

Figure 1 (part 1 of 2)

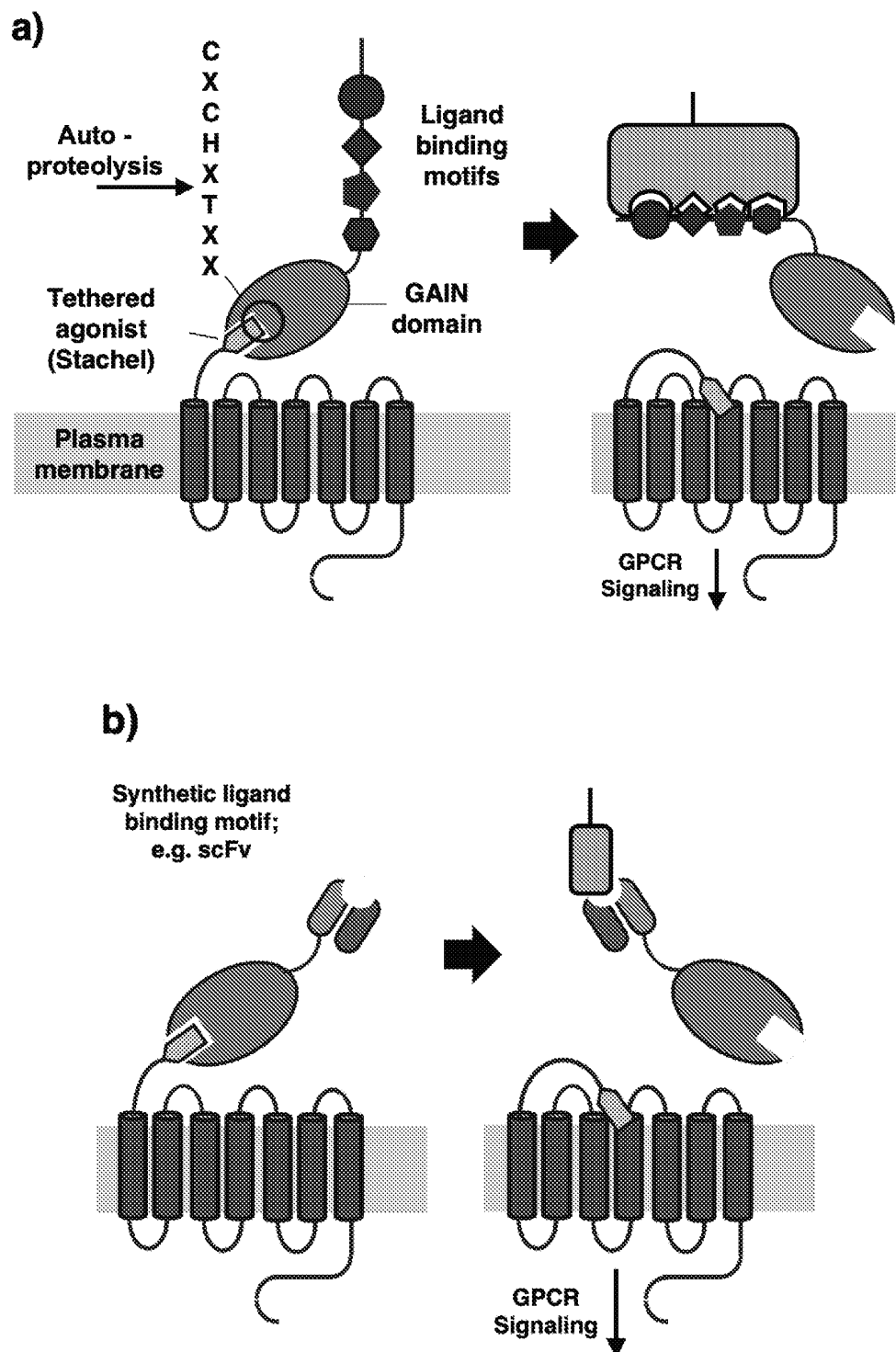


Figure 1 (part 2 of 2)

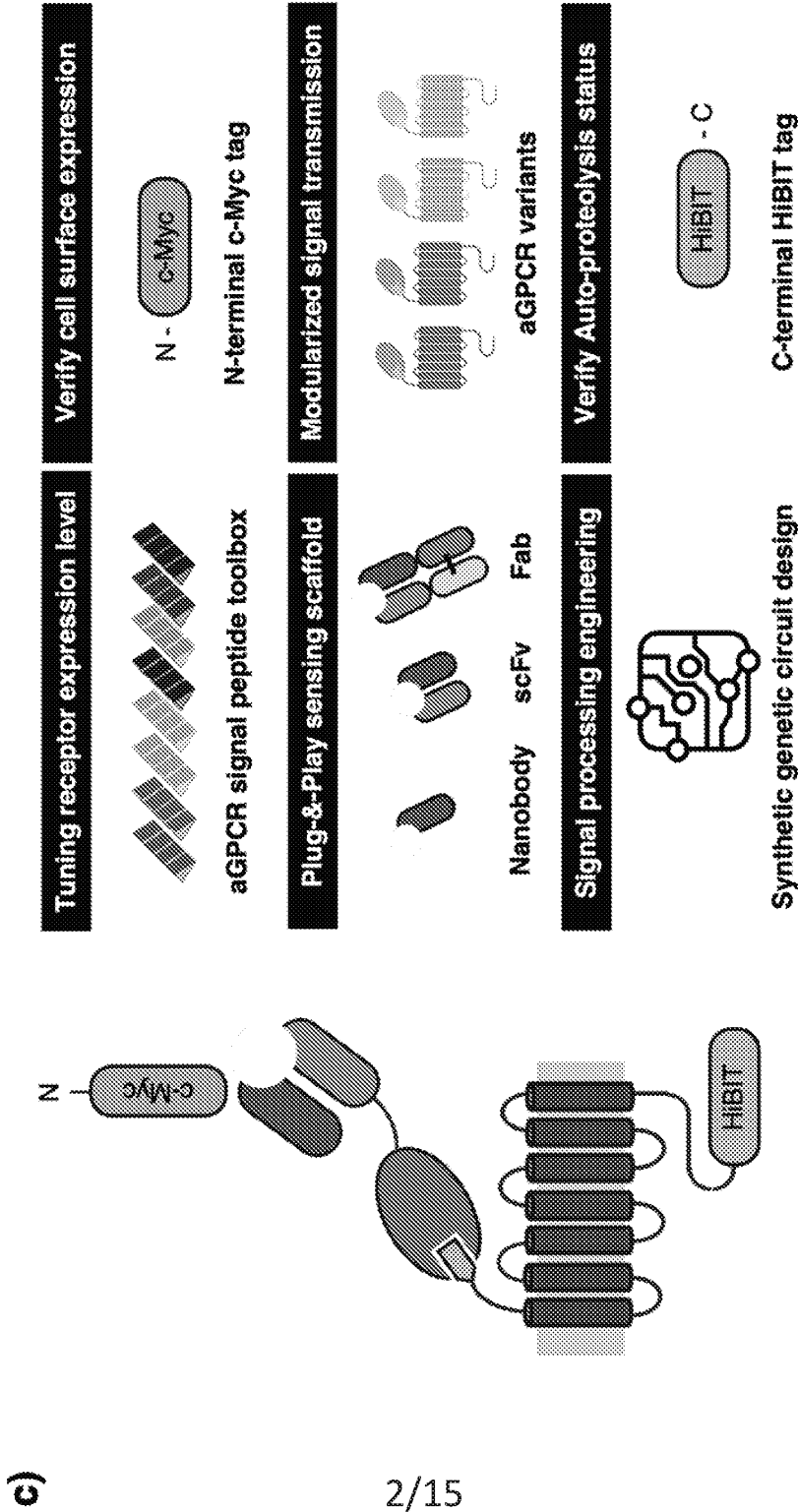


Figure 2 (part 1 of 3)

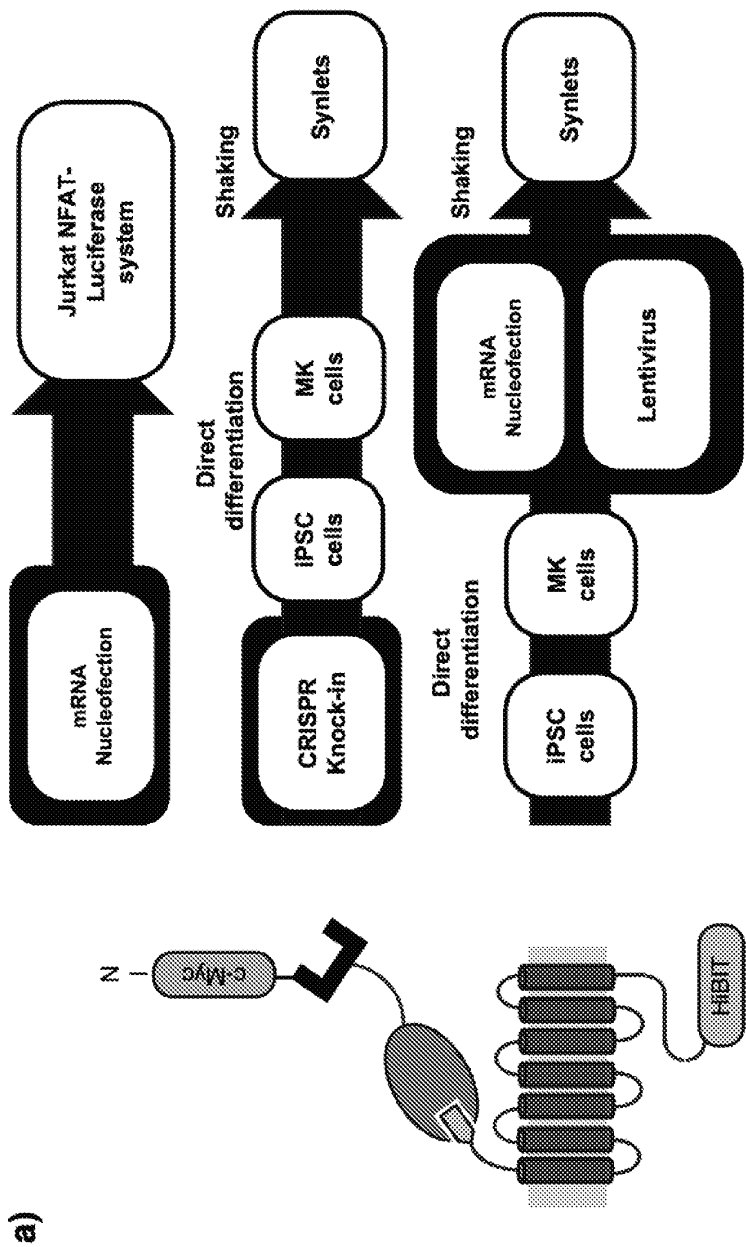


Figure 2 (part 2 of 3)

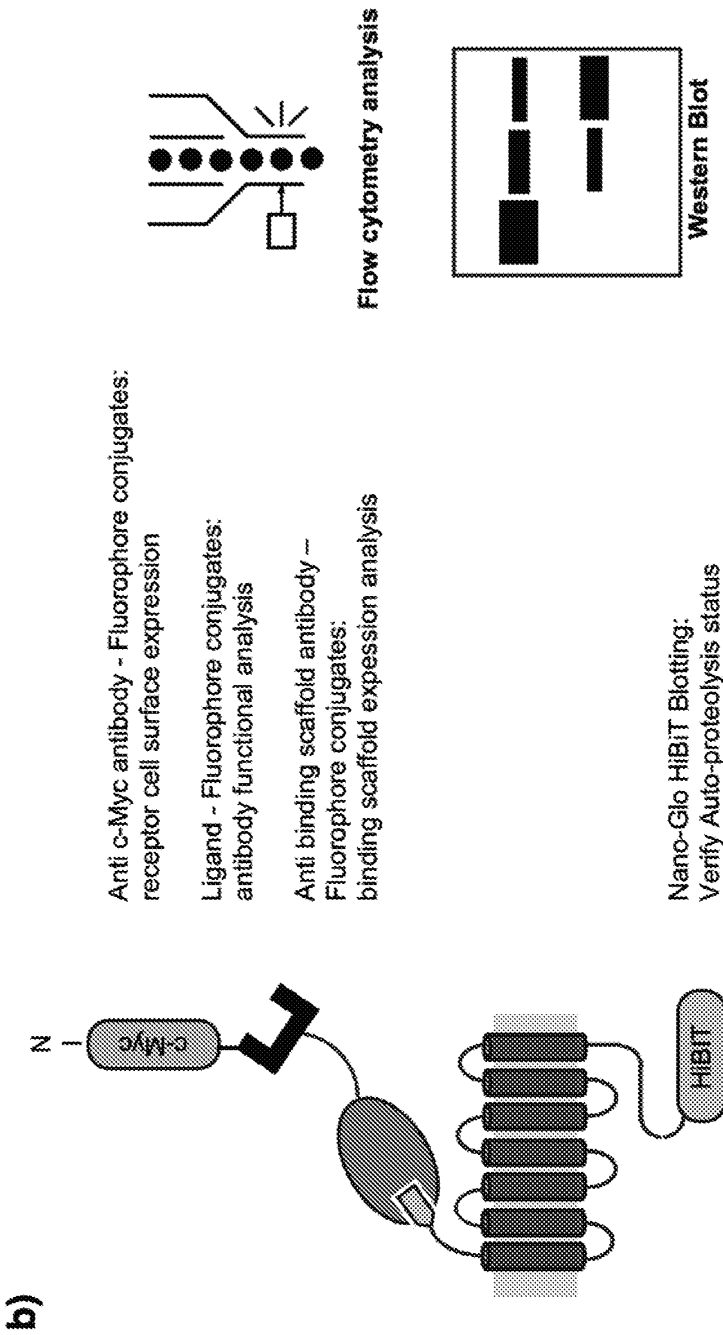


Figure 2 (part 3 of 3)

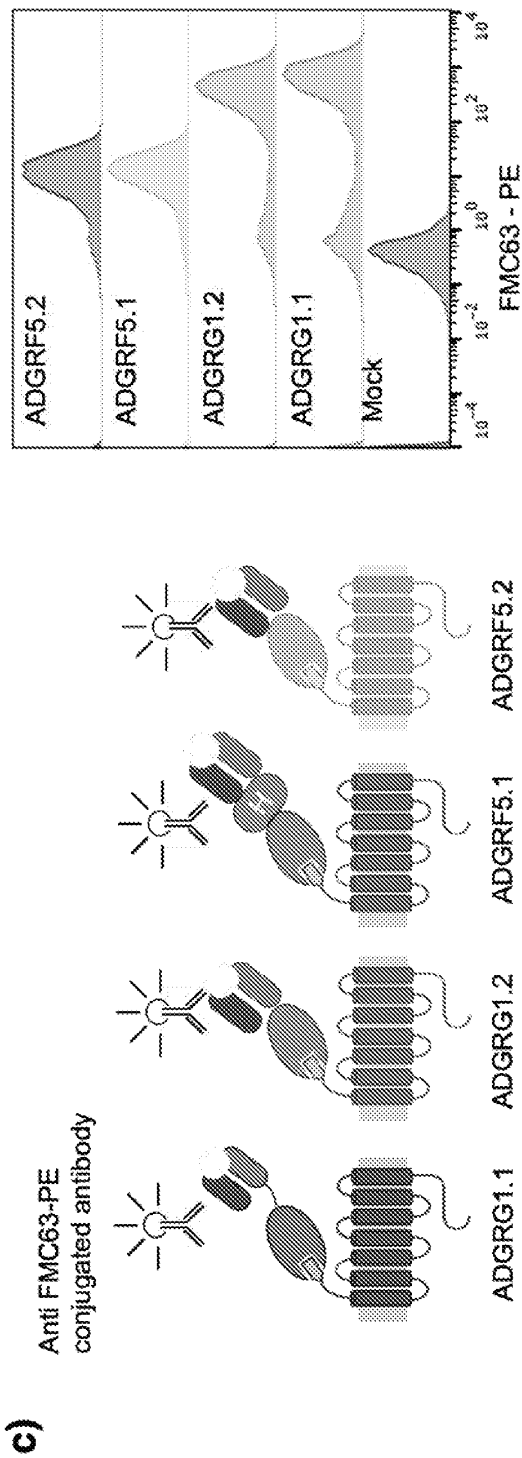


Figure 3

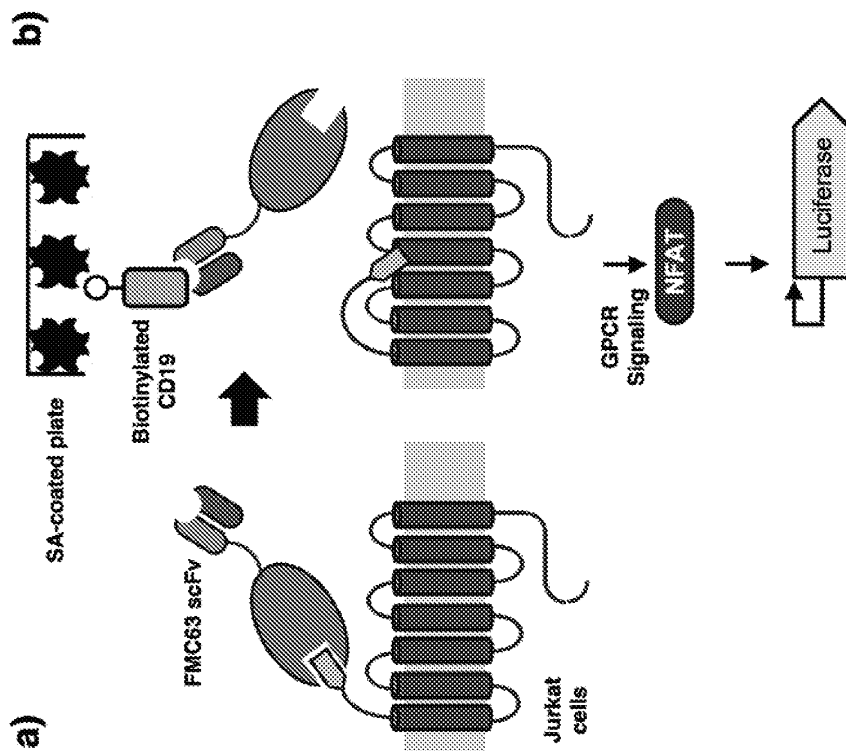
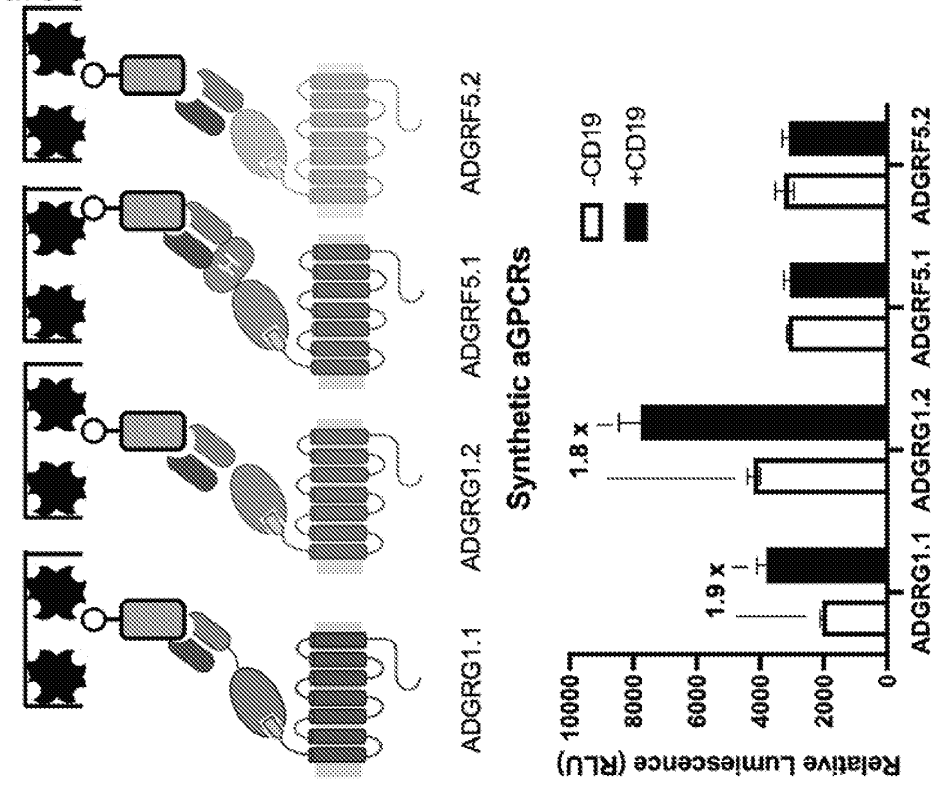


Figure 4 (part 1 of 2)

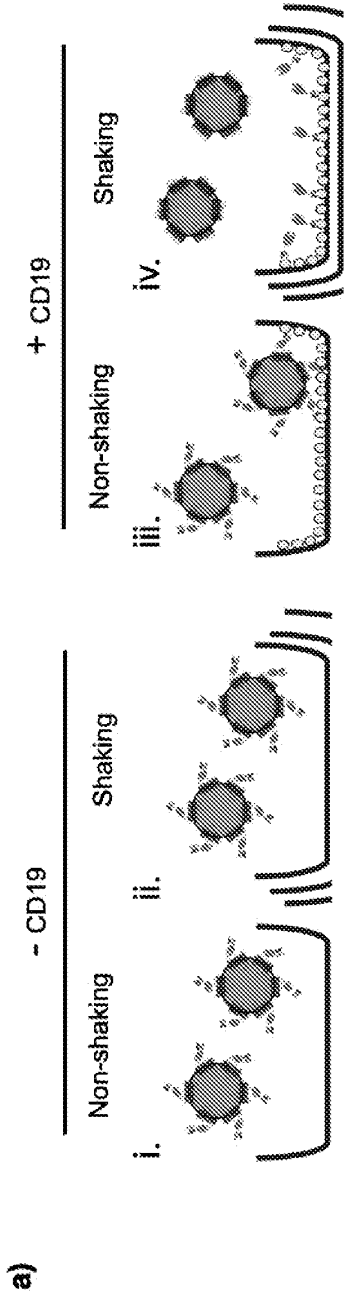
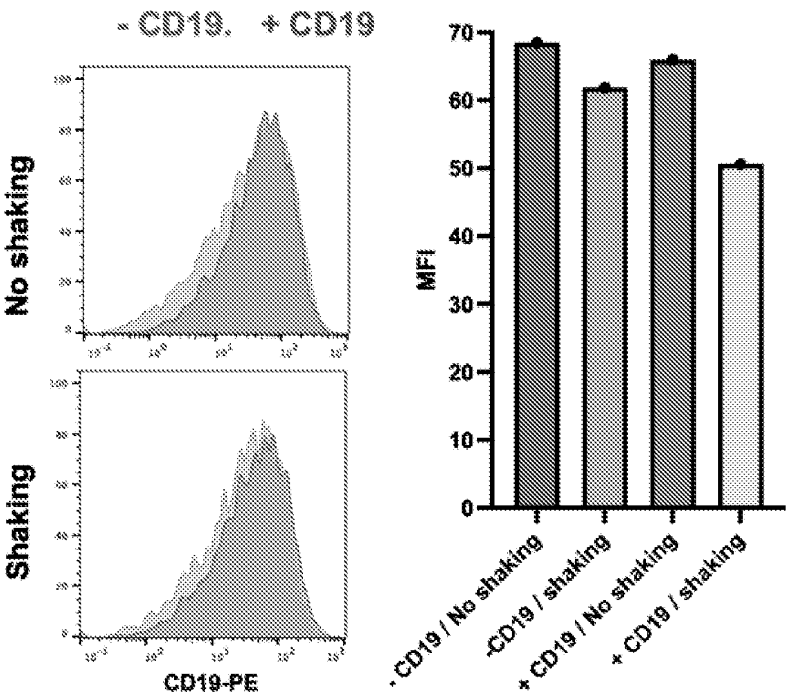


Figure 4 (part 2 of 2)

b)



c)

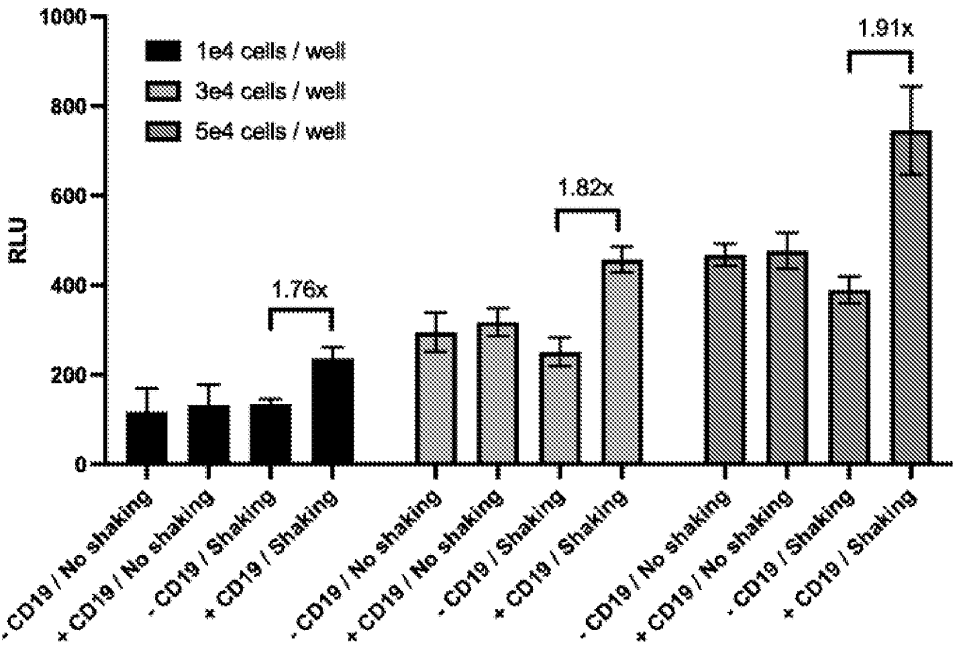


Figure 5

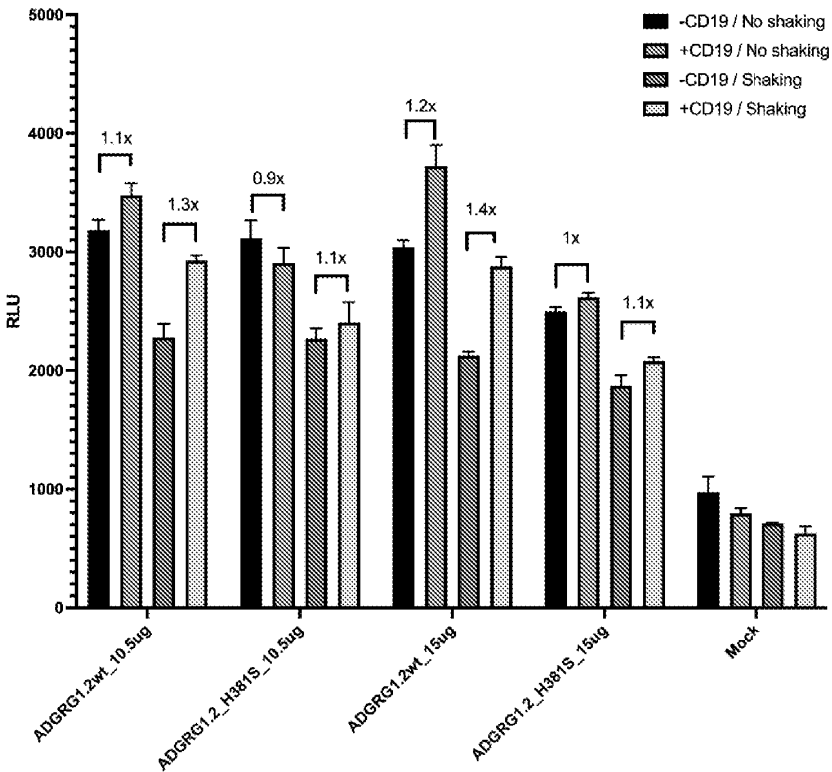


Figure 6

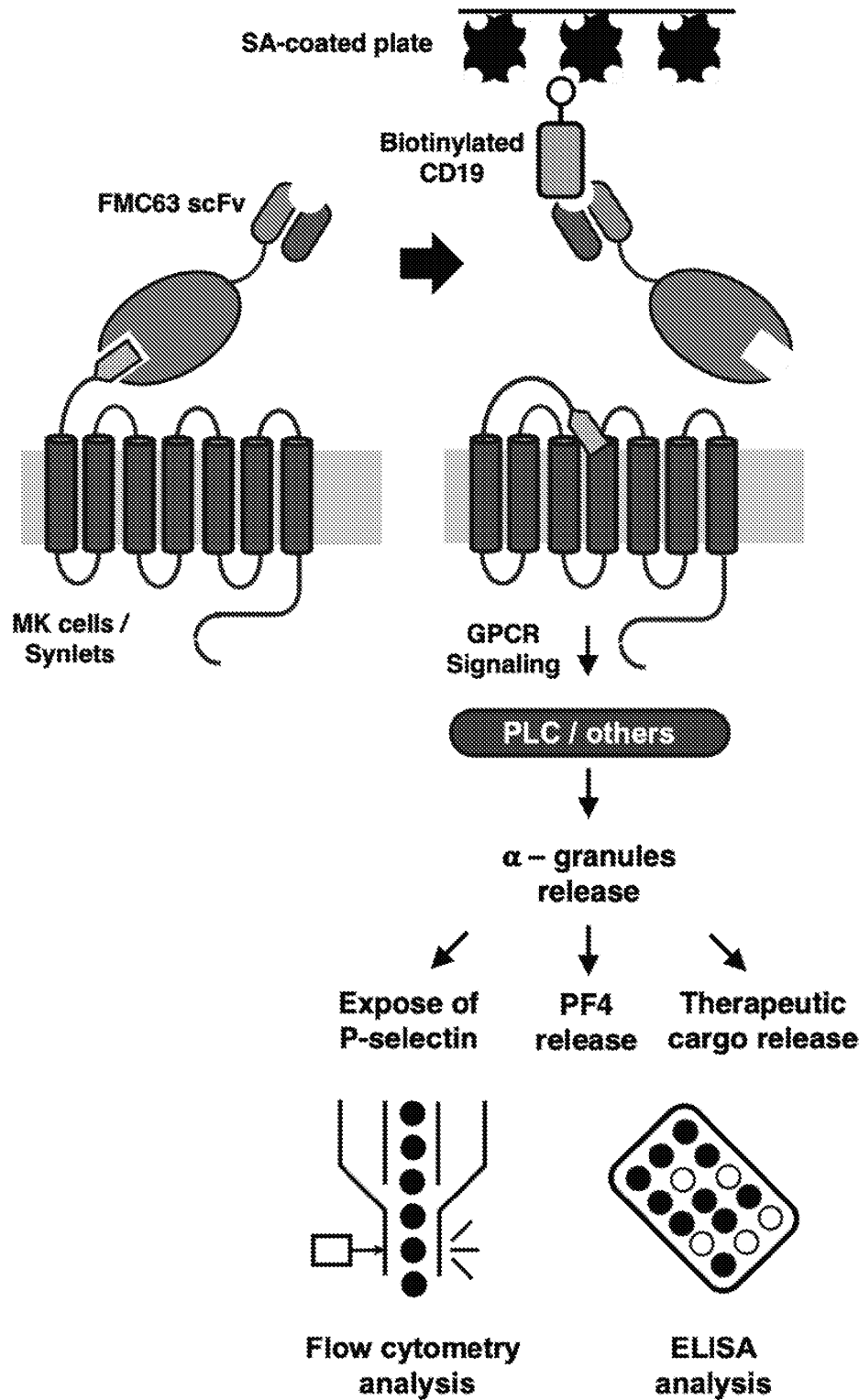


Figure 7

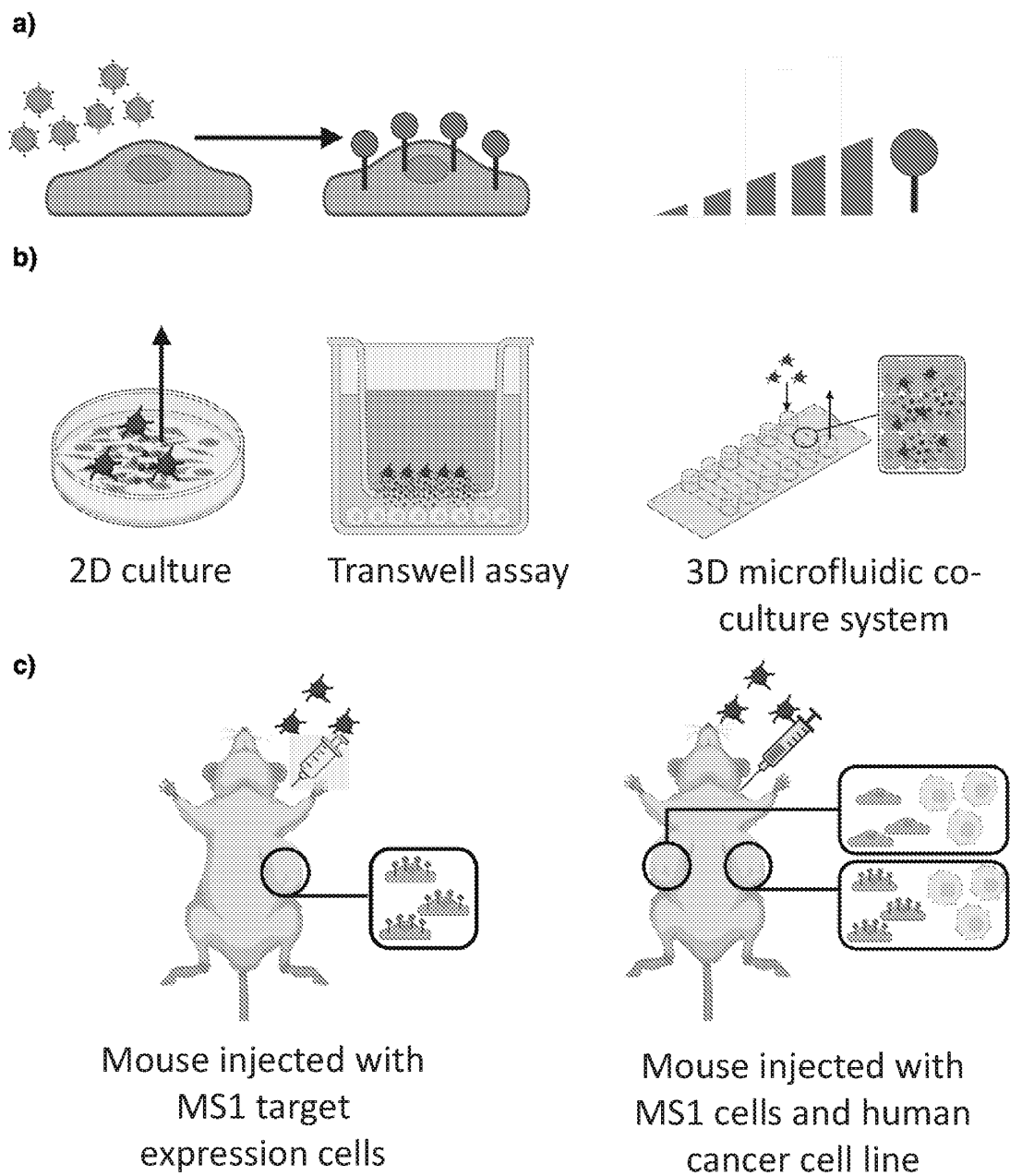


Figure 8

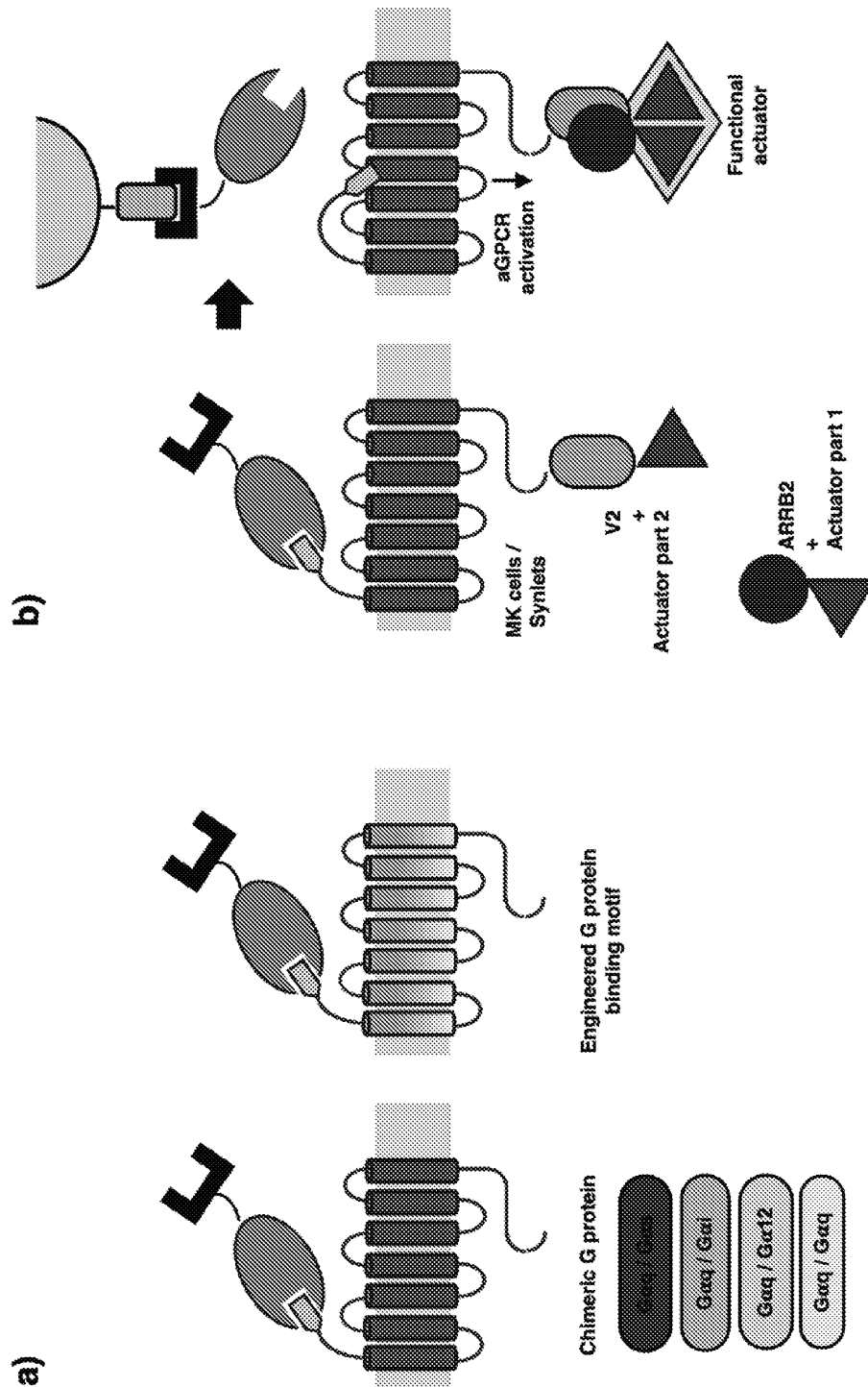


Figure 9

Receptor		HLT Cleavage Site and CTF Stalk		SEQ ID NO:
Consensus		CXC GPS β -Strand 13 Turn		
		CXCXHL TSPAVLXXXXXXXXXXXXXXXXXX-TM1		129
		TA		
I	ADGRL1 (LPHN1)	CACSHL TSPAVLNAHREIYQGRINELLSSV-TM1	97	
	ADGRL2 (LPHN2)	CACSHL TSPAILNAHREIAYKDGVEHLLTV-TM1	98	
	ADGRL3 (LPHN3)	CSCNHL TSPAVLNAHVEVKHSDAVHDLDDLVDV-TM1	99	
	ADGRL4 (ELTD1)	CRCNHL TSPAILNSSGQPSIGIKDYNILTRI-TM1	100	
II	ADGRE1 (EMR1)	CSCNQK-ANLAVINASGELTMDPSL-TM1	101	
	ADGRE2 (EMR2)	CRCNHL SSPAVLNAHYDVQEDDPVLT-TM1	102	
	ADGRE3 (EMR3)	CNCNHL SSPAVLNAHTSQEDDPVLT-TM1	103	
	ADGRE4 (EMR4)	CKCPHL SSPAVLVALAPKEDPVLT-TM1	104	
	ADGRE5 (CD97)	CQCSHL SSPAILNAHYDVEDWKLTLITR-TM1	105	
III	ADGRA1 (GPR123)	N/A*		
	ADGRA2 (GPR124)	LHCQHL-GNVAVLNELSAFPREVGGAGAGLH-TM1	106	
	ADGRA3 (GPR125)	IQCYSL-SNYAVLMDLTGSELYTQAASLLHP-TM1	107	
IV	ADGRC1 (CELSR1)	CQCSHT-ASPAVLMDISRRENGVEVLPLKI-TM1	108	
	ADGRC2 (CELSR2)	CQCNNM TSPAVLMDVSRRENGEILPLKT-TM1	109	
	ADGRC3 (CELSR3)	CRCNHT-GTPGVLDASPRERLEGDLLEL-TM1	110	
V	ADGRD1 (GPR133)	CRCNHL TSPAILNQVVPLELARGHQVALSS-TM1	111	
	ADGRD2 (GPR144)	CFCNHS-TSPAILQIYEVQSGPEEESLLR-TM1	112	
VI	ADGRF1 (GPR110)	CQCTHL TSPSILMSPFVPSTIFFPVVKWIT-TM1	113	
	ADGRF2 (GPR111)	CKCRPSKLP-TSPSILMSPHILES-TM1	114	
	ADGRF3 (GPR113)	CLCQHL TSPSVLMSPTVPEEPALALLTQ-TM1	115	
	ADGRF4 (GPR115)	CRCNYTSVV-MSPSILMSSEKSMTEK-TM1	116	
	ADGRF5 (GPR116)	CICDHL TSPSILMSPDSPDPSSLLGILLD-TM1	117	
VII	ADGRB1 (BAI1)	CLCDHL STFAILQLSADANMEKATLP-TM1	118	
	ADGRB2 (BAI2)	CQCQHL STFAVLAQPPKDLTLELAGSPSVP-TM1	119	
	ADGRB3 (BAI3)	CLCDHL STFAILQPPREIINESSGTPSVT-TM1	120	
VIII	ADGRG1 (GPR56)	CFCNHL TSPAVLVSSVEVDVAVHKHYLS-TM1	121	
	ADGRG2 (GPR64)	CTCSHL TSPGVLDLSRTSVLPQMMAL-TM1	122	
	ADGRG3 (GPR97)	CCCDHL TFPALLRFTLDQSTVHILTR-TM1	123	
	ADGRG4 (GPR112)	CQCDEL TSPGVLDLSSTVDSVNEQIL-TM1	124	
	ADGRG5 (GPR114)	CRCNHL TSPAVLQLSPALVPAELLAPL-TM1	125	
	ADGRG6 (GPR126)	CLCNHF TSPGVLDLPSSASQLDARNTKVL-TM1	126	
	ADGRG7 (GPR128)	CRCNHT-TSPAVLTFKKDYQPKSLD-TM1	127	
IX	ADGRV1 (VLGR1)	CACSHM SVYAVIARTQNLSSYNE-TM1	128	

Figure 10

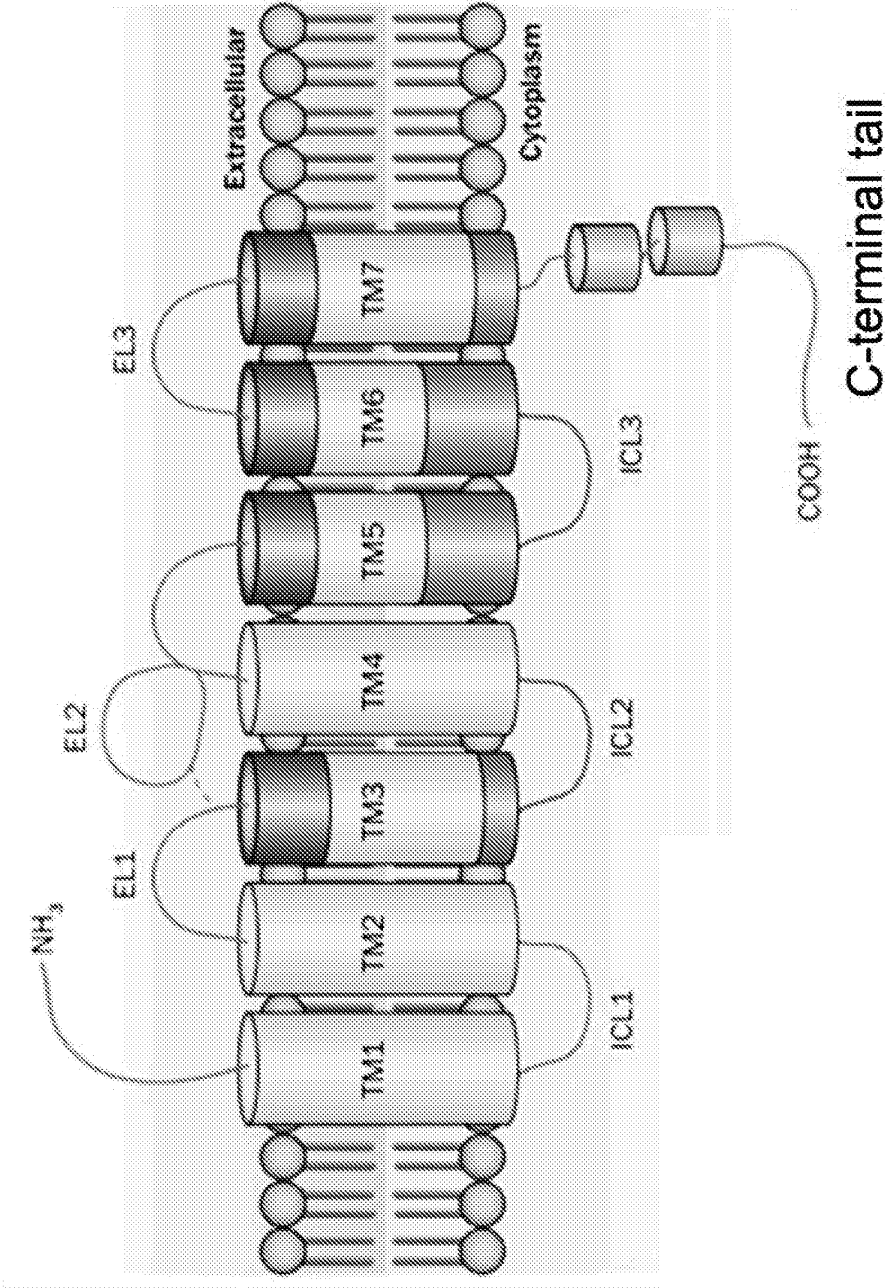


Figure 11

