

Fig.1

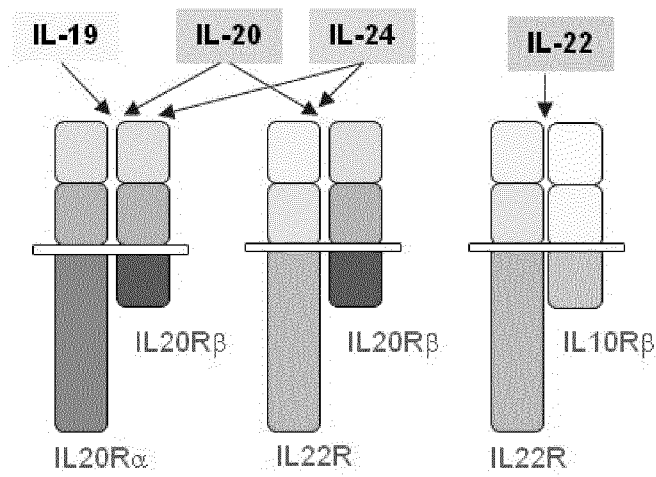


Fig.2

1	MRTLLTILTV	GSLAAHAPED	PSDLLQHVKF	QSSNFENILT	WDSGPEGTPD
51	TVYSIEYKTY	GERDWWAKKG	CQRITRKSCN	LTVETGNLTE	LYYARVTAVS
101	AGGRSATKMT	DRFSSLQHTT	LKPPDVTCIS	KVRSIQMIVH	PTPTPIRAGD
151	GHRLTLEDIF	HDLFYHLELQ	VNRTYQMHLG	GKQREYEFFG	LTPDTEFLGT
201	IMICVPTWAK	ESAPYMCRVK	TLPDRTWTYS	FSGAFLFSMG	FLVAVLCYLS
251	YRYVTKPPAP	PNSLNVQRVL	TFQPLRFIQE	HVLIPVFDLS	GPSSLAQPVQ
301	YSQIRVSGPR	EPAGAPQRHS	LSEITYLGQP	DISILQPSNV	PPPQILSPLS
351	YAPNAAPEVG	PPSYAPQVTP	EAQFFFYAPQ	AISKVQPSSY	APQATPDSWP
401	PSYGVCMEGS	GKDSPTGTLS	SPKHLRPKGQ	LQKEPPAGSC	MLGGLSLQEV
451	TSLAMEESQE	AKSLHQPLGI	CTDRTSDPNV	LHSGEEGTPQ	YKKGQLPLLS
501	SVQIEGHPMS	LPLQPPSRPC	SPSDQGPSPW	GLLESLVCPK	DEAKSPAPET
551	SDLEQPTELD	SLFRGLALTV	QWES		

Fig.3

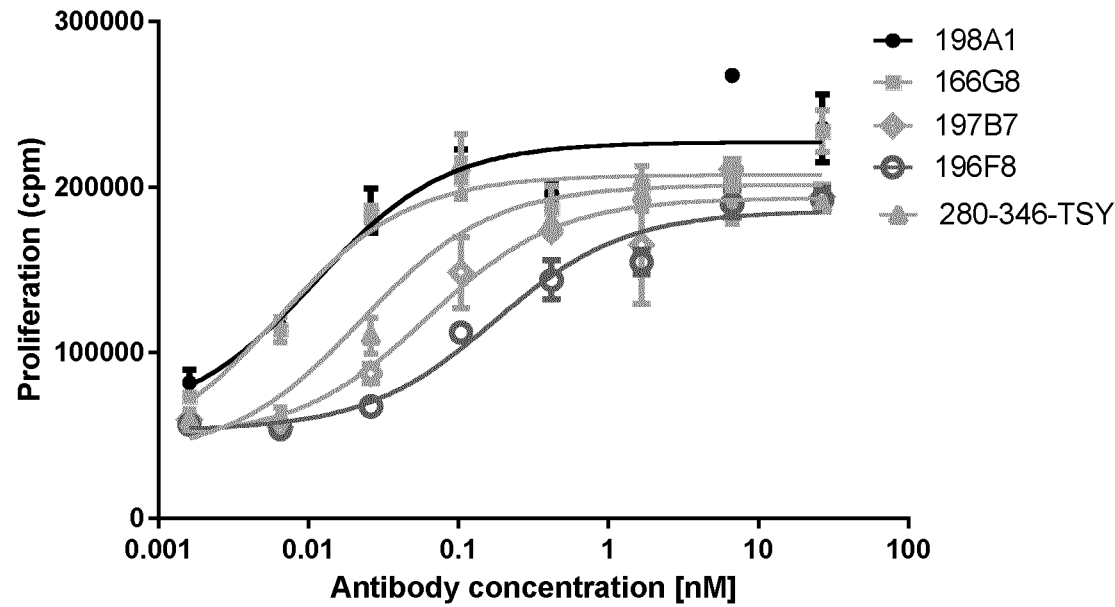
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1   ATGAGGACGC TGCTGACCAT CTTGACTGTG GGATCCCTGG CTGCTCACGC CCCTGAGGAC
61  CCCTCGGATC TGCTCCAGCA CGTGAAATTC CAGTCCAGCA ACTTTGAAAA CATCCTGACG
121 TGGGACAGCG GGCCGGAGGG CACCCCAGAC ACGGTCTACA GCATCGAGTA TAAGACGTAC
181 GGAGAGAGGG ACTGGGTGGC AAAGAAGGGC TGTCAGCGGA TCACCCGGAA GTCTGCAAC
241 CTGACGGTGG AGACGGGCAA CCTCACGGAG CTCTACTATG CCAGGGTCAC CGCTGTCAGT
301 GCGGGAGGCC GGTGAGCCAC CAAGATGACT GACAGGTTCA GCTCTCTGCA GCACACTACC
361 CTCAAGCCAC CTGATGTGAC CTGTATCTCC AAAGTGAGAT CGATTGAGAT GATTGTTCAT
421 CCTACCCCCA CGCCCATCCG TGCAGGCGAT GGCCACCGGC TAACCCTGGA AGACATCTTC
481 CATGACCTGT TCTACCACTT AGAGCTCCAG GTCAACCGCA CCTACCAAAT GCACCTTGGA
541 GGAAGCAGA GAGAATATGA GTTCTTCGGC CTGACCCCTG ACACAGAGTT CTTGGCACC
601 ATCATGATTT GCGTTCCCAC CTGGGCCAAG GAGAGTGCCC CCTACATGTG CCGAGTGAAG
661 AACTGCCAG ACCGGACATG GACCTACTCC TTCTCCGGAG CCTTCCTGTT CTCCATGGGC
721 TTCCTCGTCG CAGTACTCTG CTACCTGAGC TACAGATATG TCACCAAGCC GCCTGCACCT
781 CCCAACTCCC TGAACGTCCA GCGAGTCCTG ACTTTCCAGC CGCTGCGCTT CATCCAGGAG
841 CACGTCCTGA TCCCTGTCTT TGACCTCAGC GGCCCCAGCA GTCTGGCCCA GCCTGTCCAG
901 TACTCCCAGA TCAGGGTGTC TGGACCCAGG GAGCCTGCAG GAGCTCCACA GCGGCATAGC
961 CTGTCCGAGA TCACCTACTT AGGGCAGCCA GACATCTCCA TCCTCCAGCC CTCCAACGTG
1021 CCACCTCCCC AGATCCTCTC CCCACTGTCC TATGCCCCAA ACGCTGCCCC TGAGGTCGGG
1081 CCCCCATCCT ATGCACCTCA GGTGACCCCC GAAGCTCAAT TCCCATTCTA CGCCCCACAG
1141 GCCATCTCTA AGGTCCAGCC TTCCTCCTAT GCCCCCAAG CCACTCCGGA CAGCTGGCCT
1201 CCCTCCTATG GGGTATGCAT GGAAGGTTCT GGCAAAGACT CCCCCACTGG GACACTTTCT
1261 AGTCCTAAAC ACCTTAGGCC TAAAGGTCAG CTTGAGAAAG AGCCACCAGC TGGAAGCTGC
1321 ATGTTAGGTG GCCTTTCTCT GCAGGAGGTG ACCTCCTTGG CTATGGAGGA ATCCCAAGAA
1381 GCAAATCAT TGCACCAGCC CCTGGGGATT TGCACAGACA GAACATCTGA CCCAAATGTG
1441 CTACACAGTG GGGAGGAAGG GACACCACAG TACCTAAAGG GCCAGCTCCC CCTCCTCTCC
1501 TCAGTCCAGA TCGAGGGCCA CCCCATGTCC CTCCCTTTGC AACCTCCTTC CCGTCCATGT
1561 TCCCCCTCGG ACCAAGGTCC AAGTCCCTGG GGCTGCTGG AGTCCCTTGT GTGTCCCAAG
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Fig.4

A.



B.

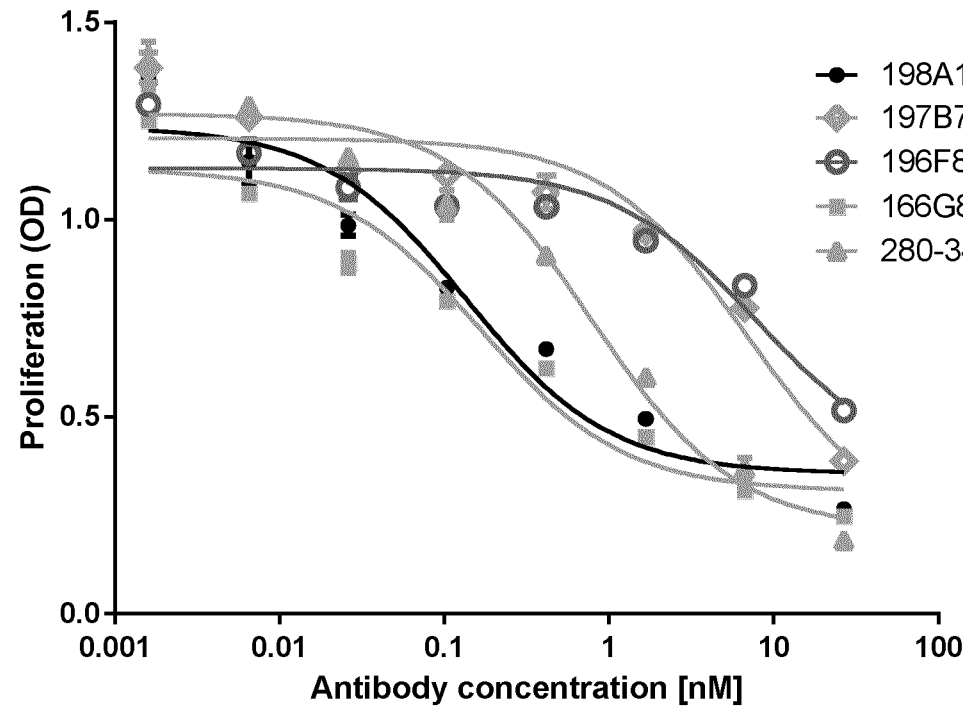


Fig.5

A

BC029273.1	VRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRITYQM--HLGGKQREYEFFGLTPDTEFLGTIMICVPTWA	SEQ ID NO: 94
IL22RA1-ECD-HIS	--.....	SEQ ID NO: 94
01113239 (rhesus)	--..... ES	SEQ ID NO: 95
FS371752 (CYNO)	 Y - S VNS	SEQ ID NO: 96
FS368027 (CYNO)	 Y - S VNS	SEQ ID NO: 97
FS371904 (CYNO)	 Y - S--.....S	SEQ ID NO: 98

*residue directly involved in IL22 binding.

B

human	1	LRLEYLRLTIGYRLNGTAATMGWSCIIILFLVATATGVHSPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDVTVYSIEYKTYGERDWAKKGCQRITRK	SEQ ID NO: 99
rhesus	1	N.....	SEQ ID NO: 100
cyno1	1	N.....	SEQ ID NO: 101
human	101	SCNLTVEITGNLTELYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTICISKVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRITYQM	
rhesus	101	H.....N.....A.....P.....	
cyno1	101	H.....N.....A.....P..... Y - S	
→huFc			
human	201	HLGGKQREYEFFGLTPDTEFLGTIMICVPTWAKESAPYMCRVKTLTPDRTW	SEQ ID NO: 99
rhesus	201	 ES.K.....R.....	SEQ ID NO: 100
cyno1	200	S.K.....R.....	SEQ ID NO: 101

loop6 (PTW; IL22 binding, next to deletion in cyIL22R)

Fig. 6

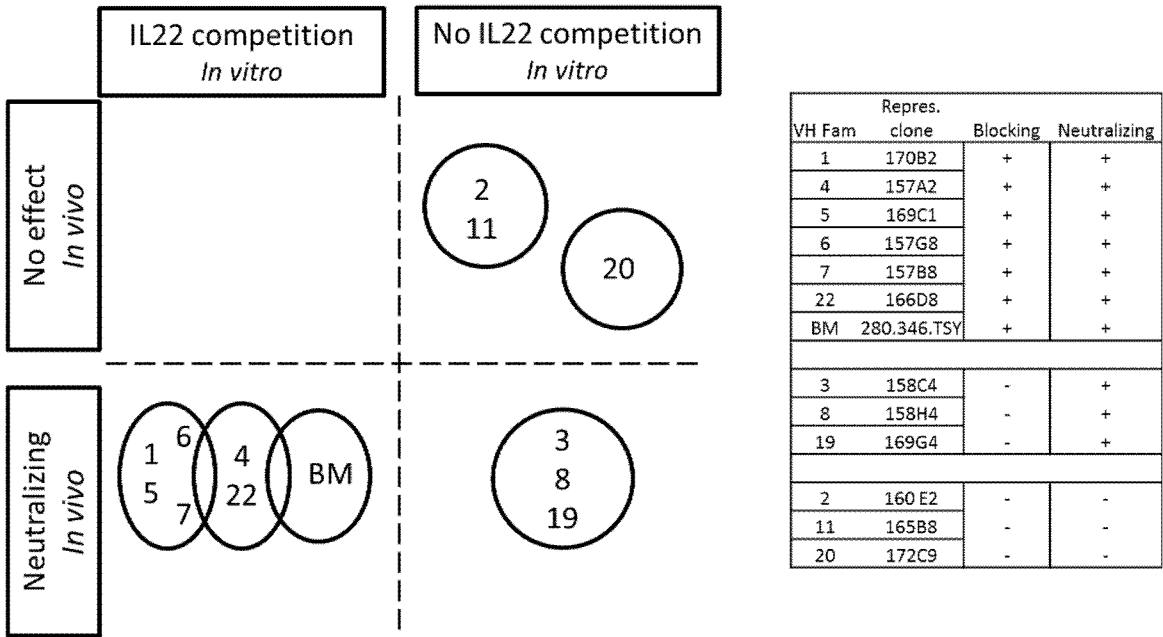


Fig. 7

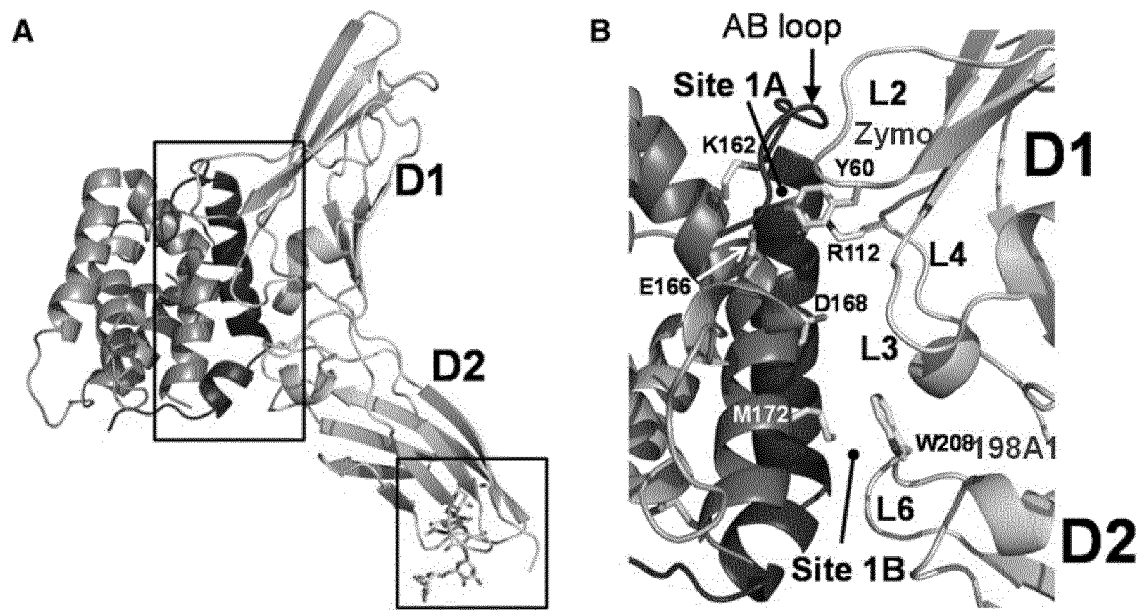


Fig. 8

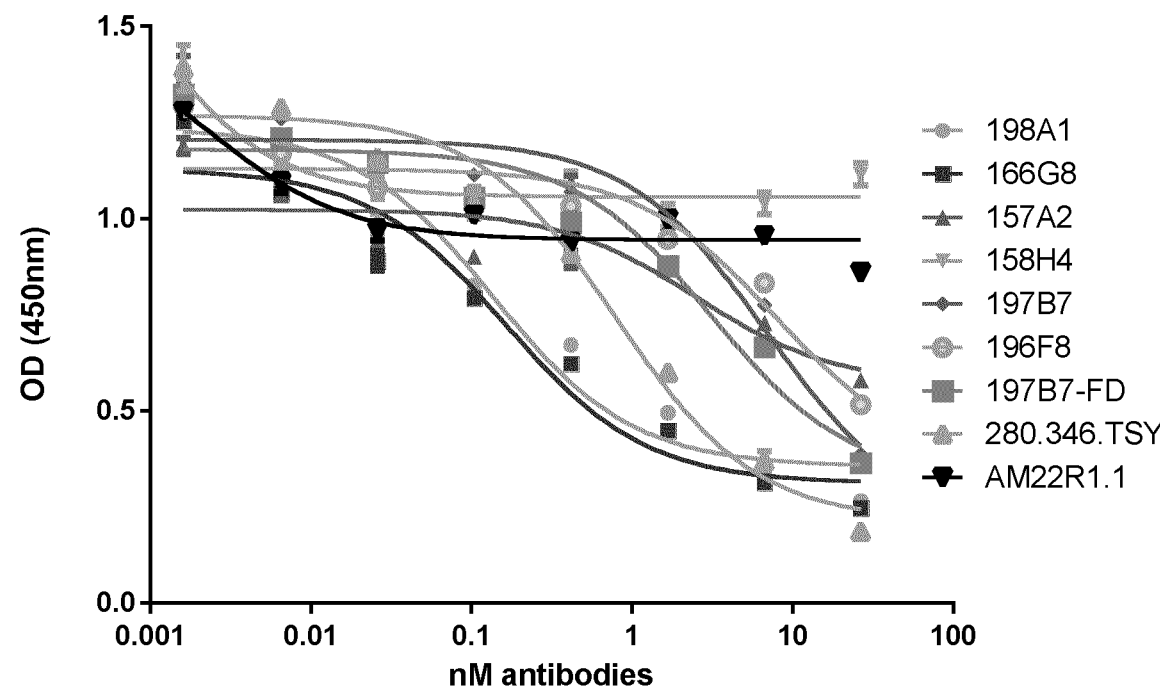
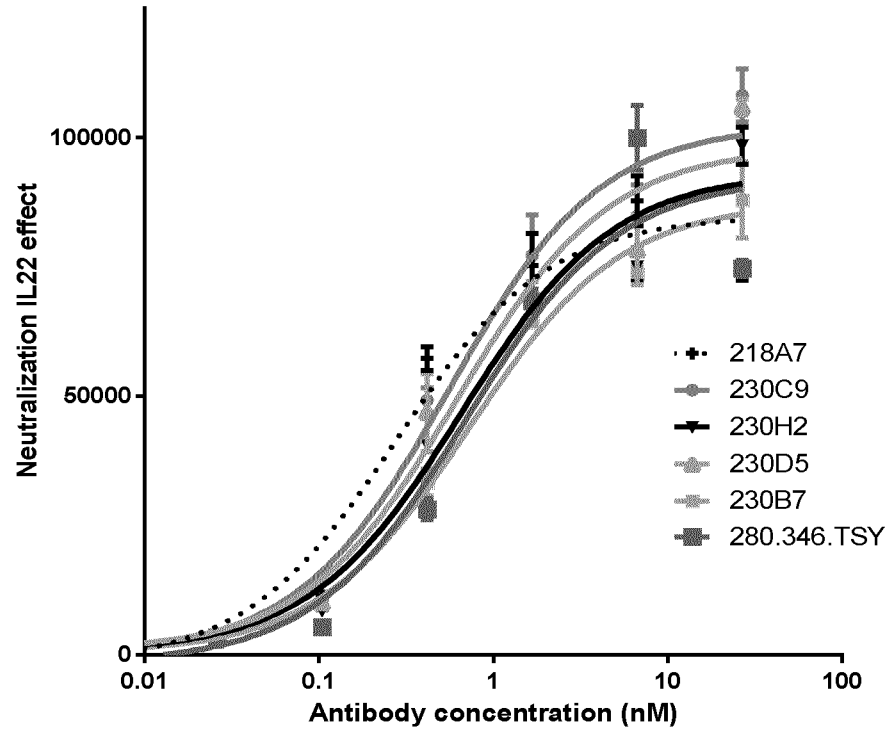


Fig. 9

A



B

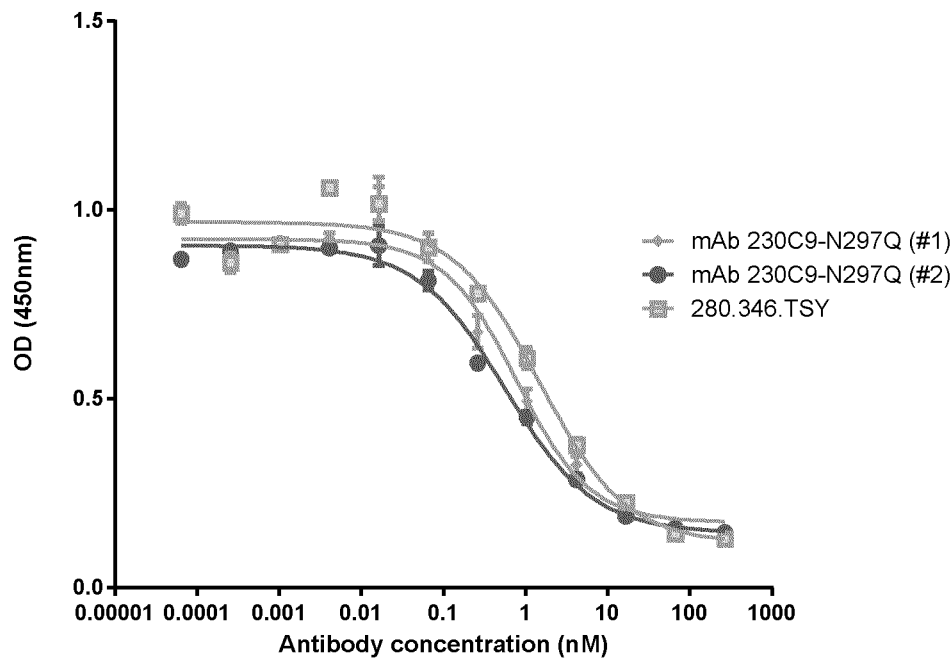


Fig. 10

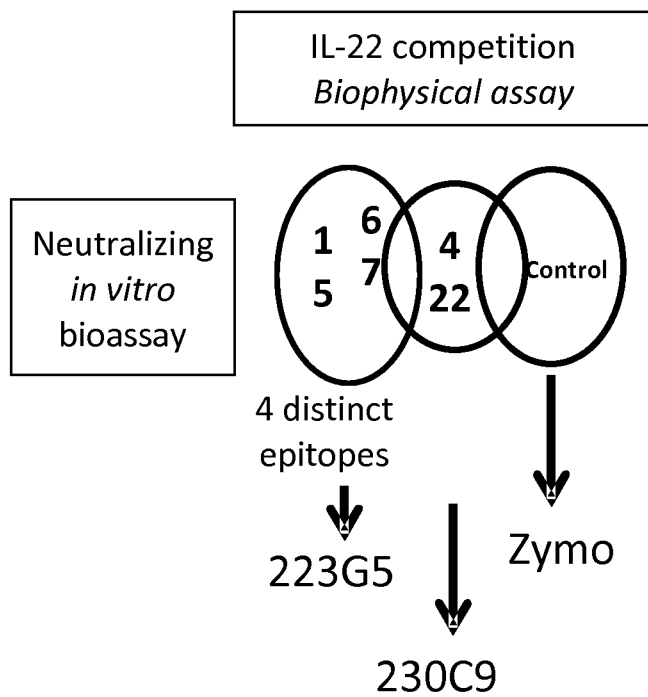


Fig. 11

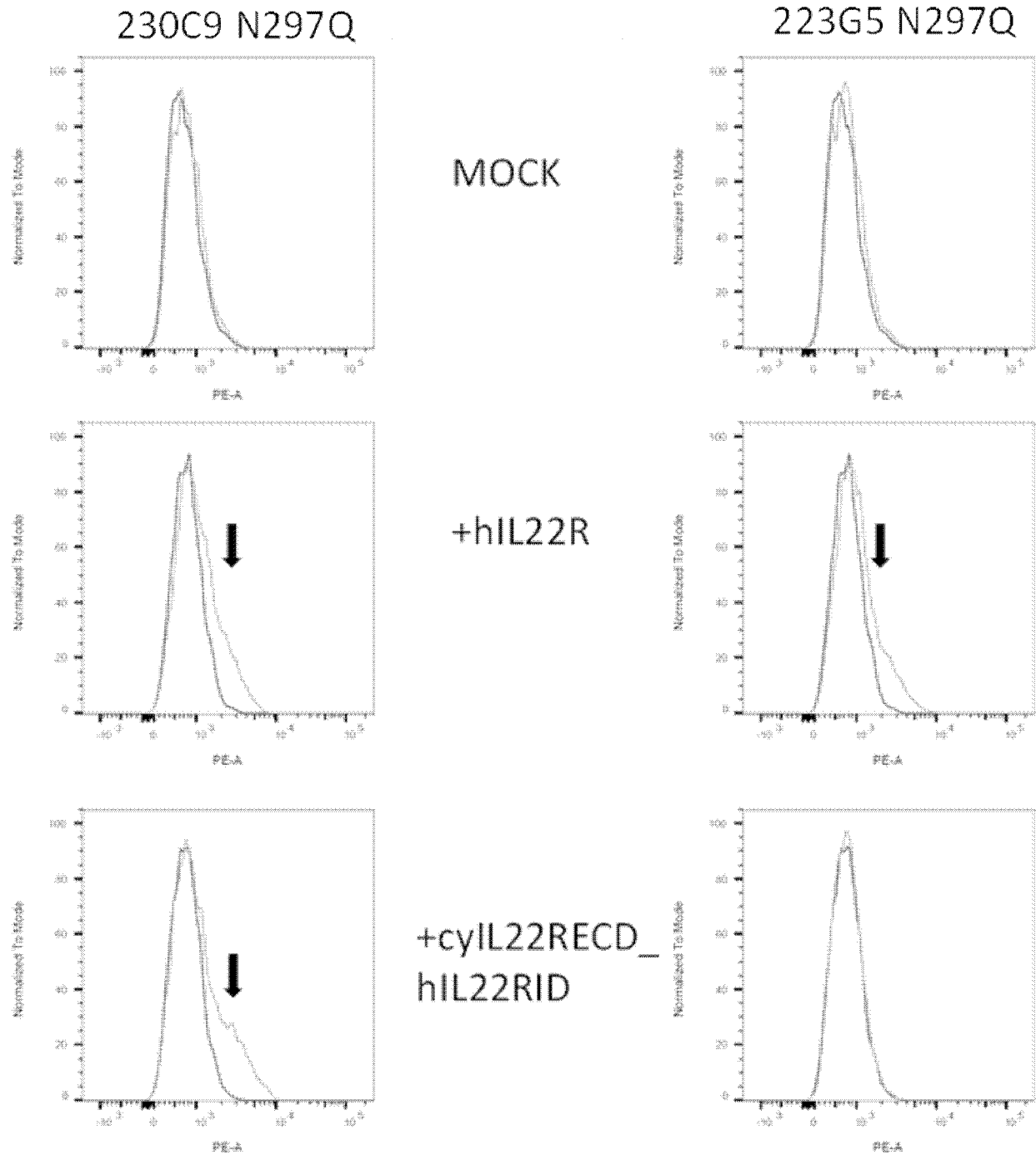


Fig. 12

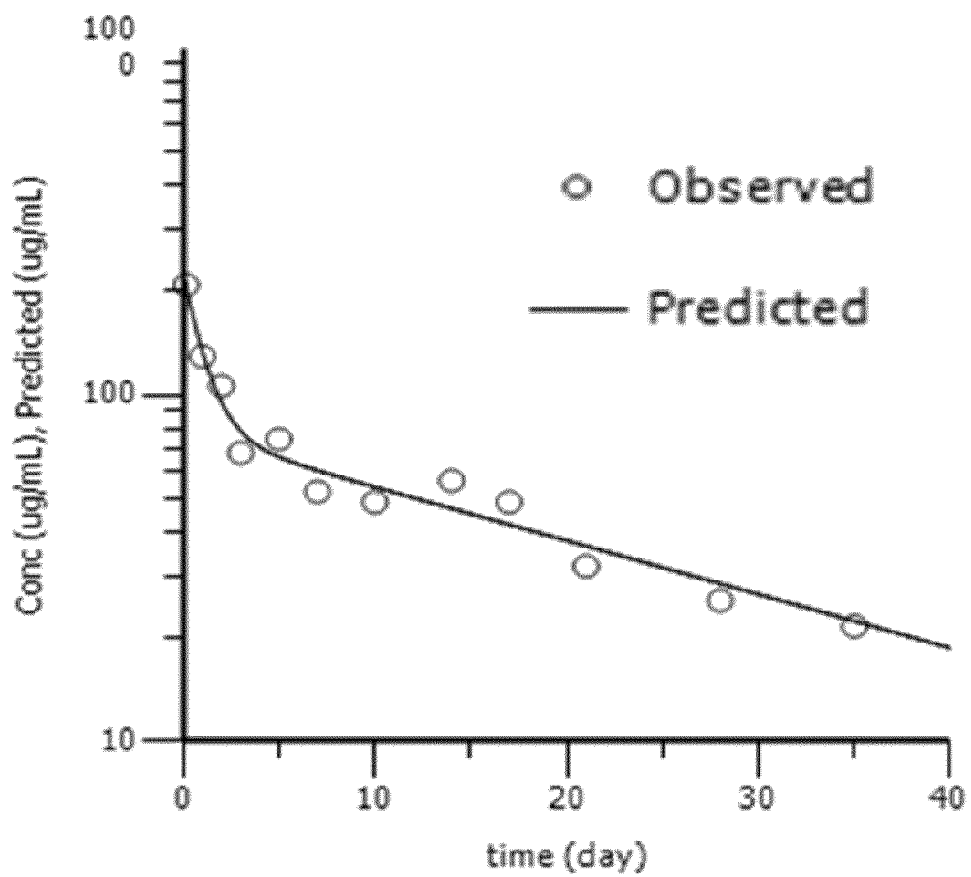
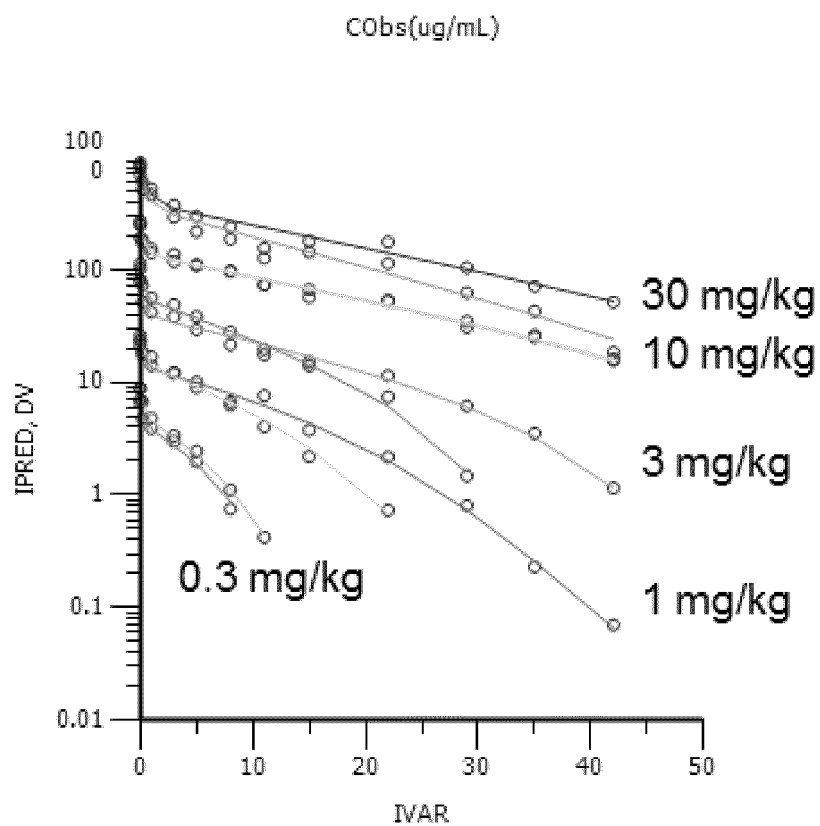


Fig. 13

A



B

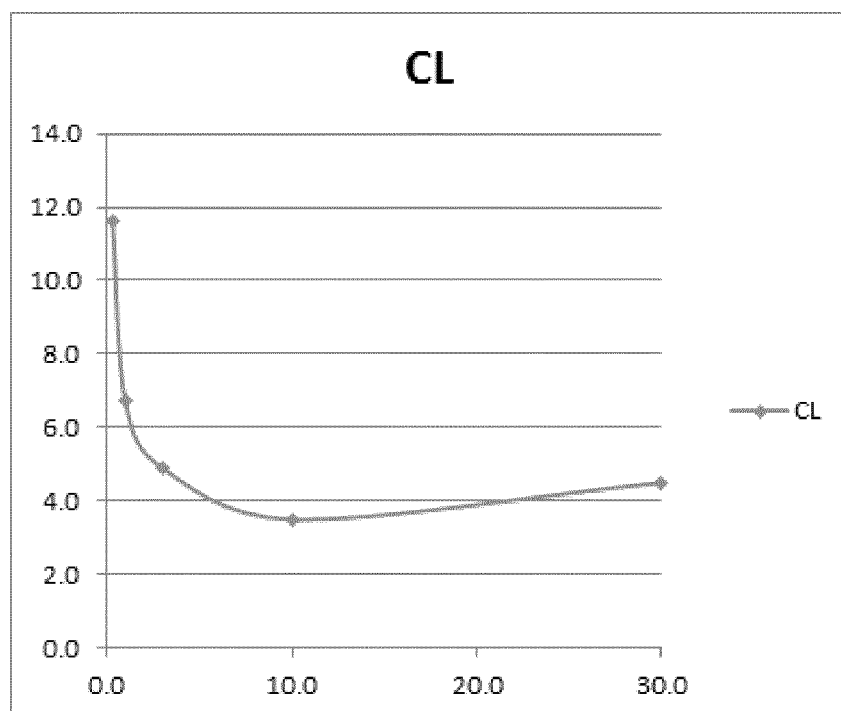
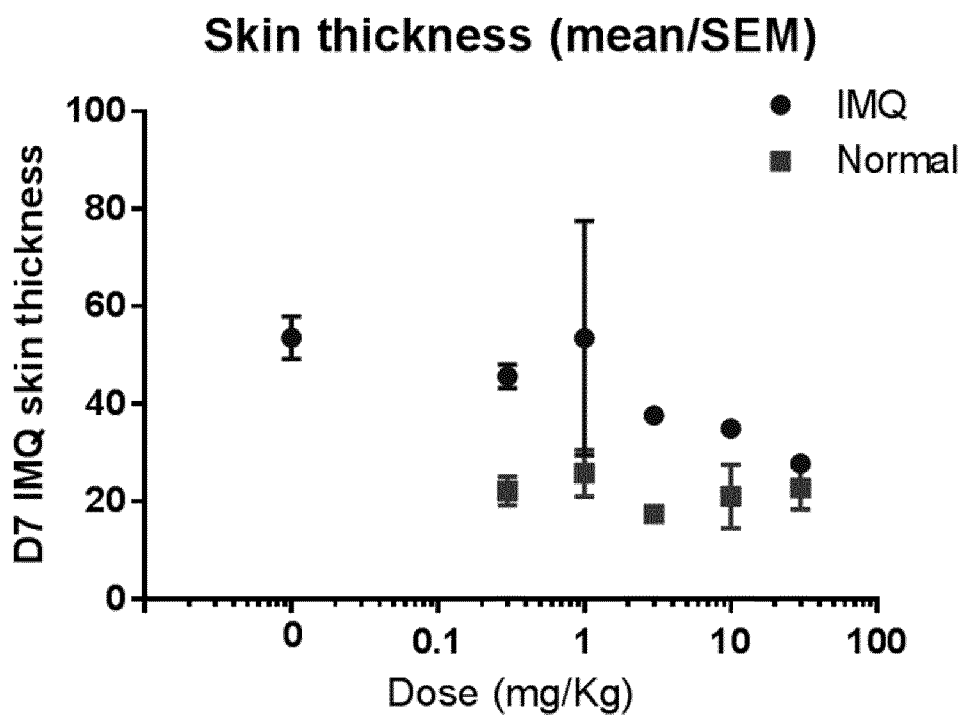


Fig. 14

A



B

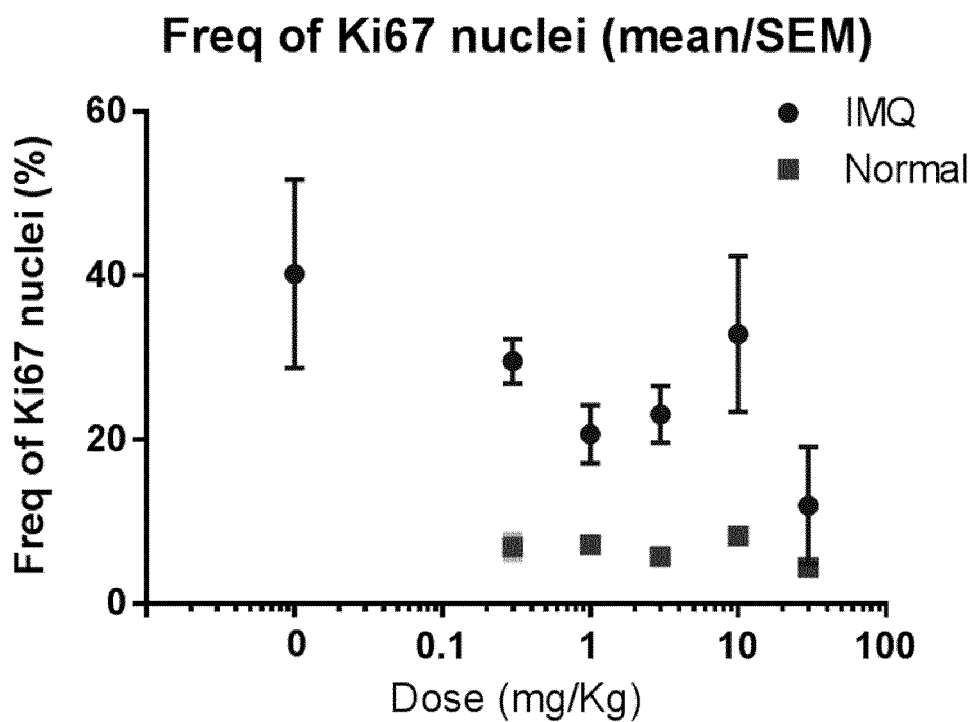


Fig. 15

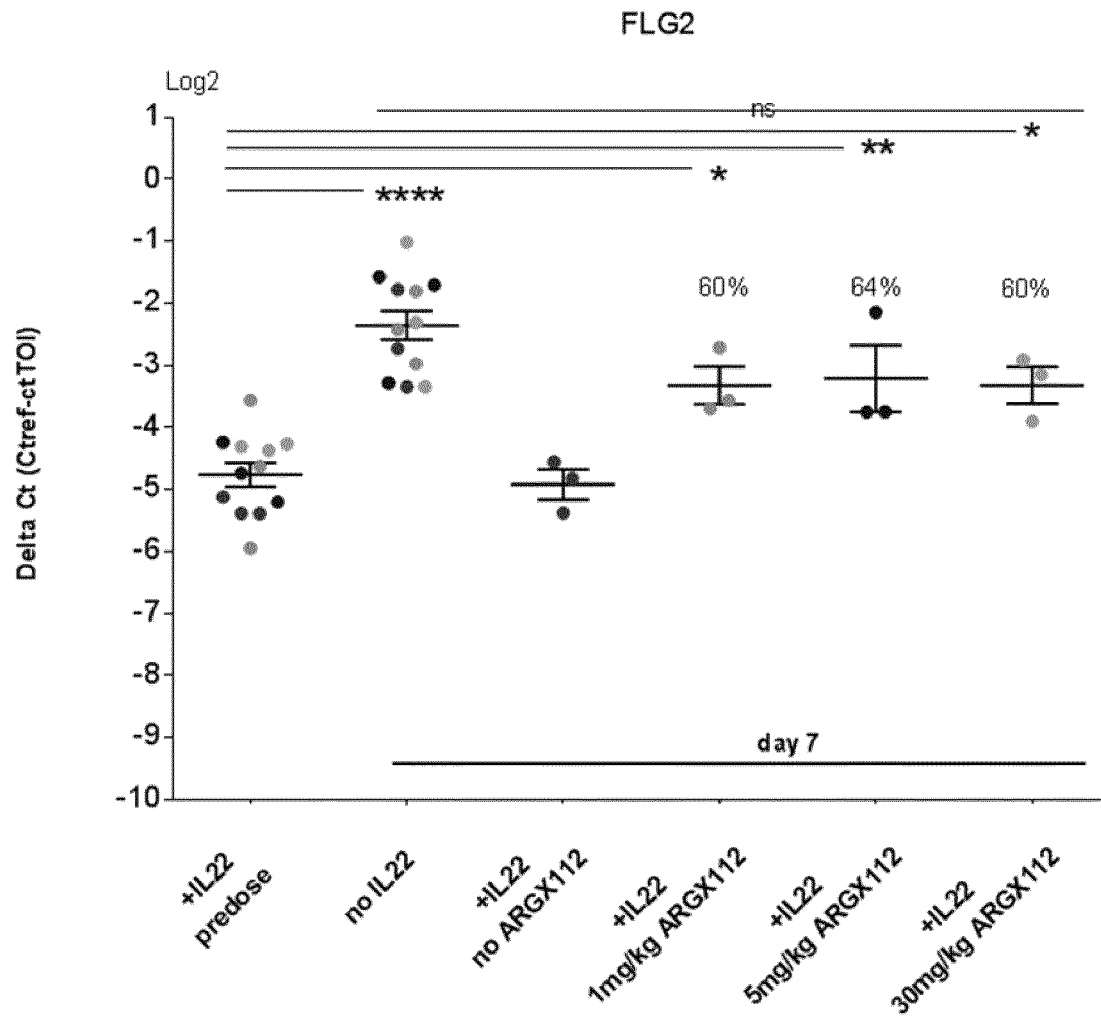


Fig. 16

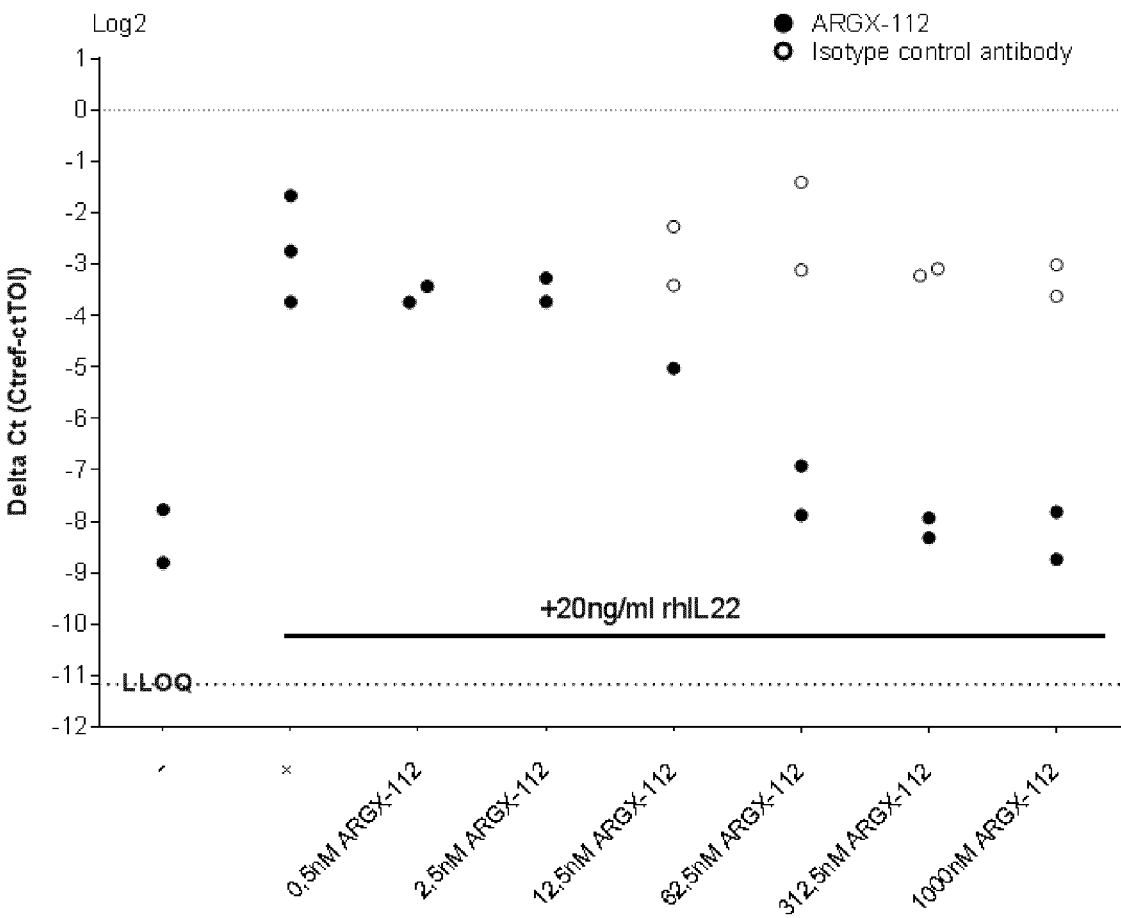
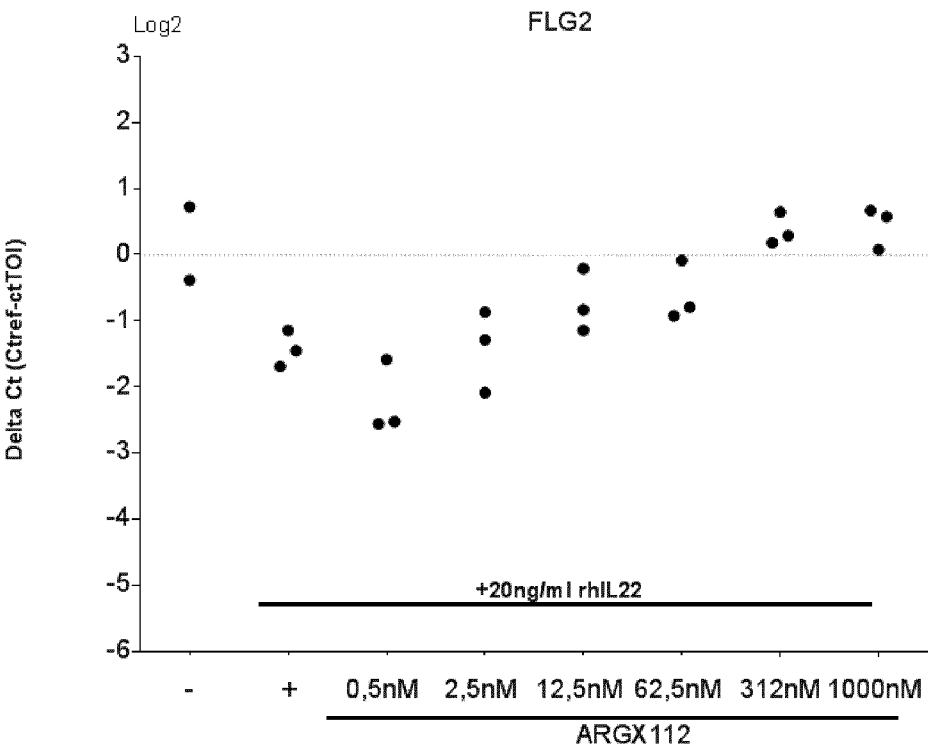


Fig. 17

A



B

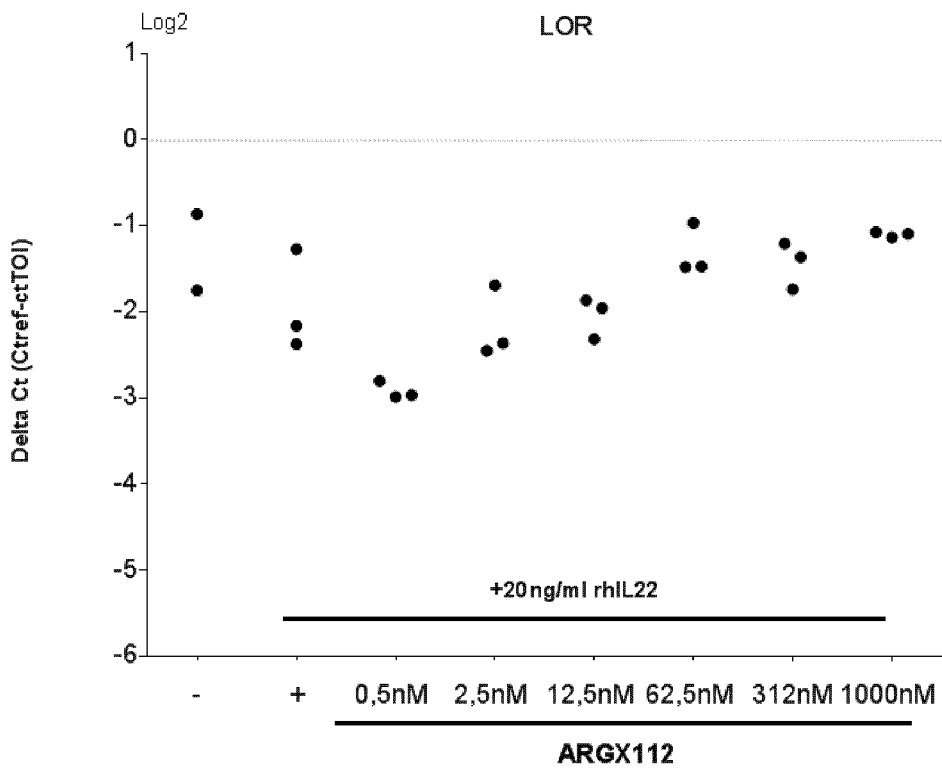


Fig. 18

