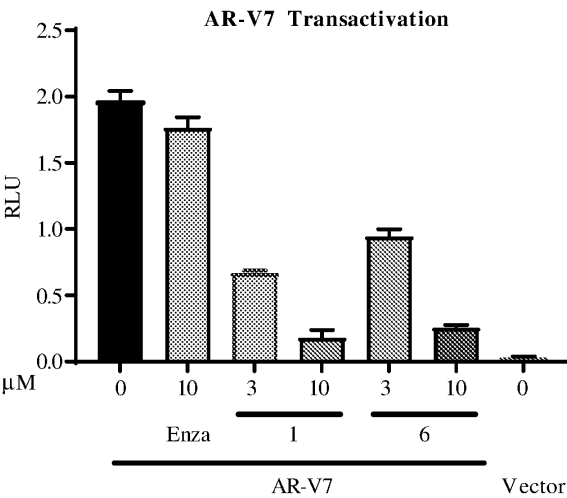


Figure 46A

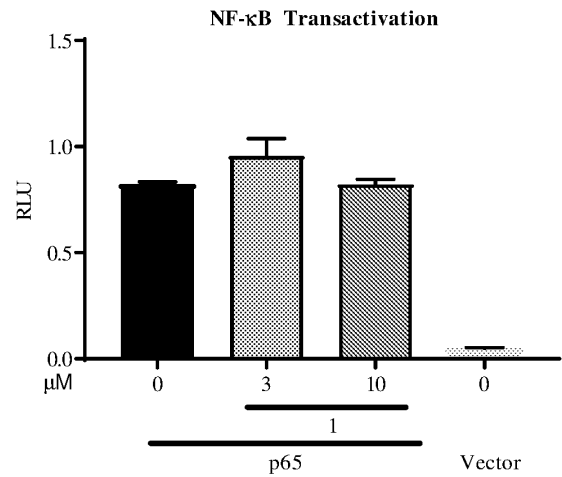


Figure 46B

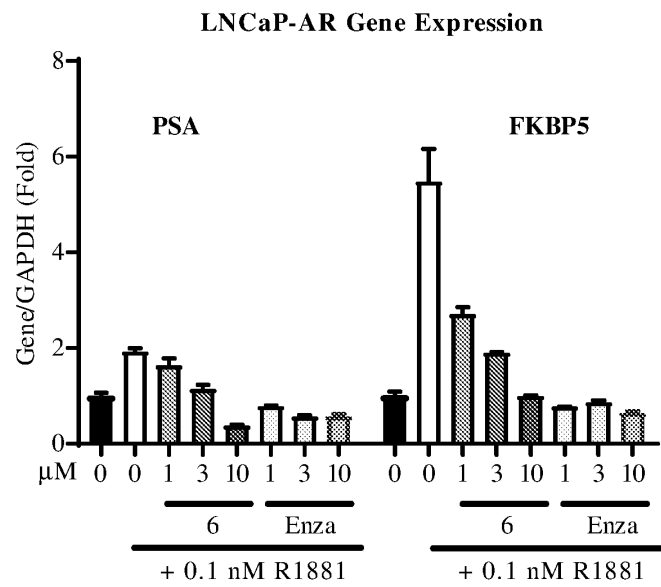


Figure 47

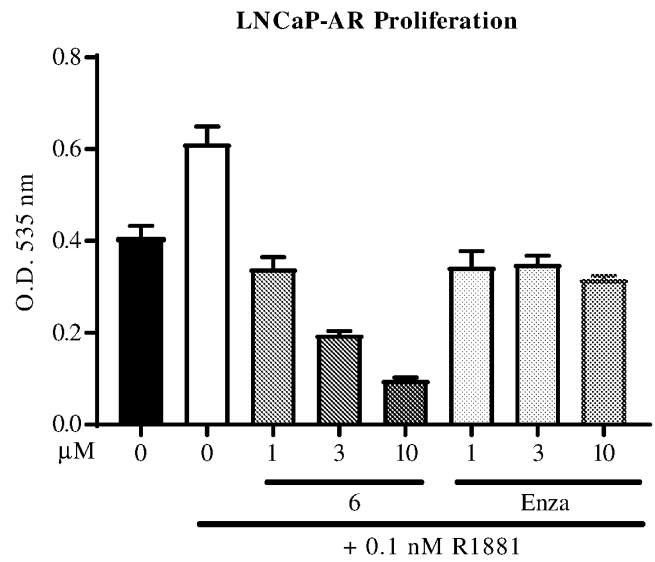


Figure 48

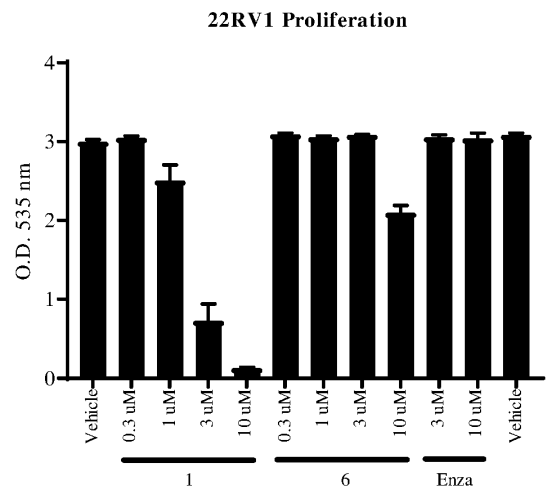


Figure 49

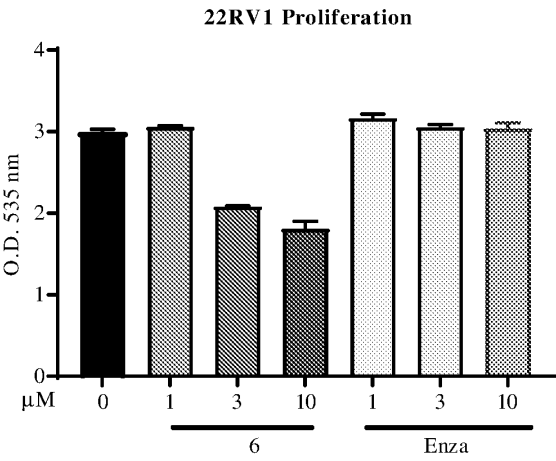


Figure 50A

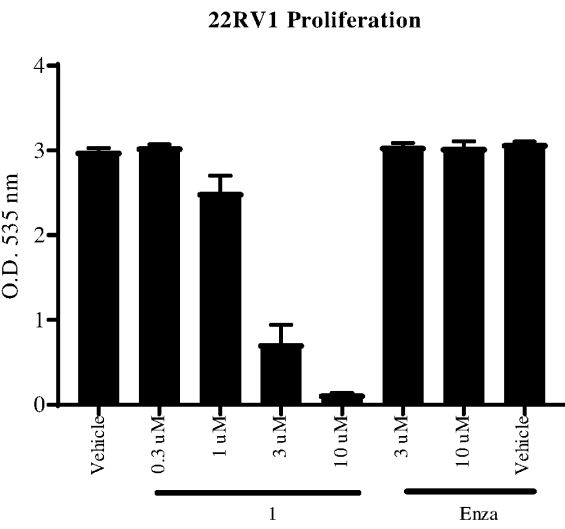


Figure 50B

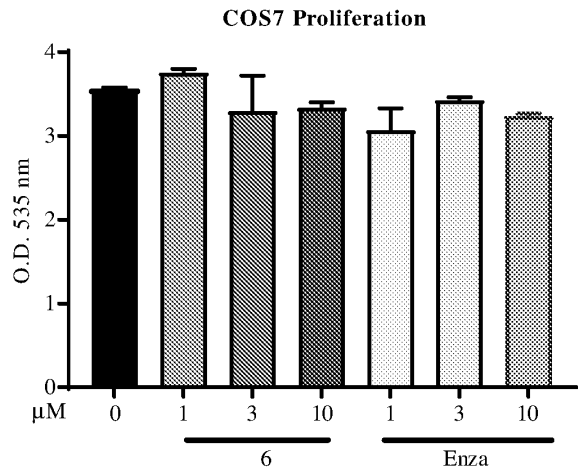


Figure 50C

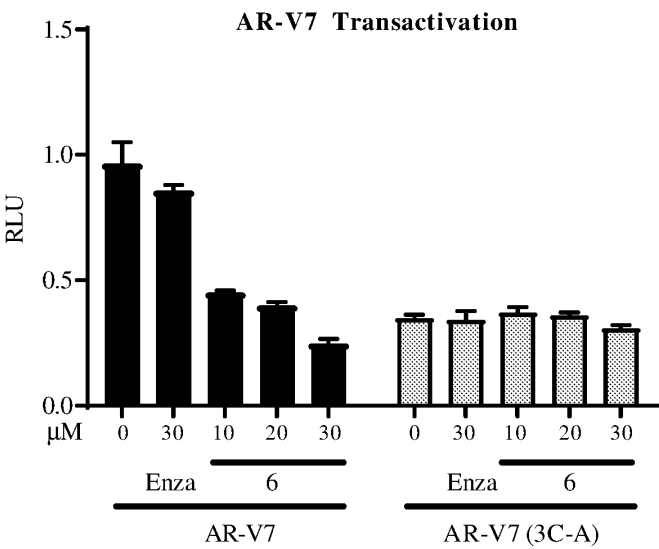


Figure 51

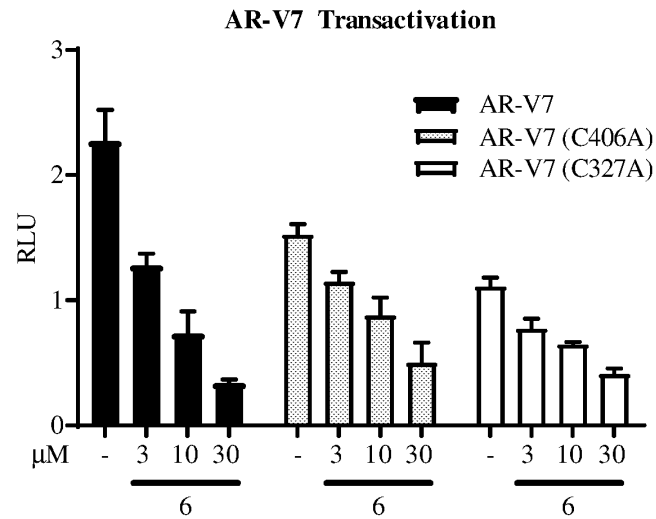


Figure 52

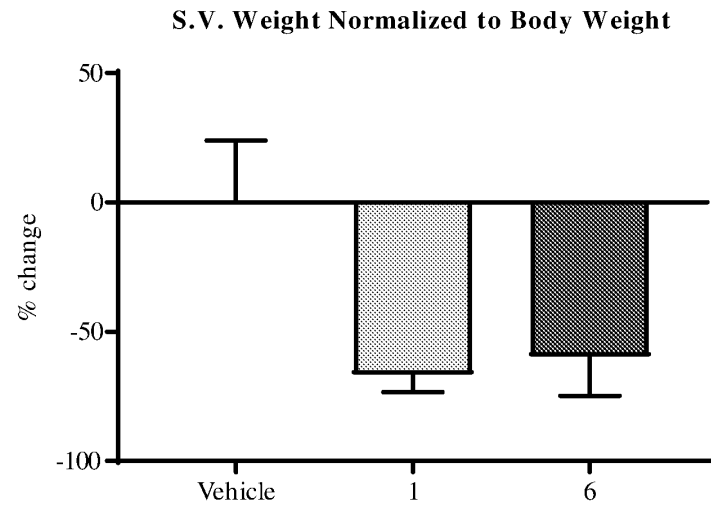
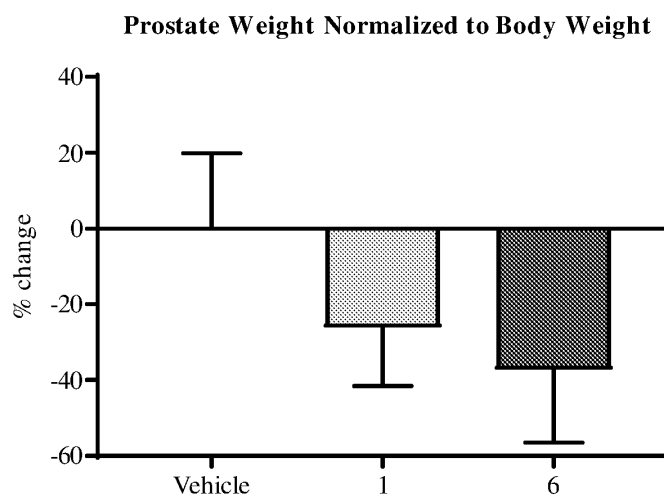
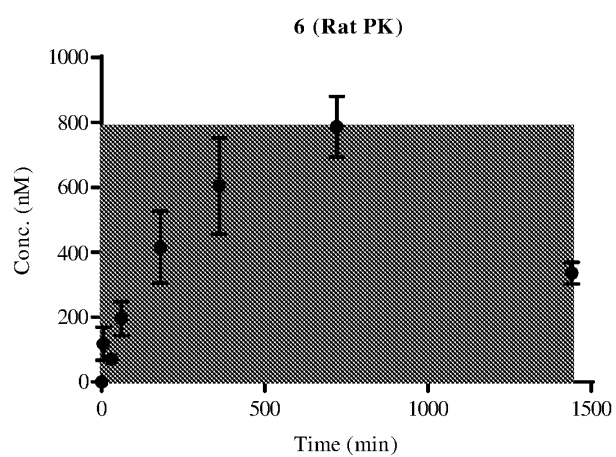


Figure 53A

**Figure 53B****Figure 54**

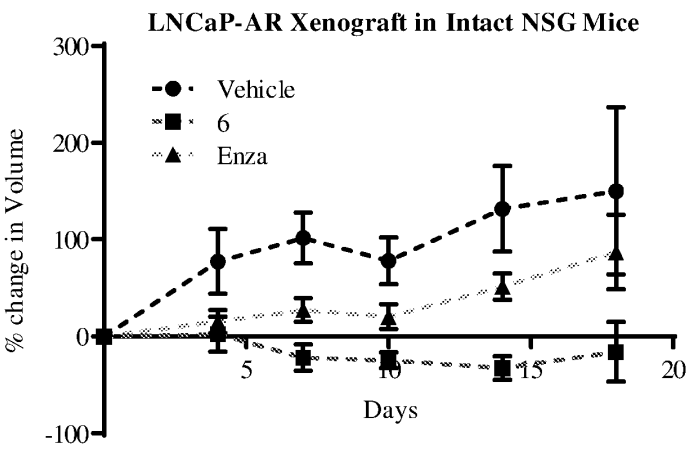


Figure 55A

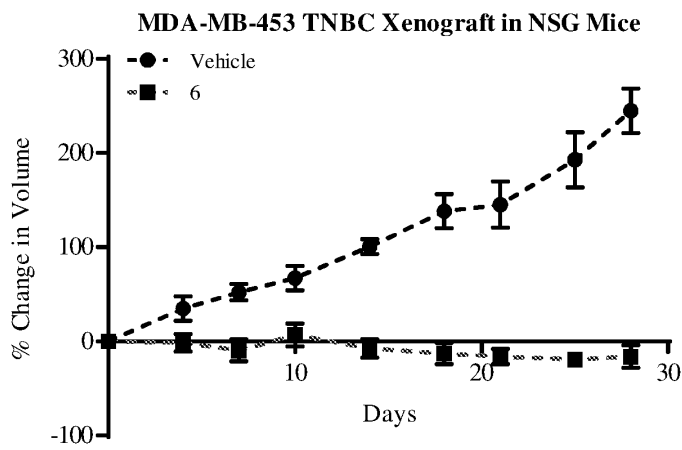


Figure 55B

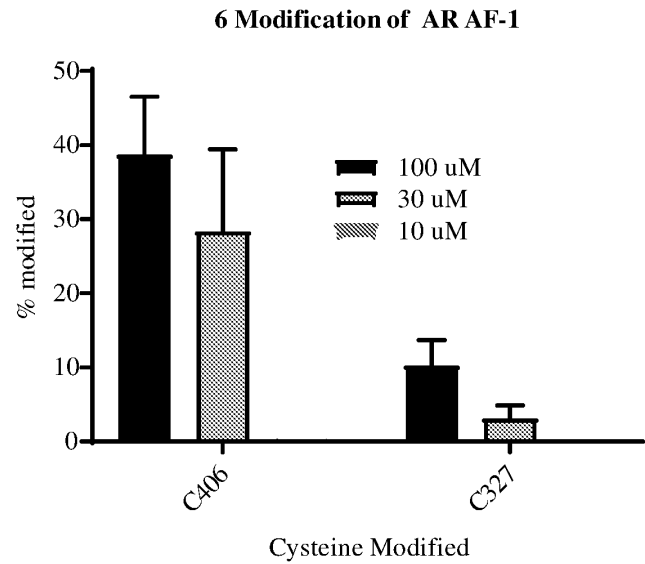


Figure 56A

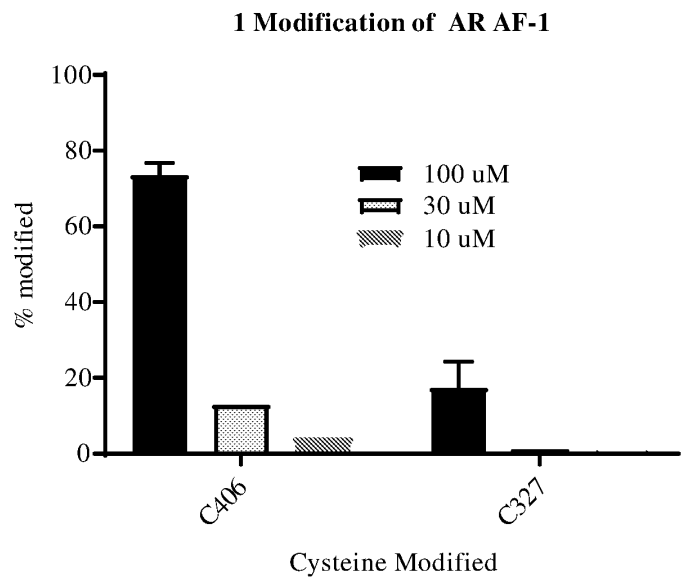


Figure 56B

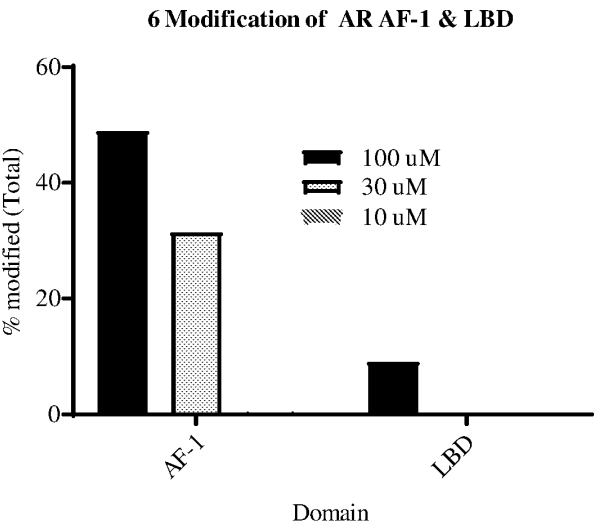


Figure 56C

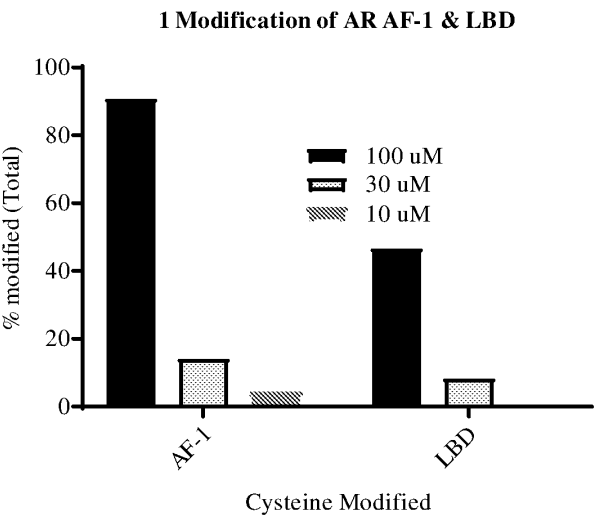


Figure 56D

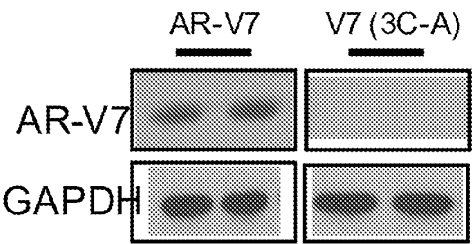


Figure 57A

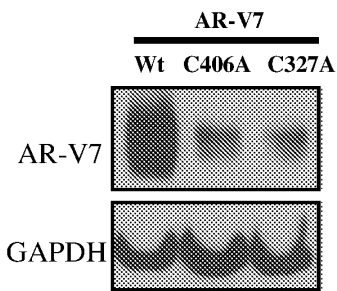


Figure 57B

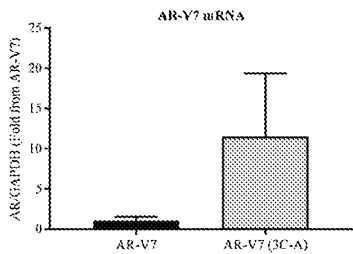
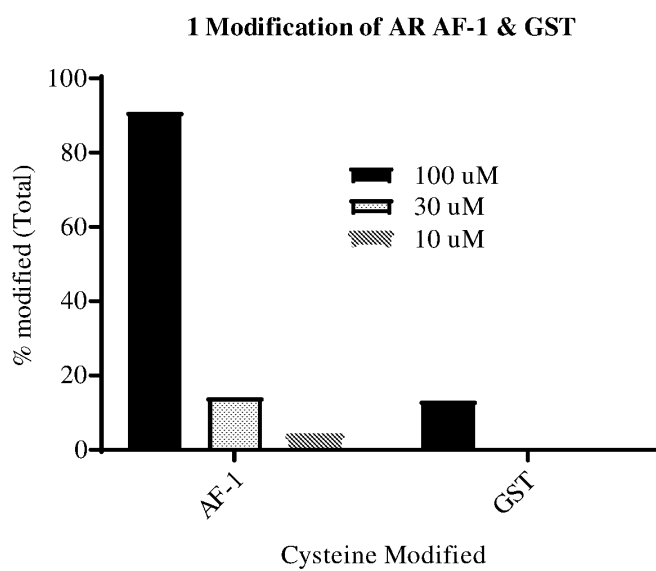
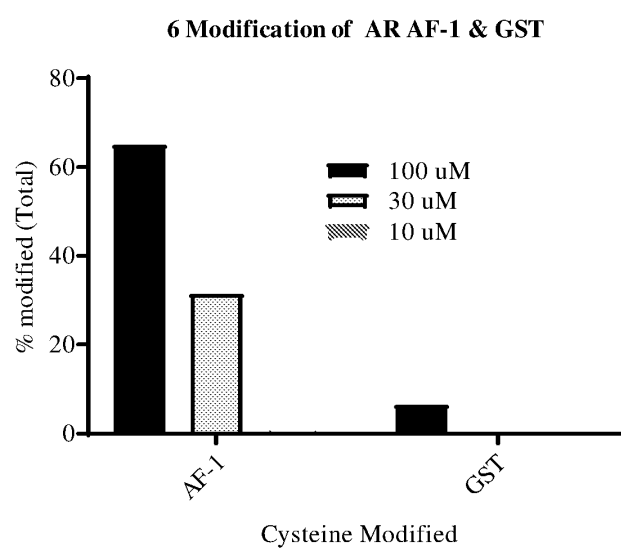


Figure 57C

**Figure 58A****Figure 58B**

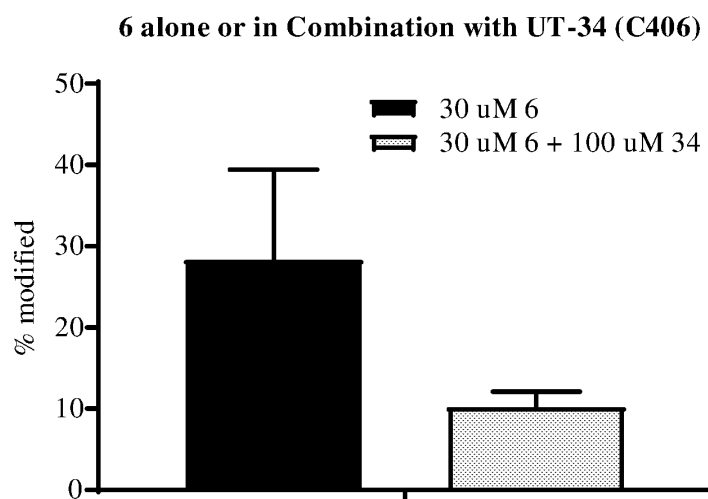


Figure 59A

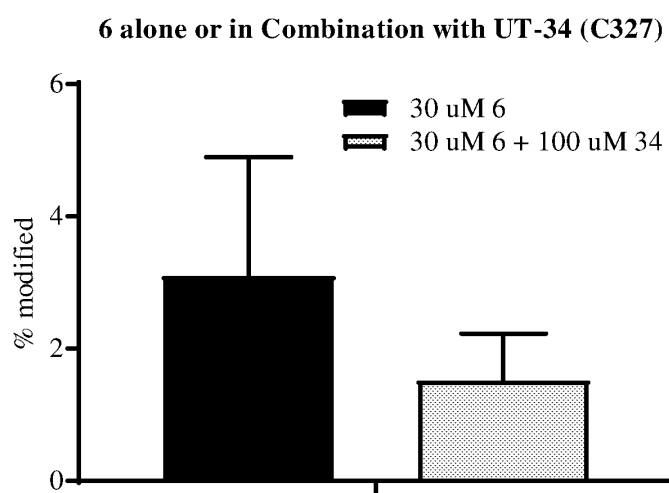


Figure 59B

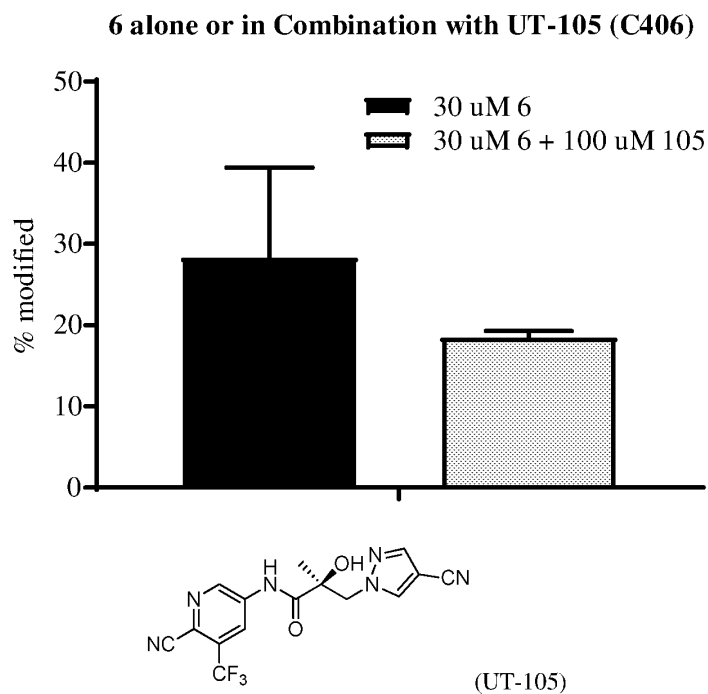


Figure 59C

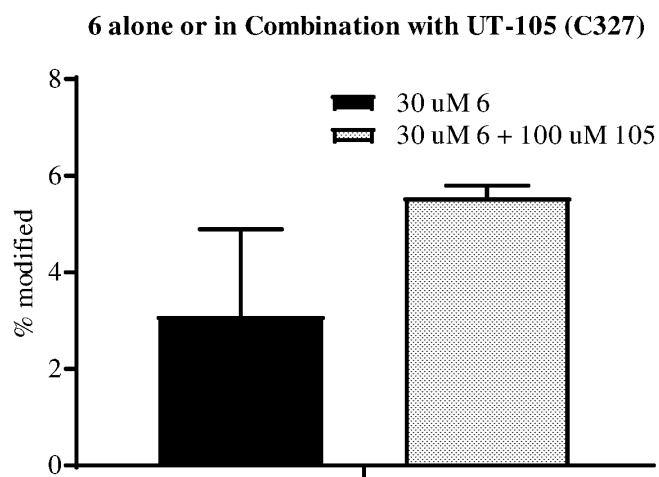


Figure 59D