

Figure 1

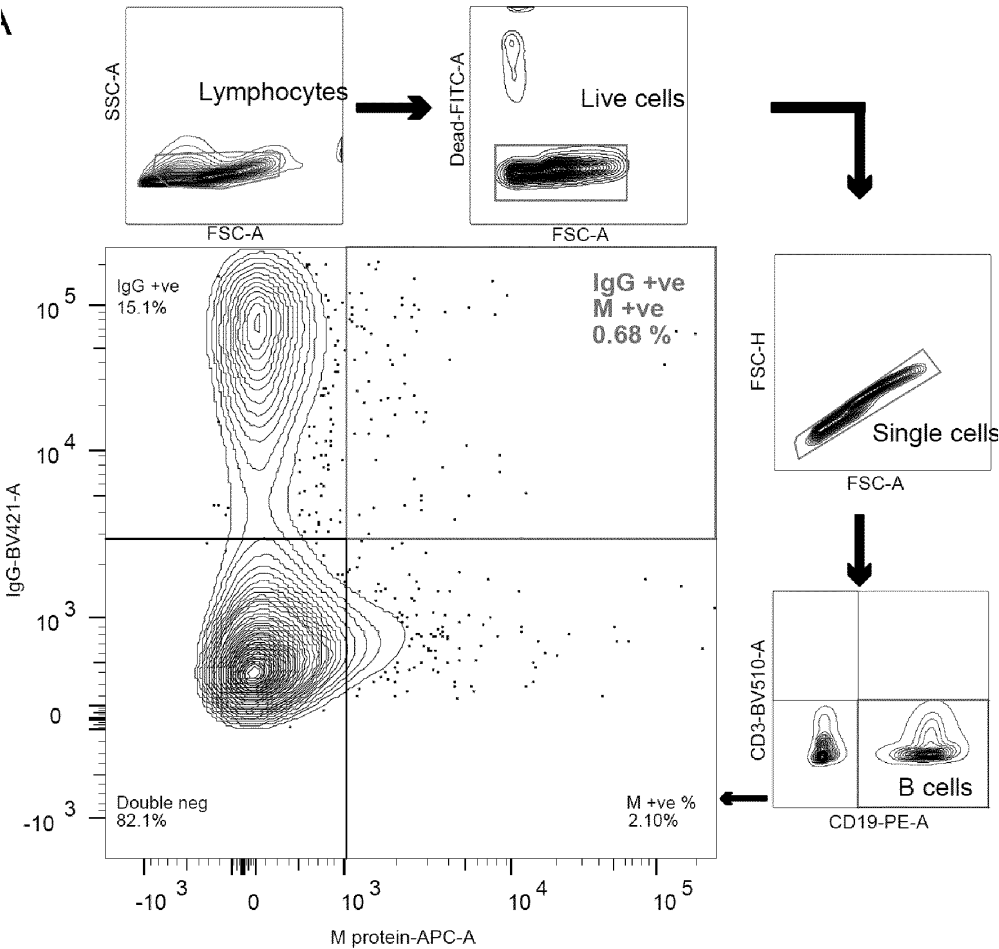


Figure 2

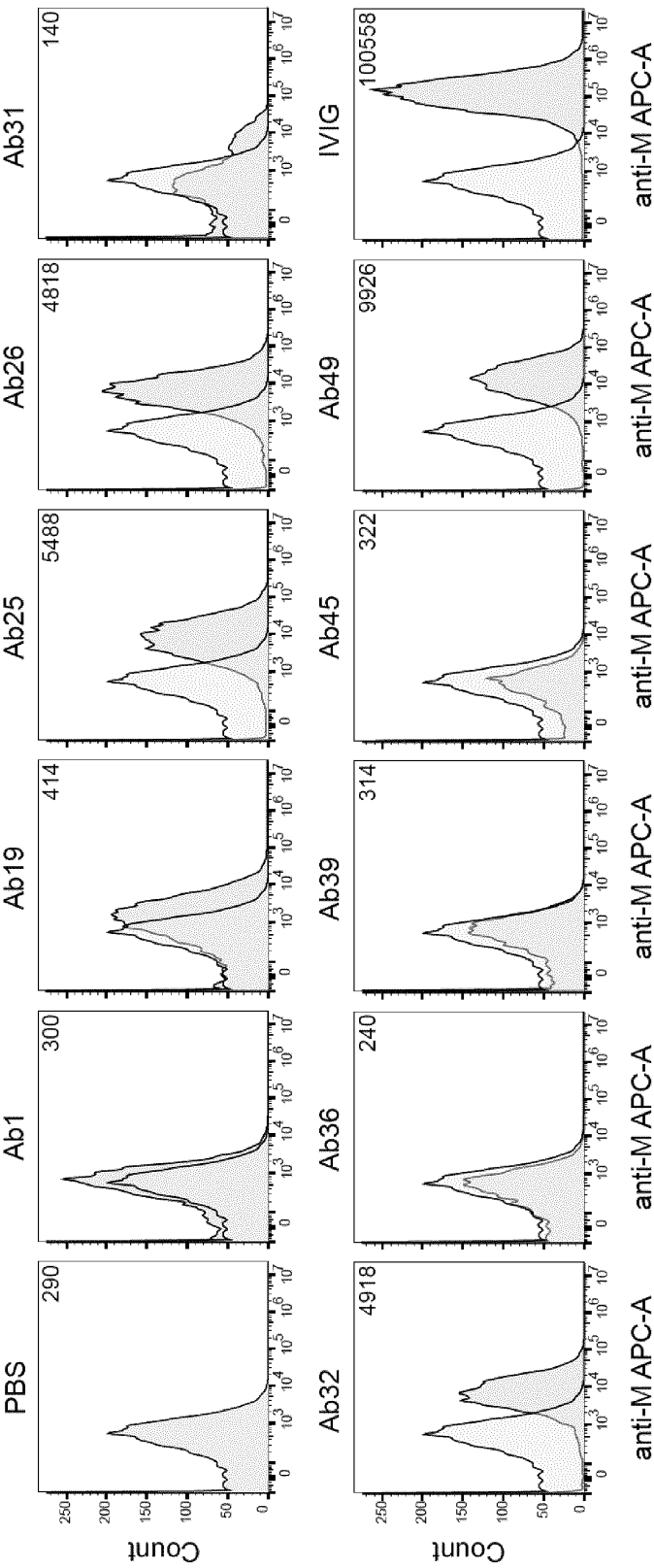


Figure 3

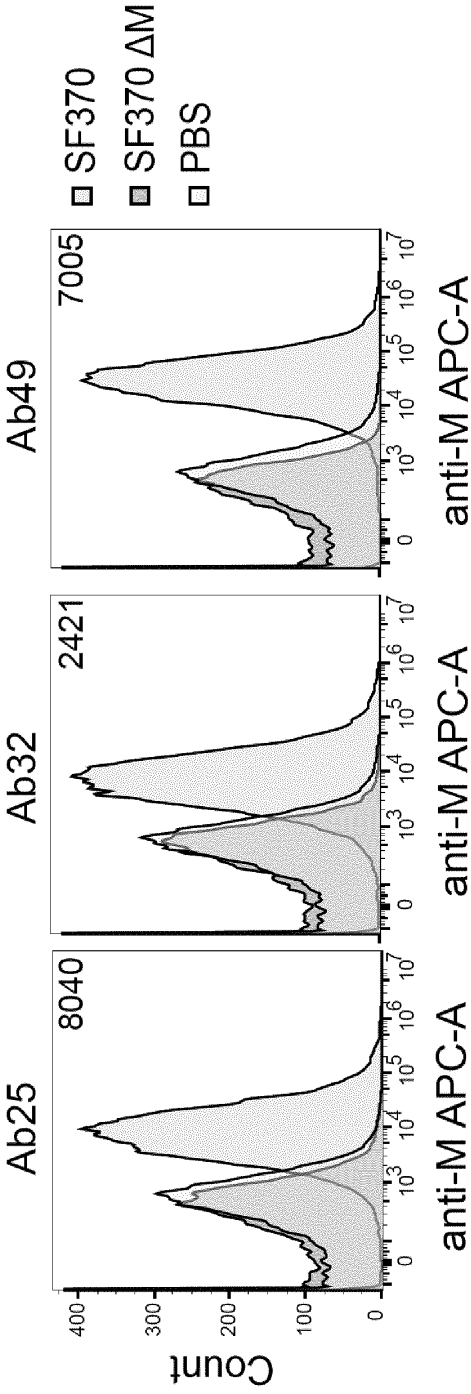


Figure 4

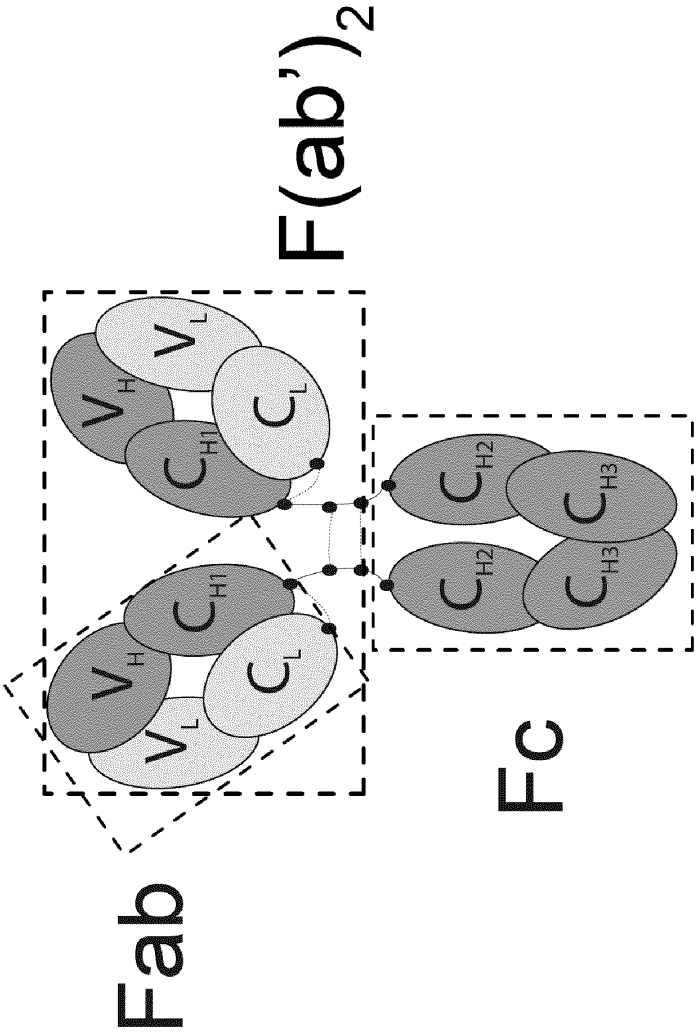


Figure 5

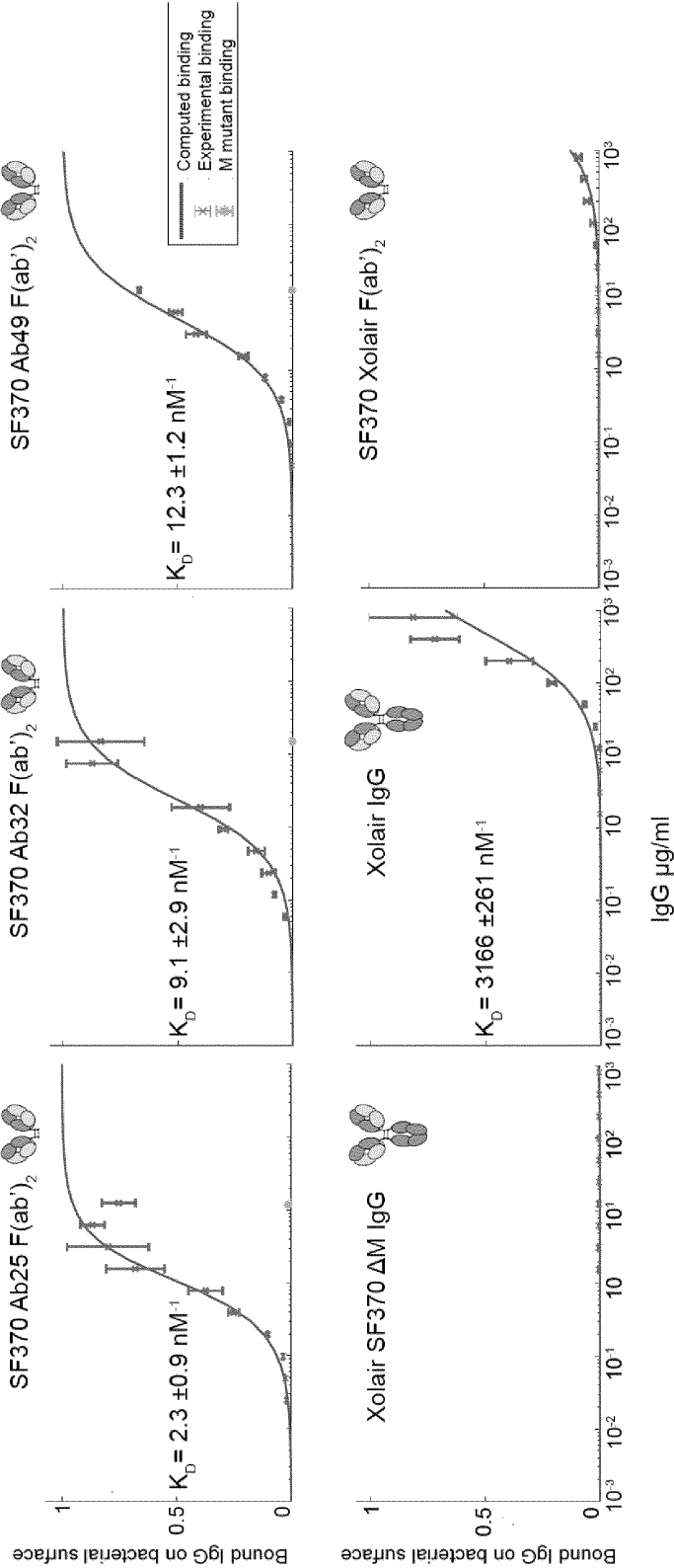


Figure 6

A SIM immunofluorescence

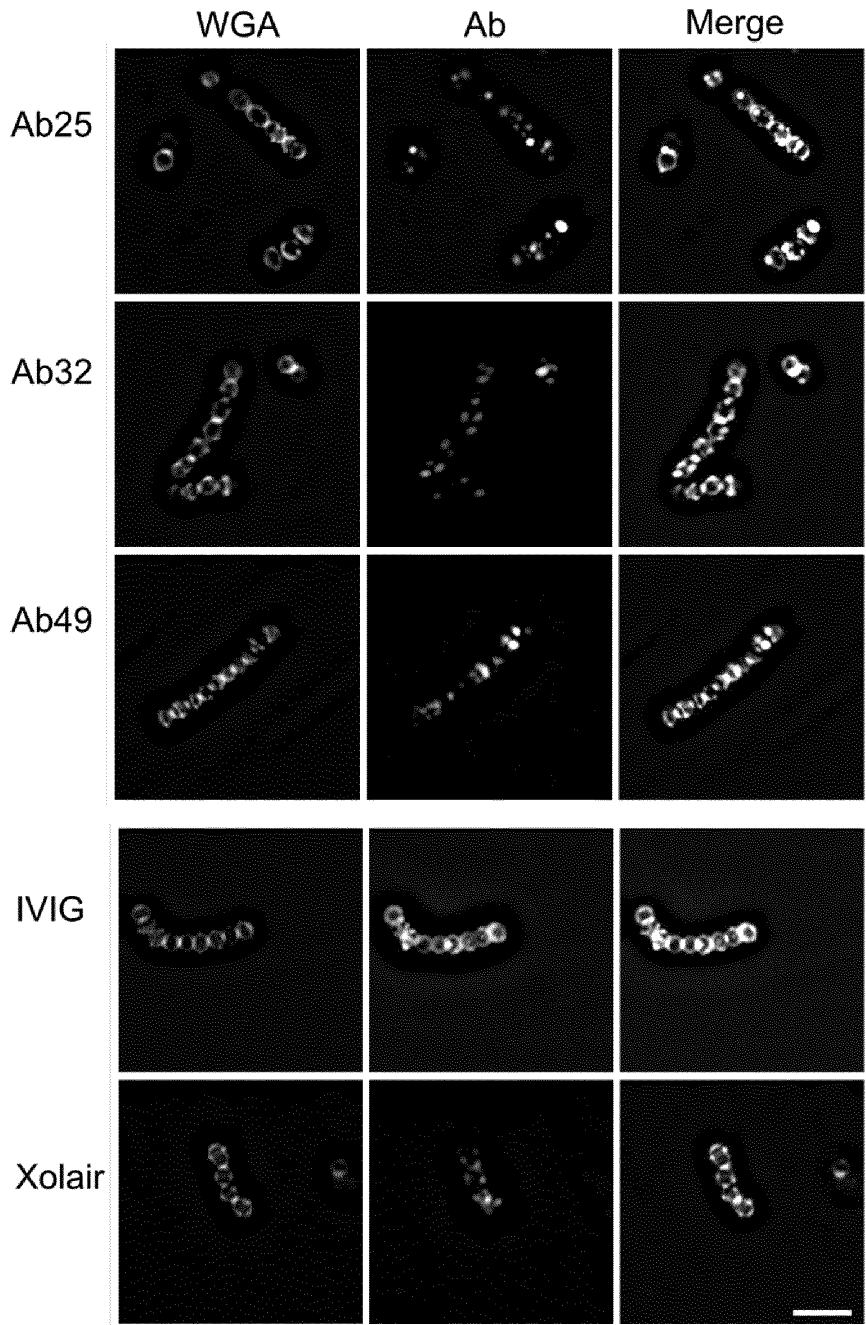


Figure 7

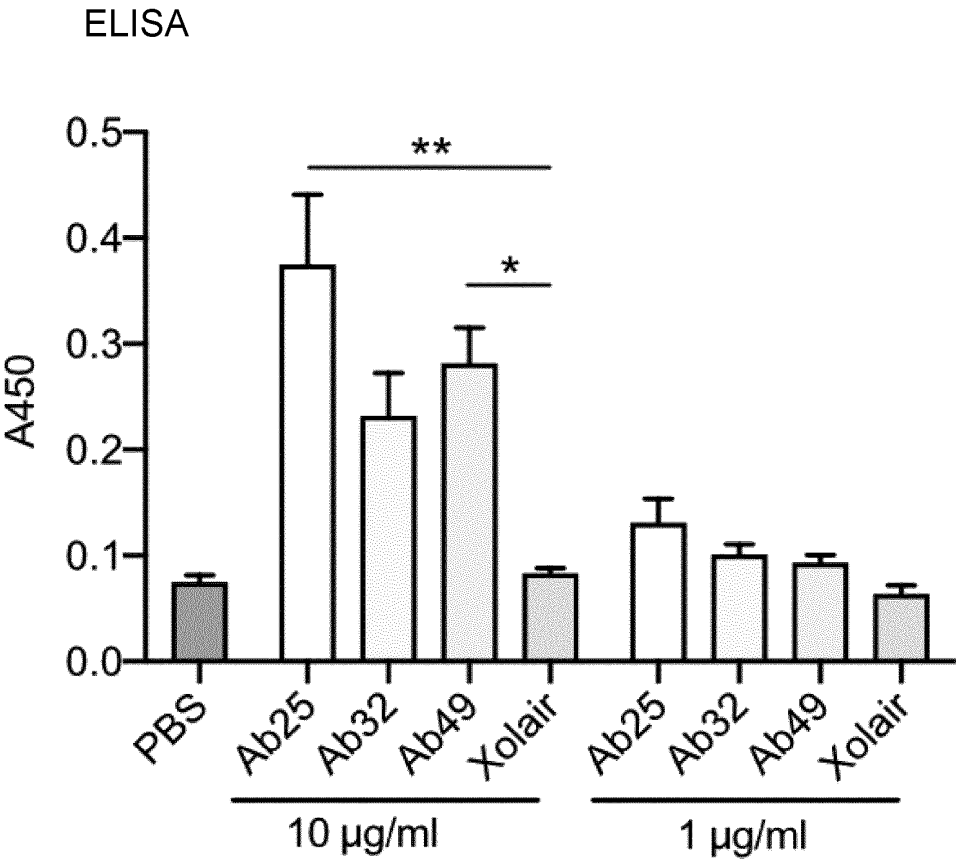


Figure 8

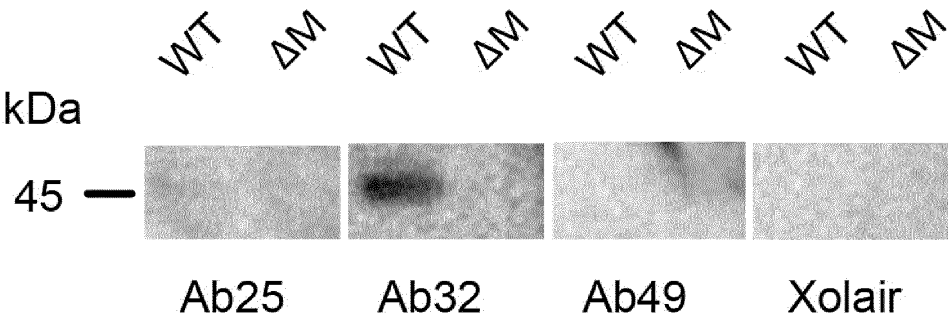


Figure 9

Agglutination

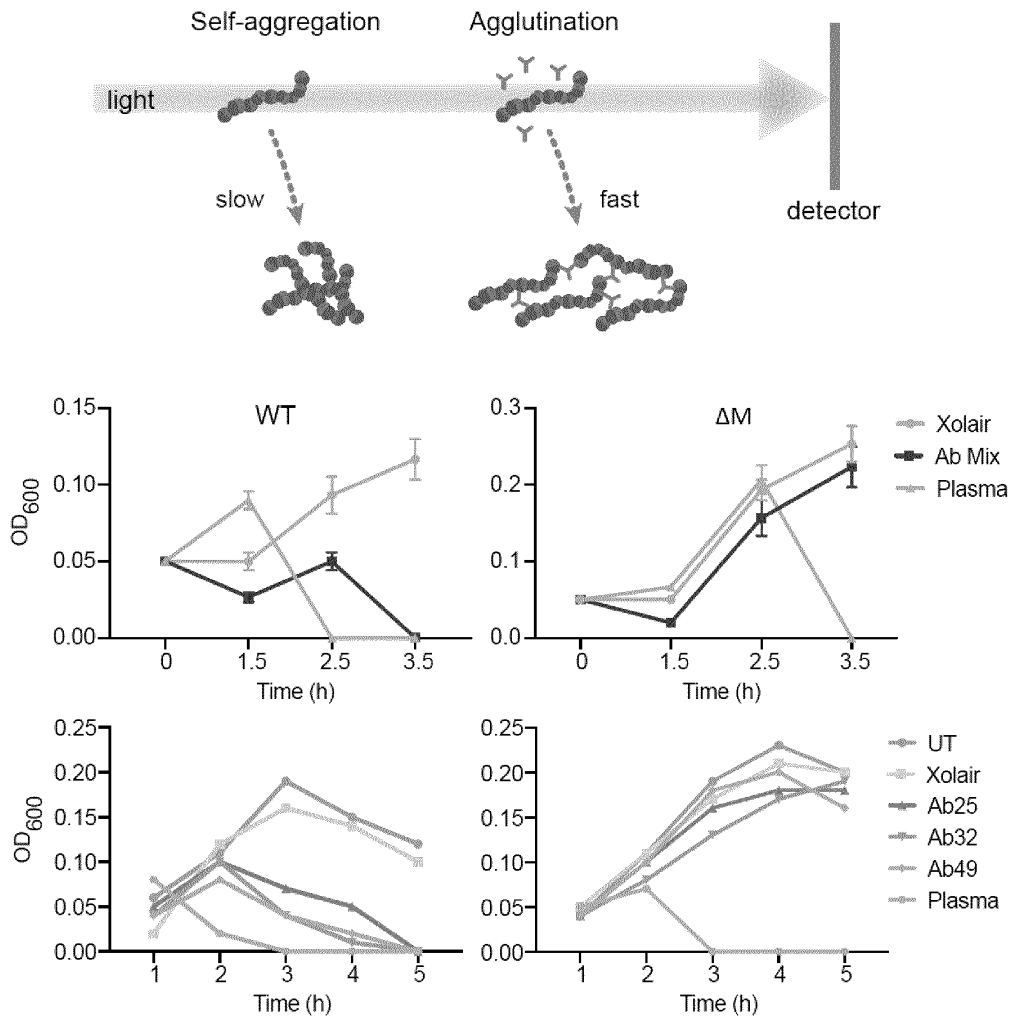


Figure 10

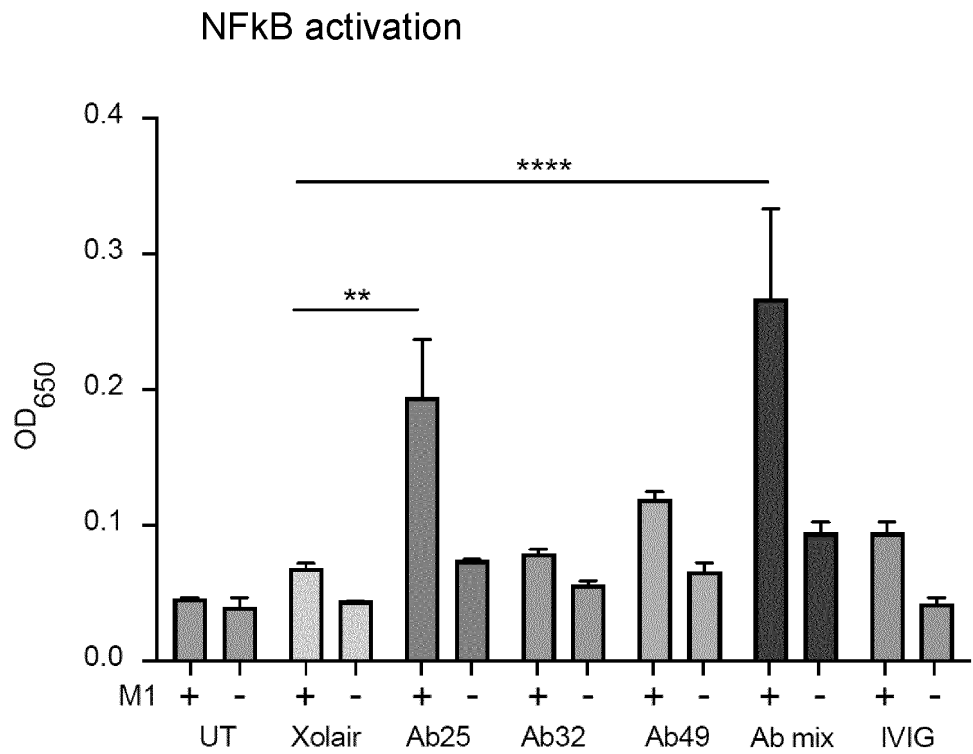


Figure 11

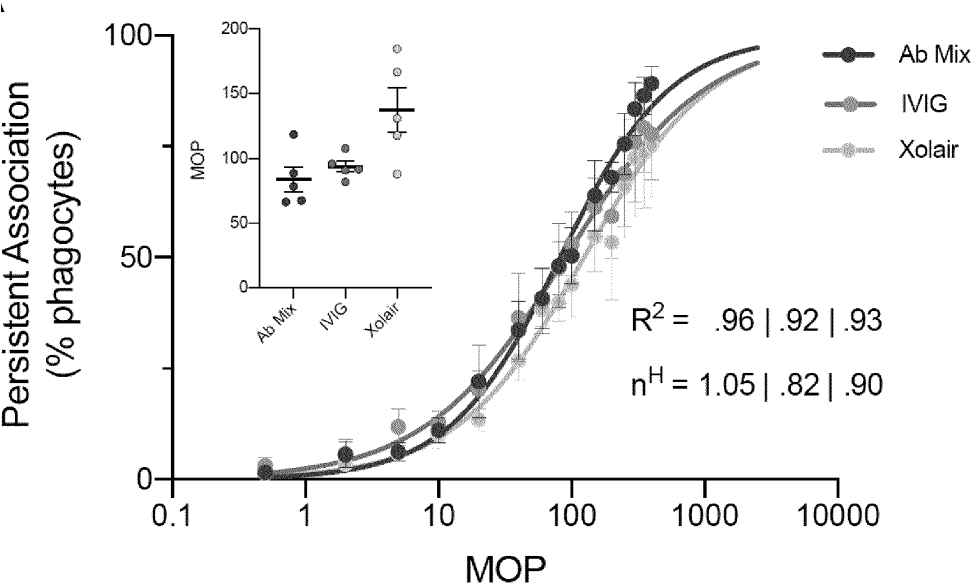
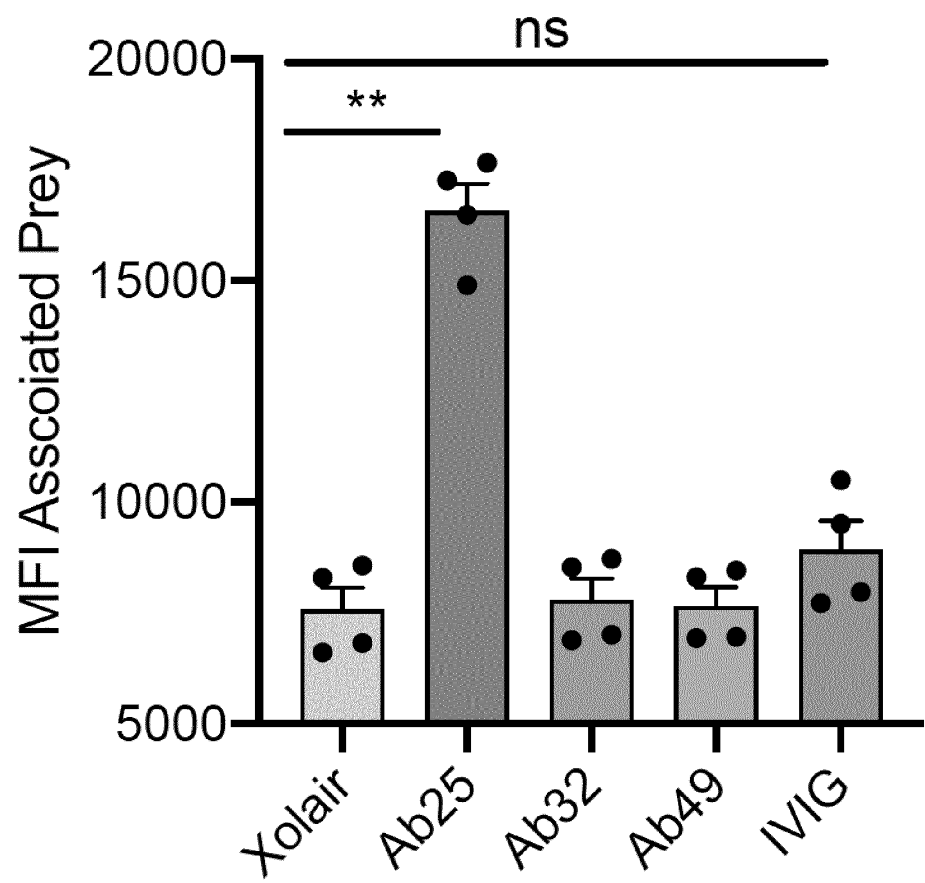


Figure 12



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Figure 13

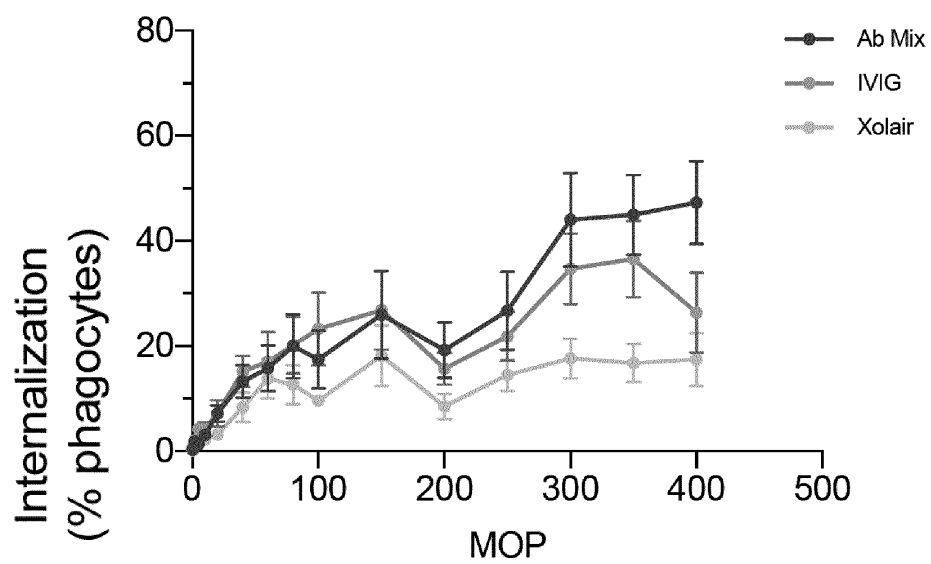


Figure 14

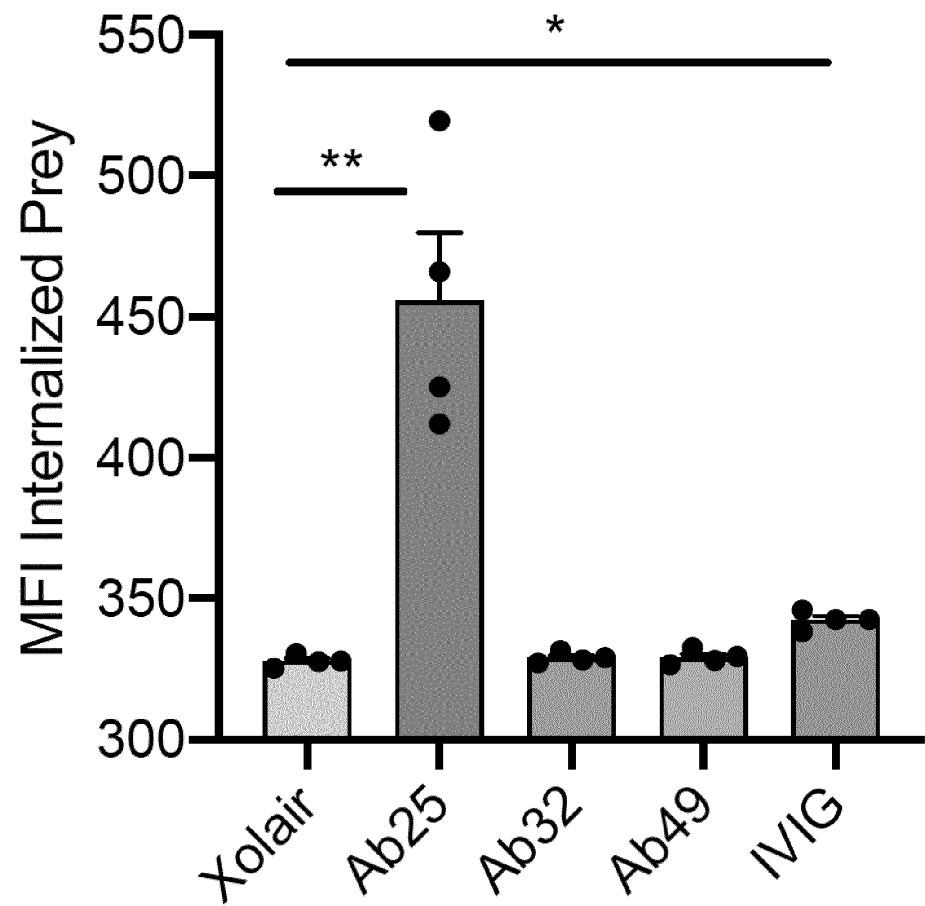


Figure 15

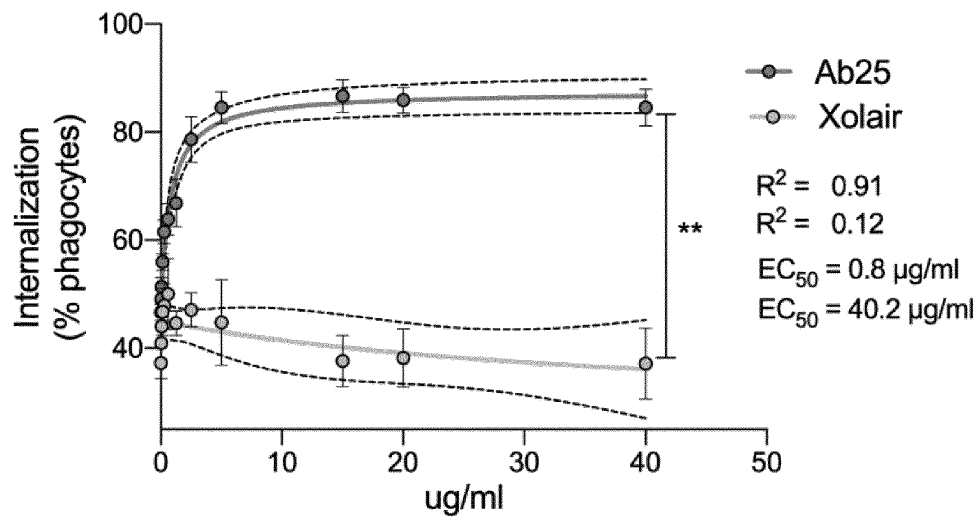


Figure 16

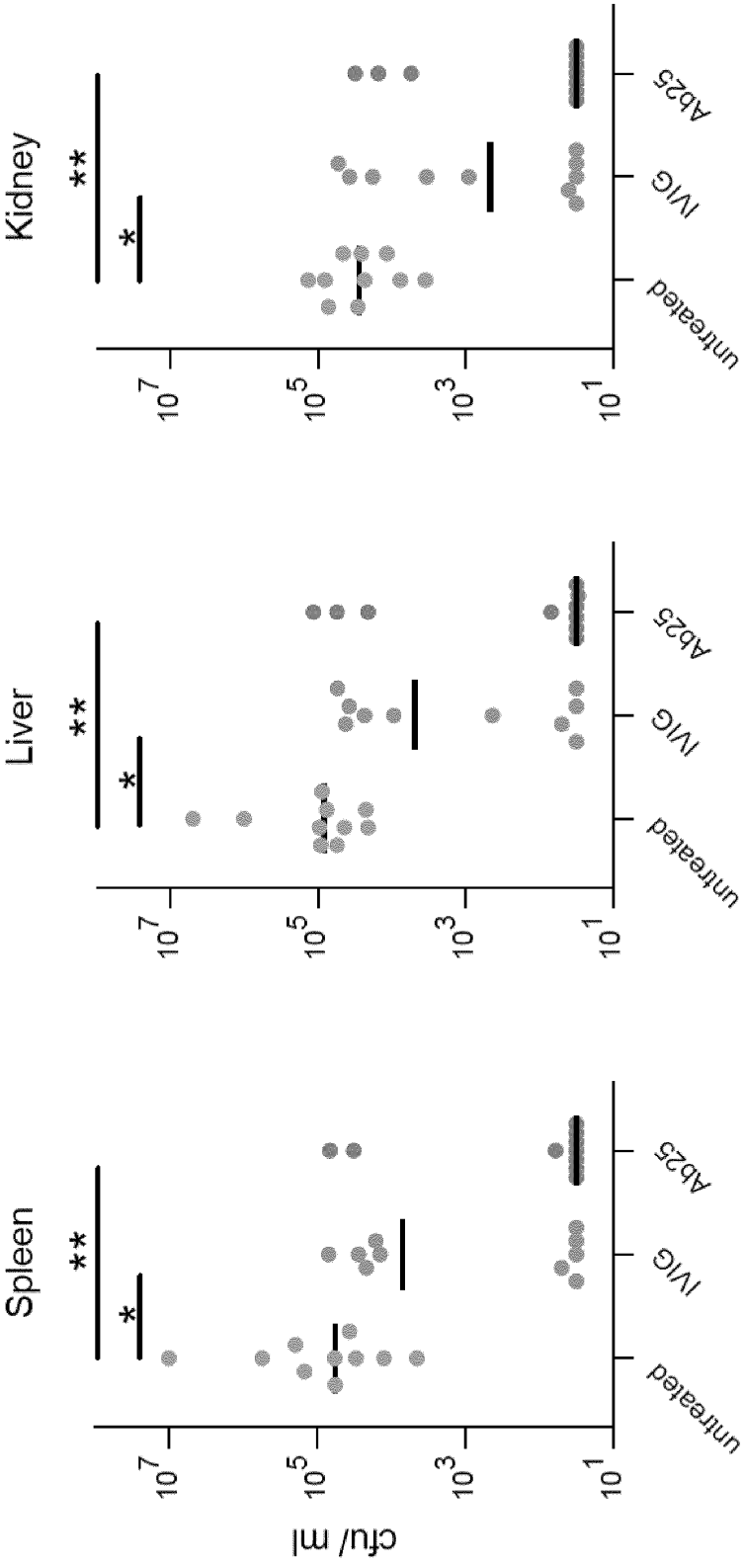


Figure 17

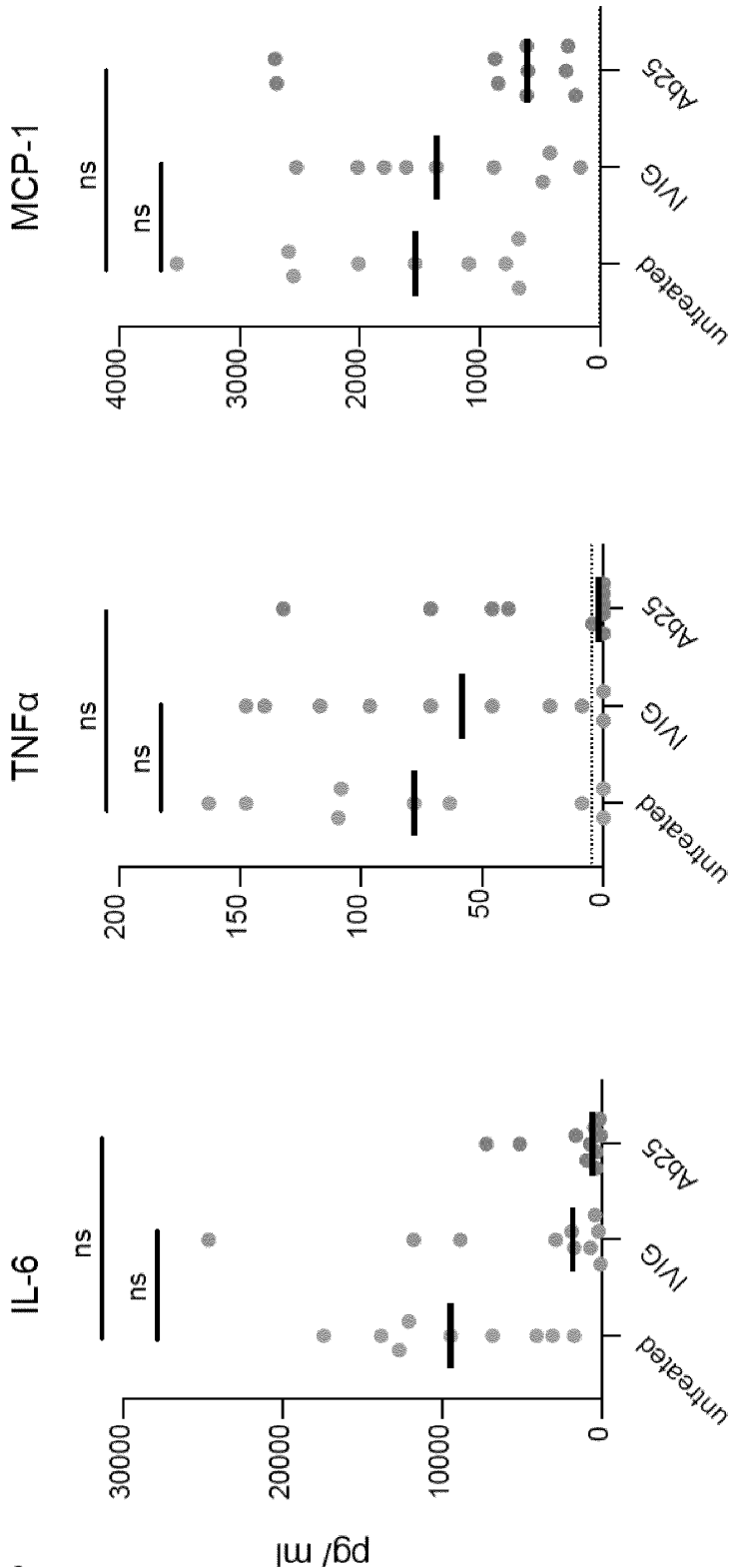


Figure 18

Ab25H	CARSYPHKRWLRPPFDYW----
Ab26H	CAKNS-RSGWY-FFFDYWGQ--
Ab32H	CARQGFDTARGE-DAFEIWG---
Ab49H	CVRD---SRFW-GIFDYWGQGT
	*.:. . *

Ab25L	QYNSYPV--TFGQGTKV
Ab26L	QYDNLPL--TFGGGTKV
Ab32L	QRSGWPSIFTFGPGTKV
Ab49L	QRSNWPP--TFGQGTKV
	* . . * *** ****

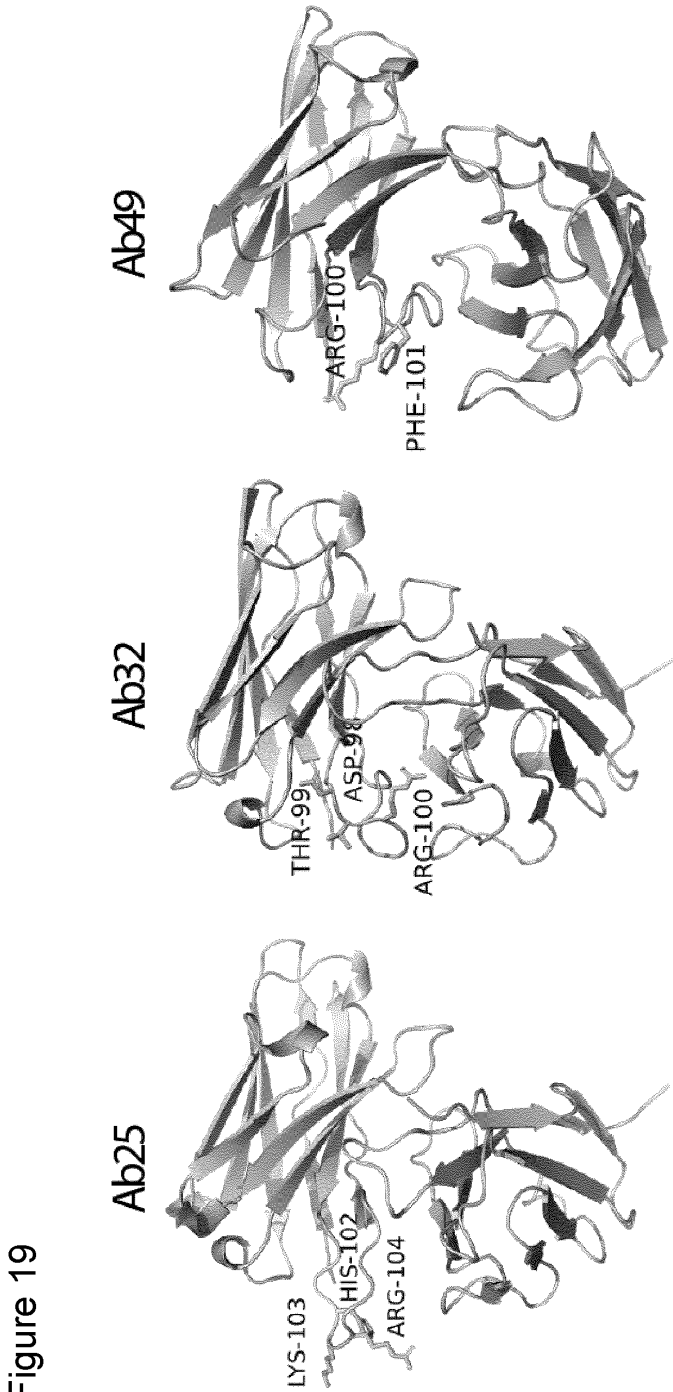
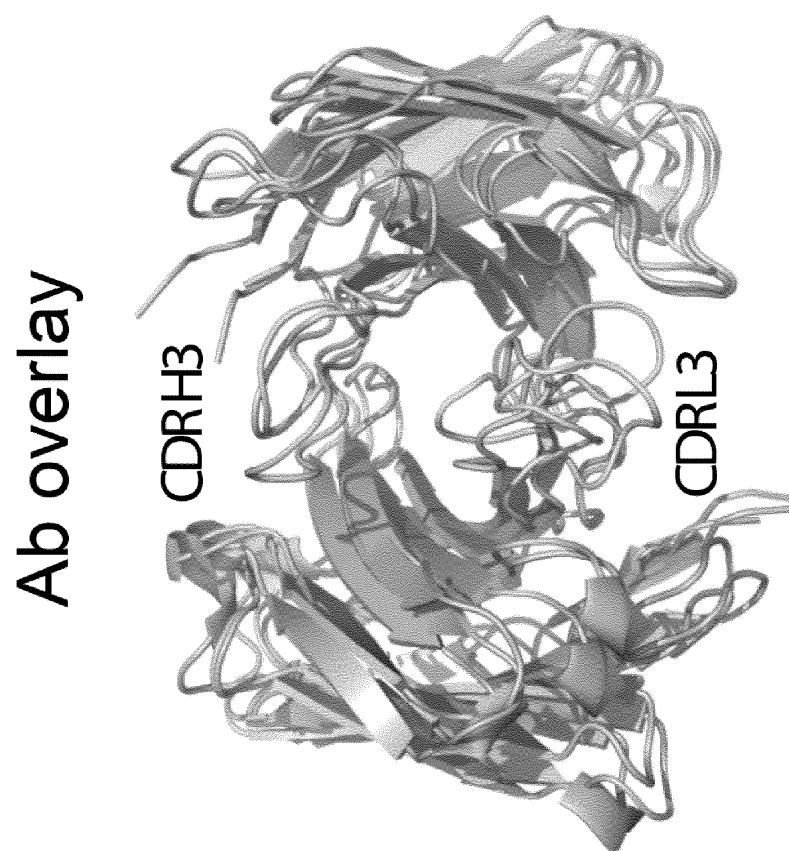


Figure 20



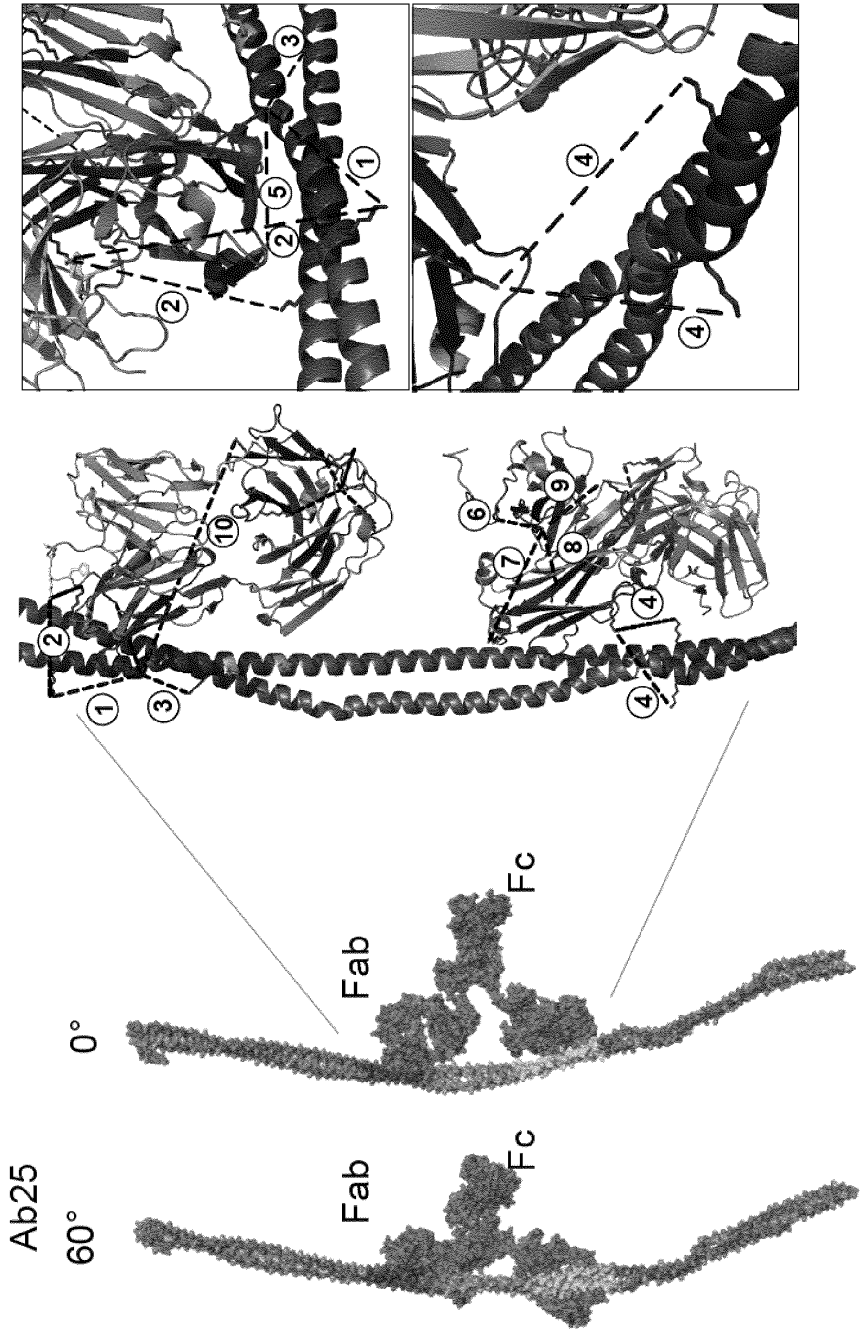


Figure 21

Figure 22

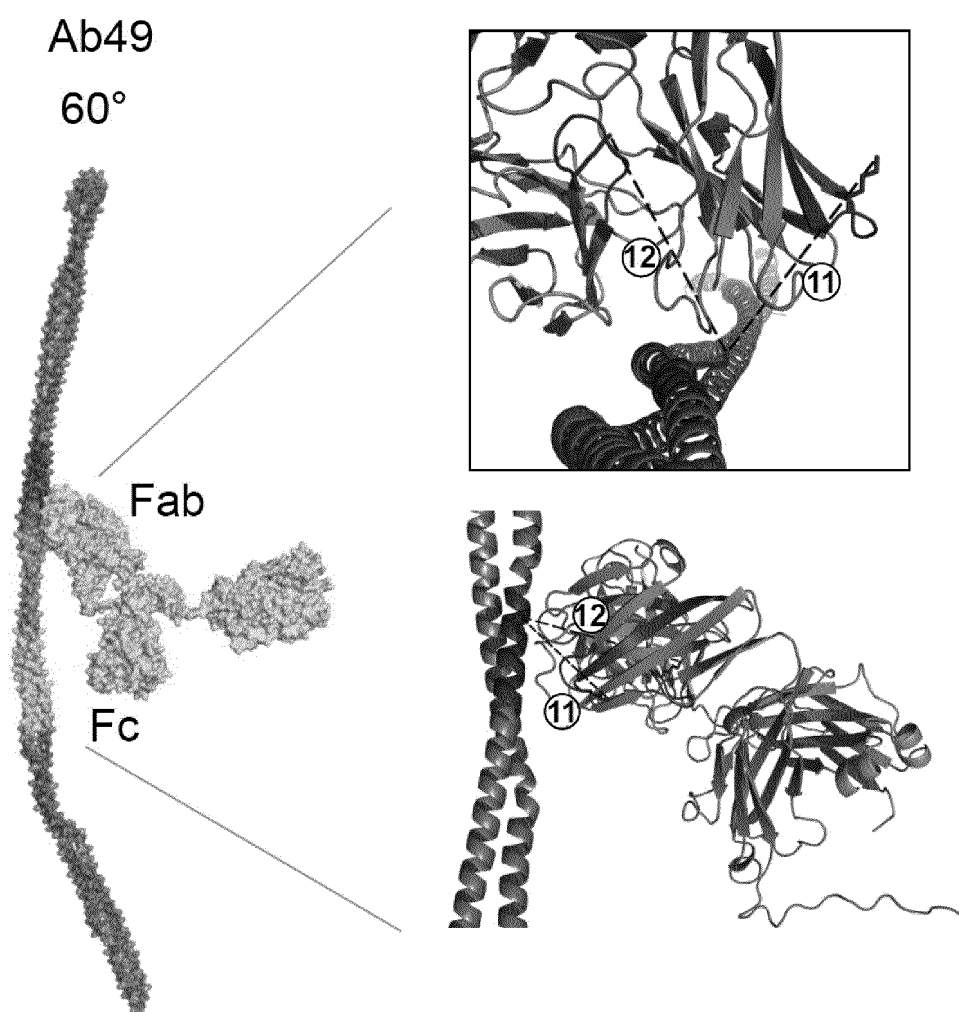


Figure 23

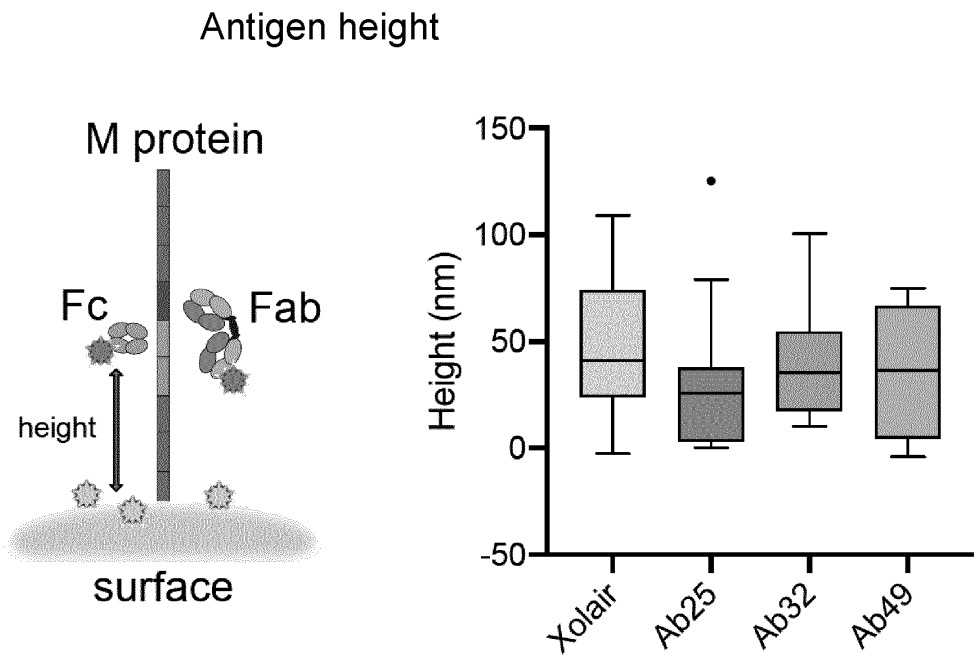


Figure 24

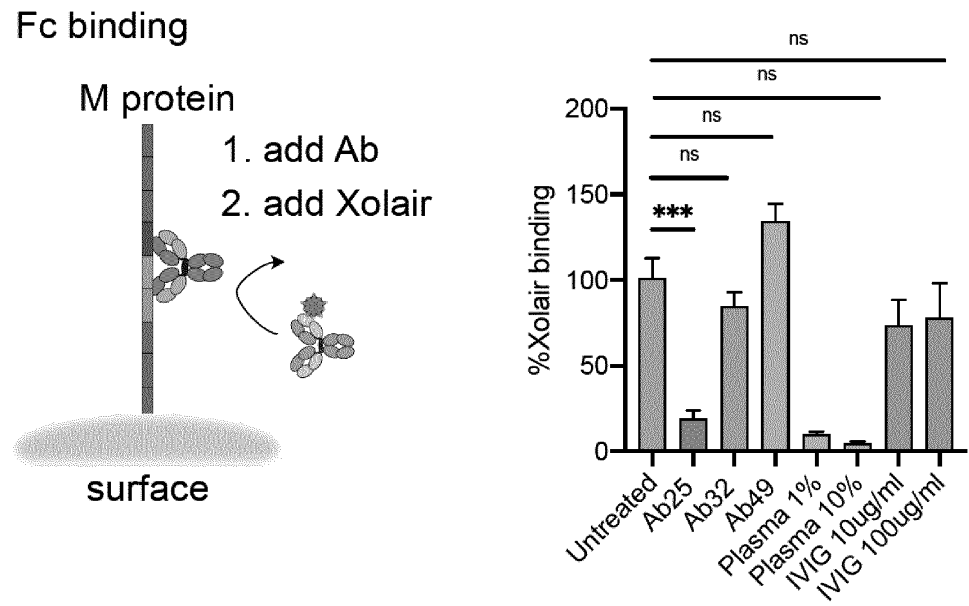


Figure 25

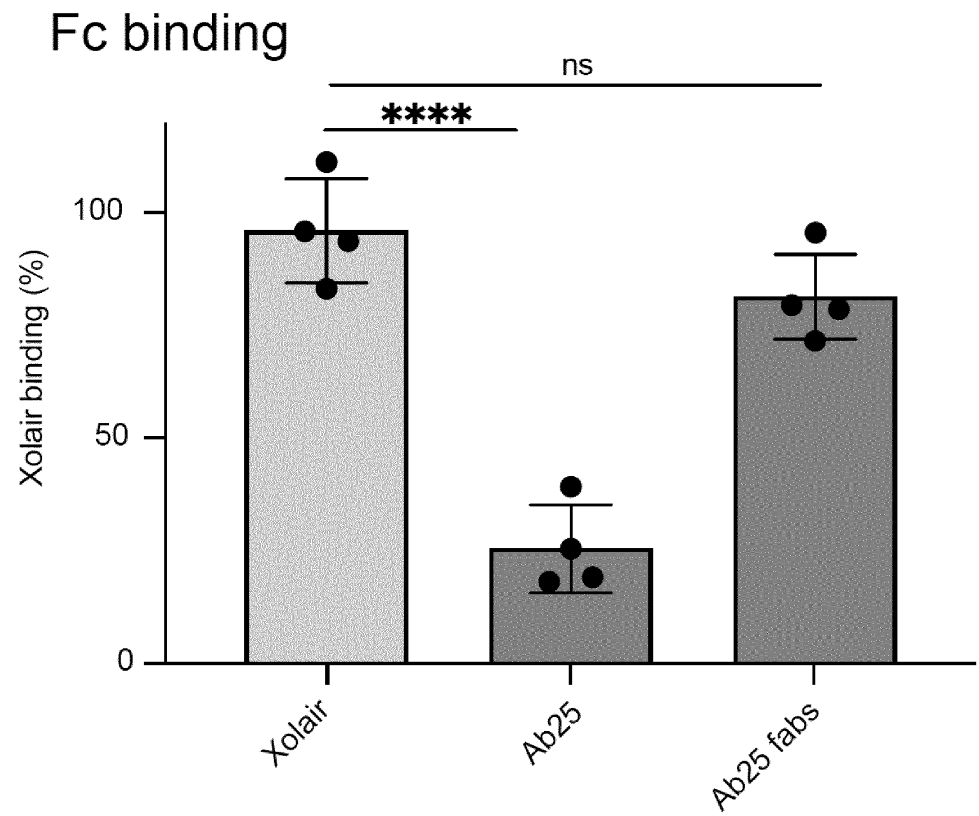


Figure 26

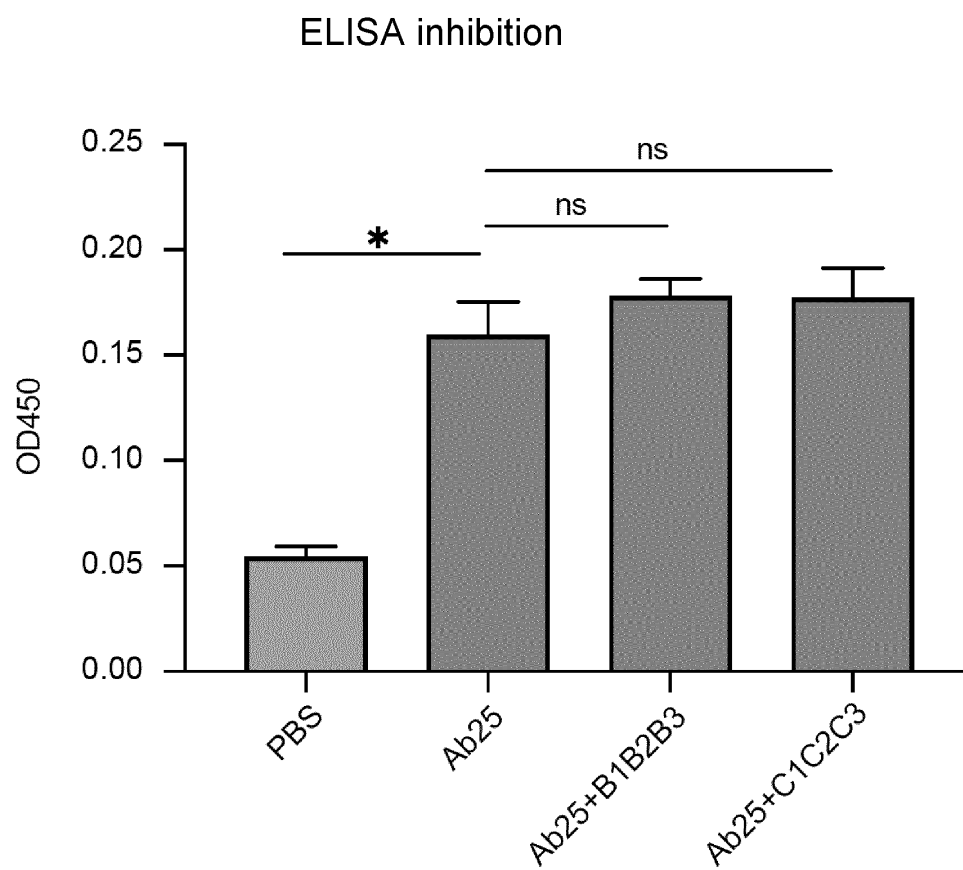


Figure 27

Bacteria binding

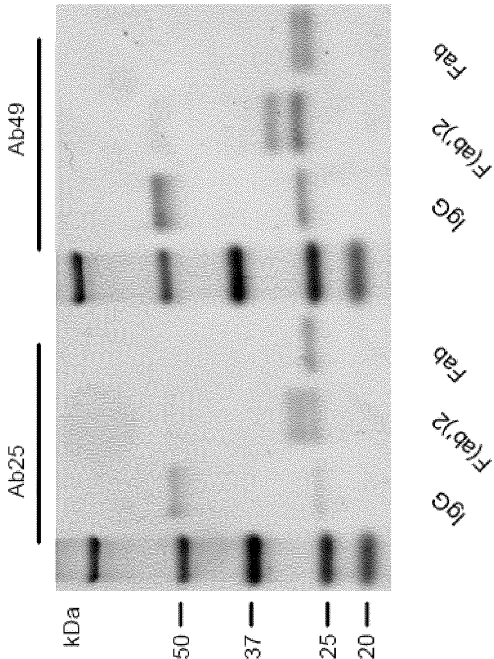
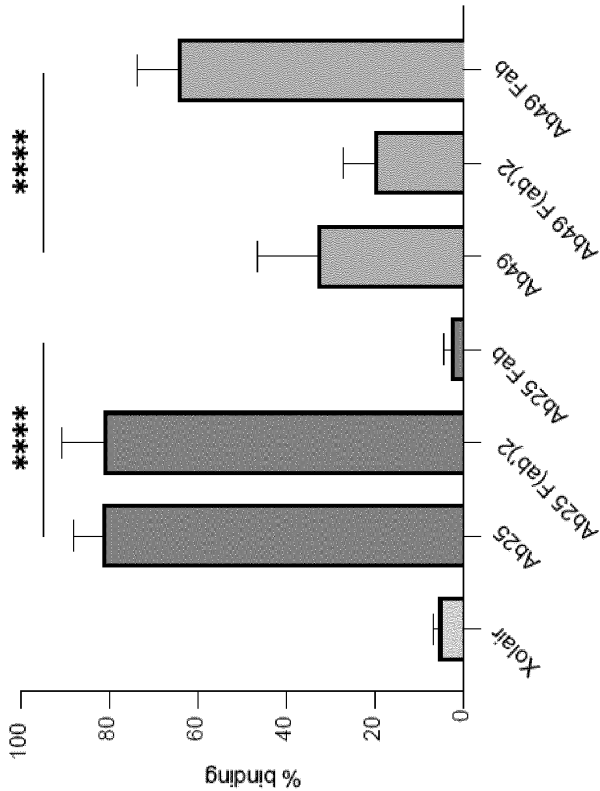


Figure 28

Fab affinity

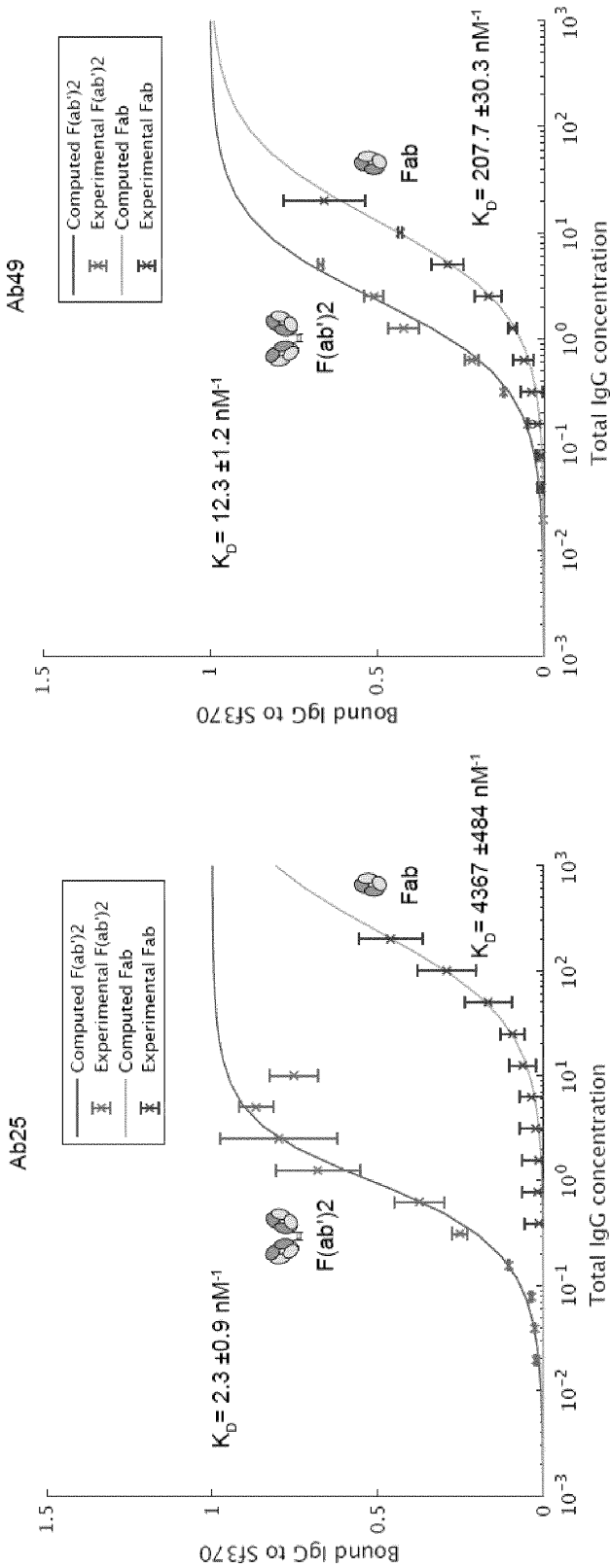
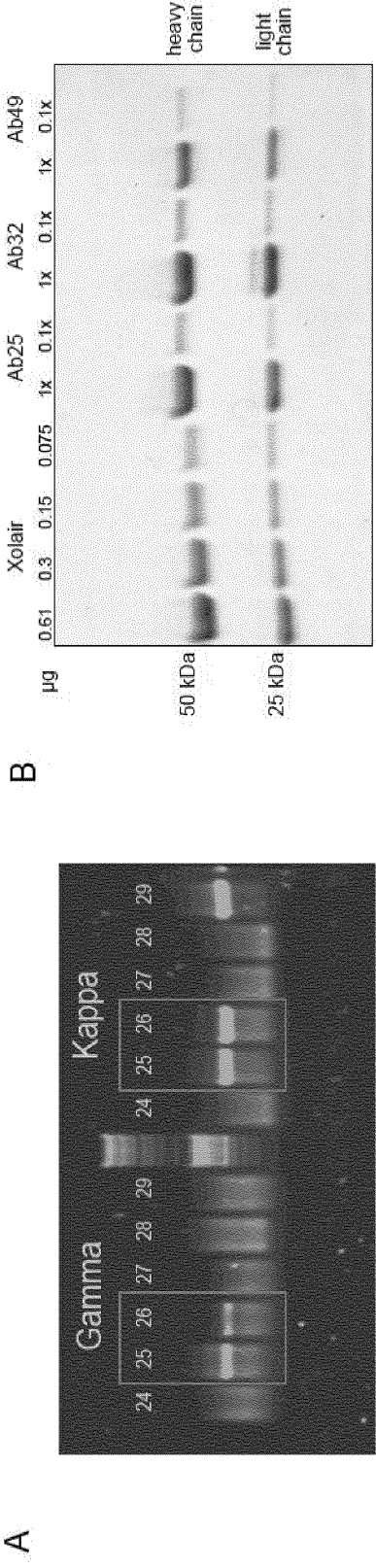


Figure 29



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Figure 30

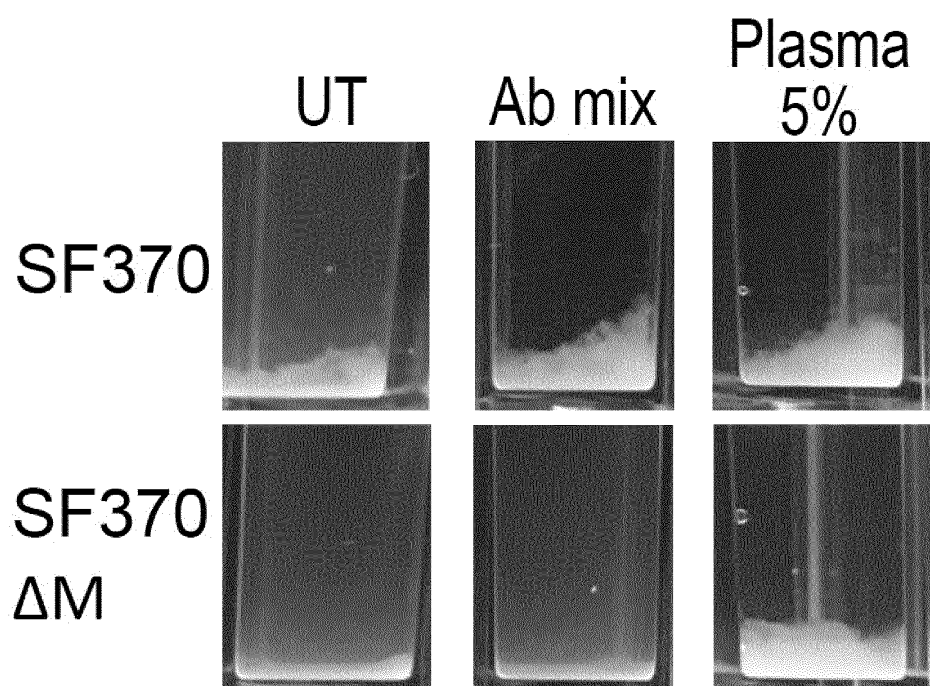


Figure 31

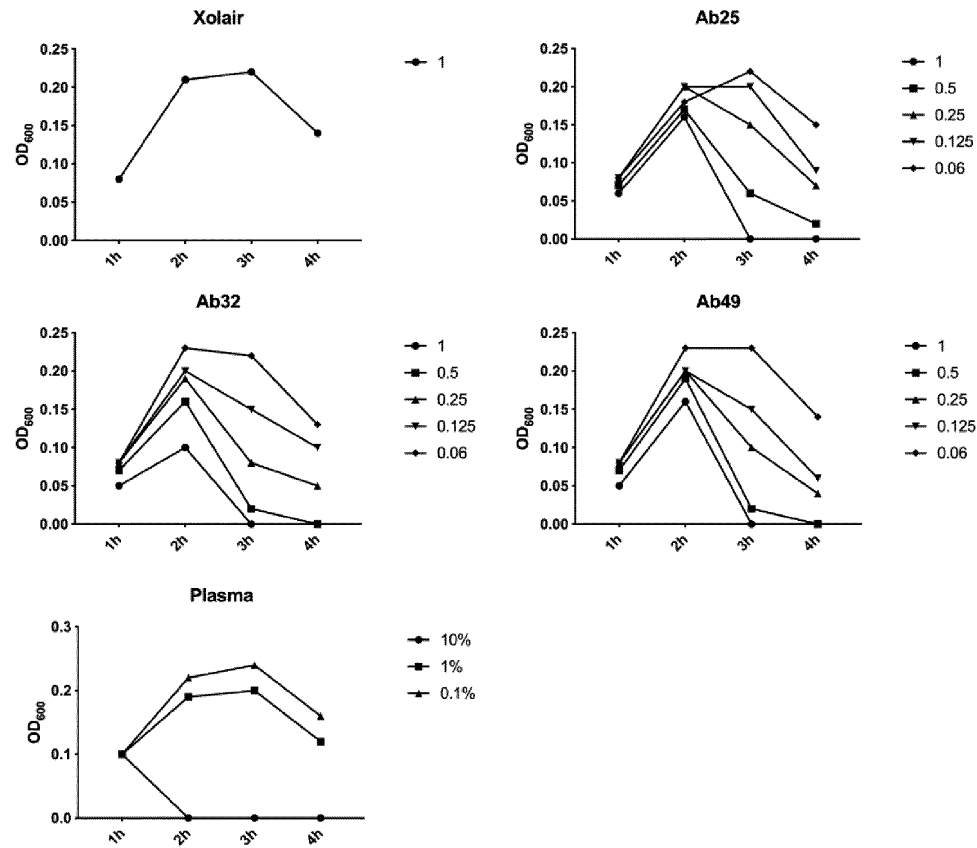


Figure 32

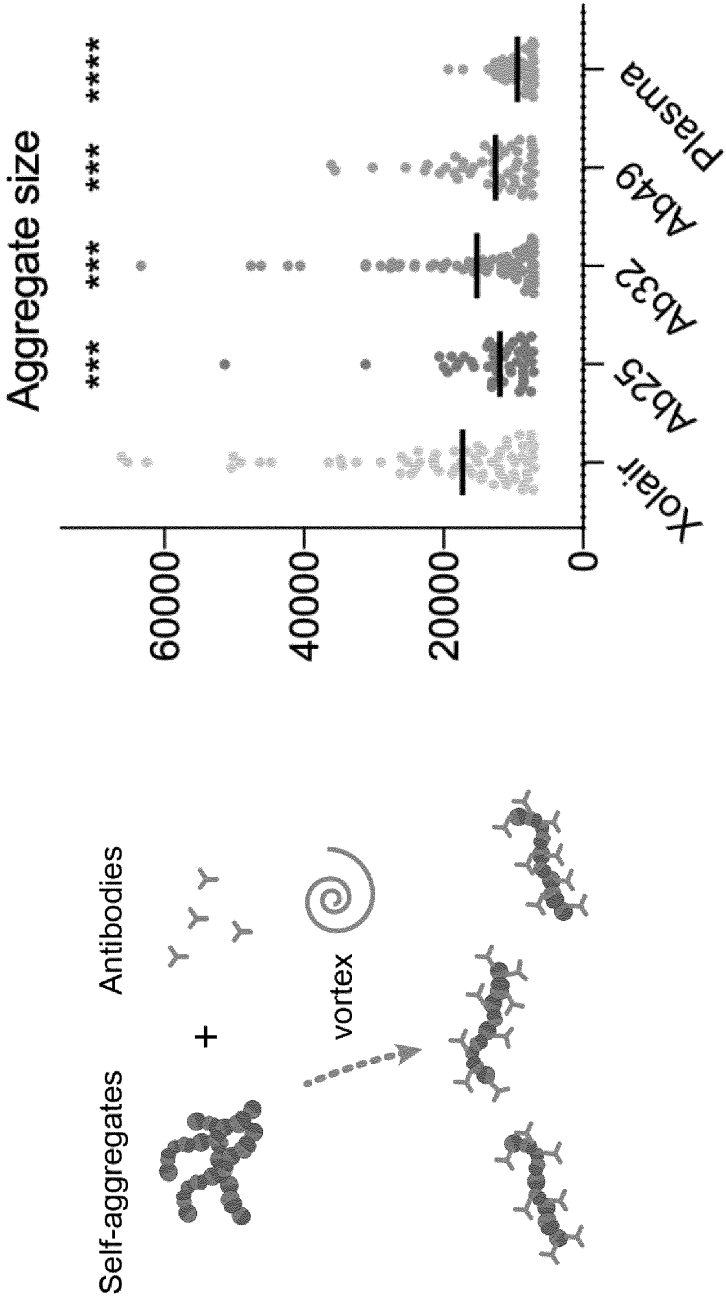


Figure 33A

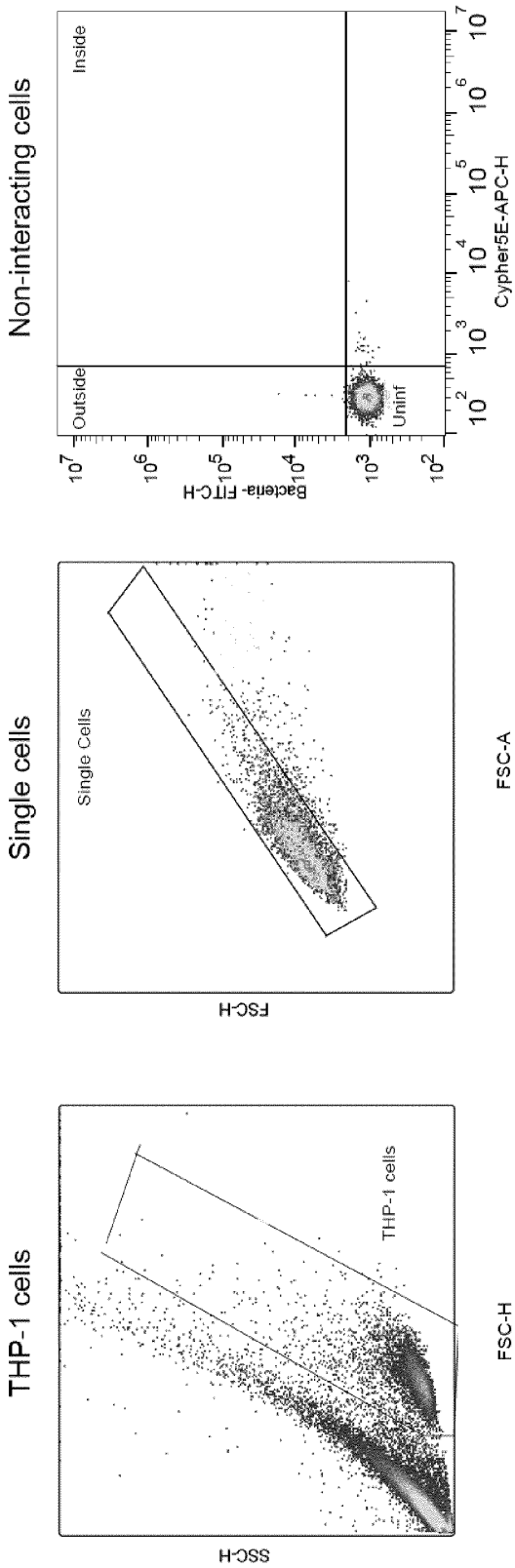


Figure 33B

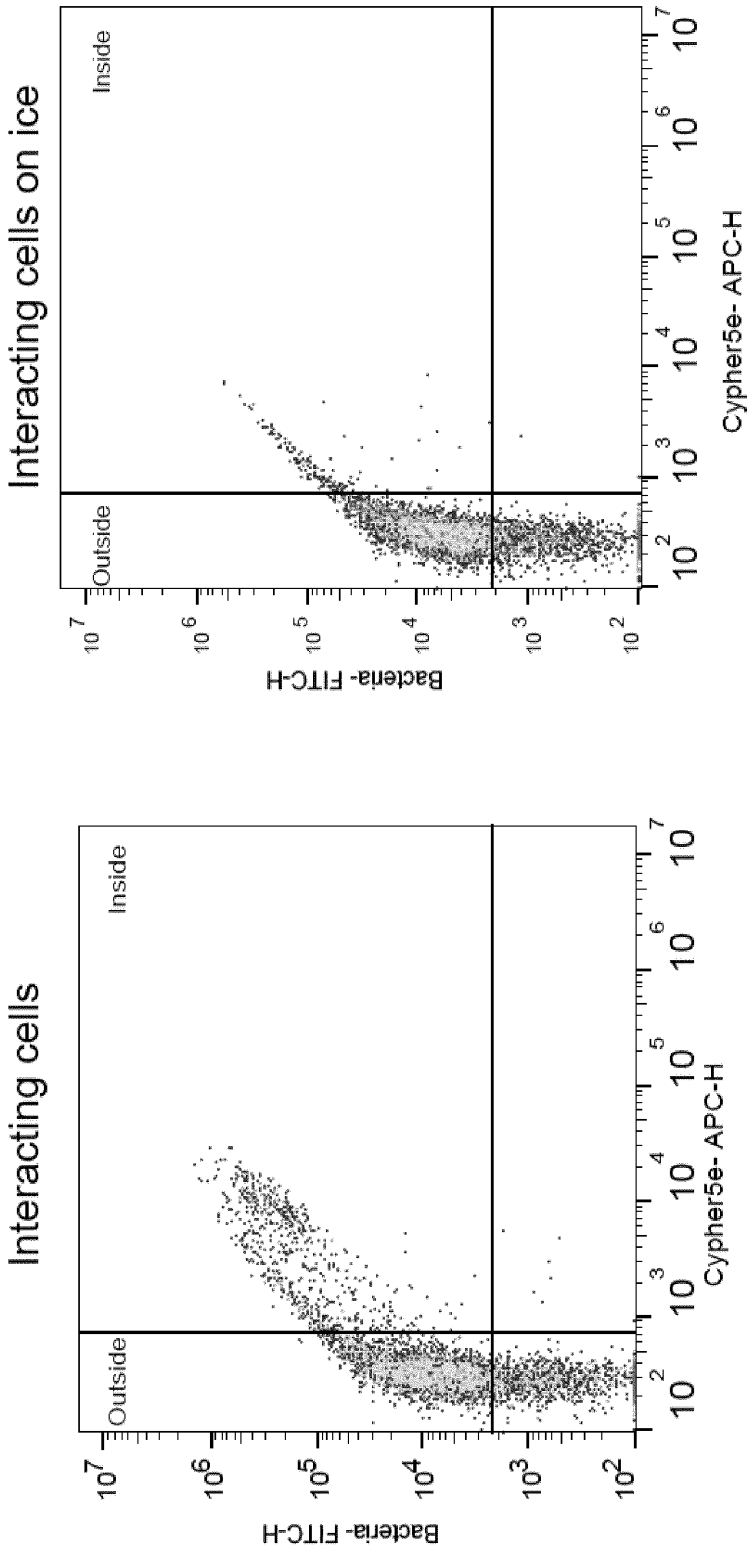
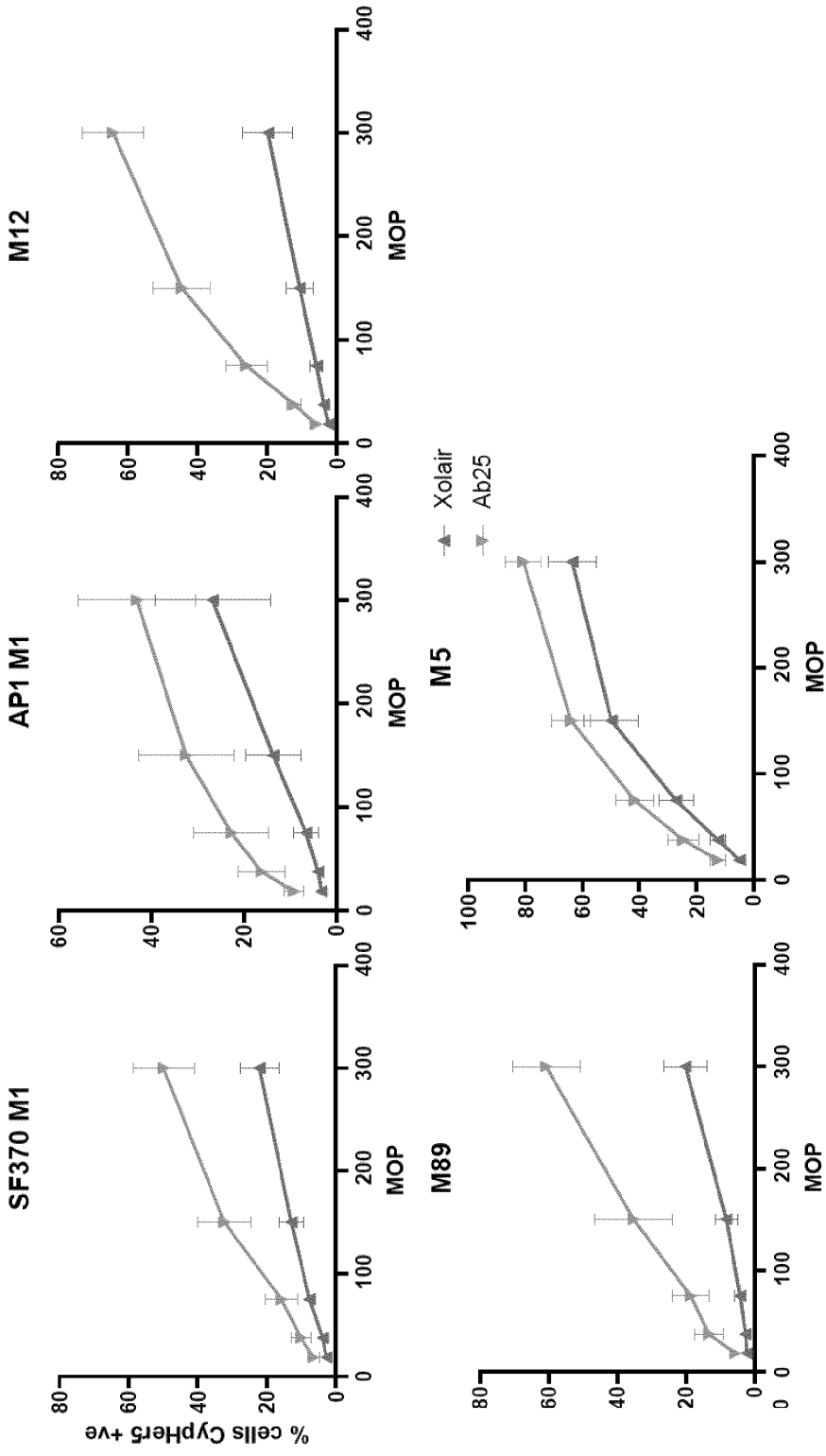


Figure 34



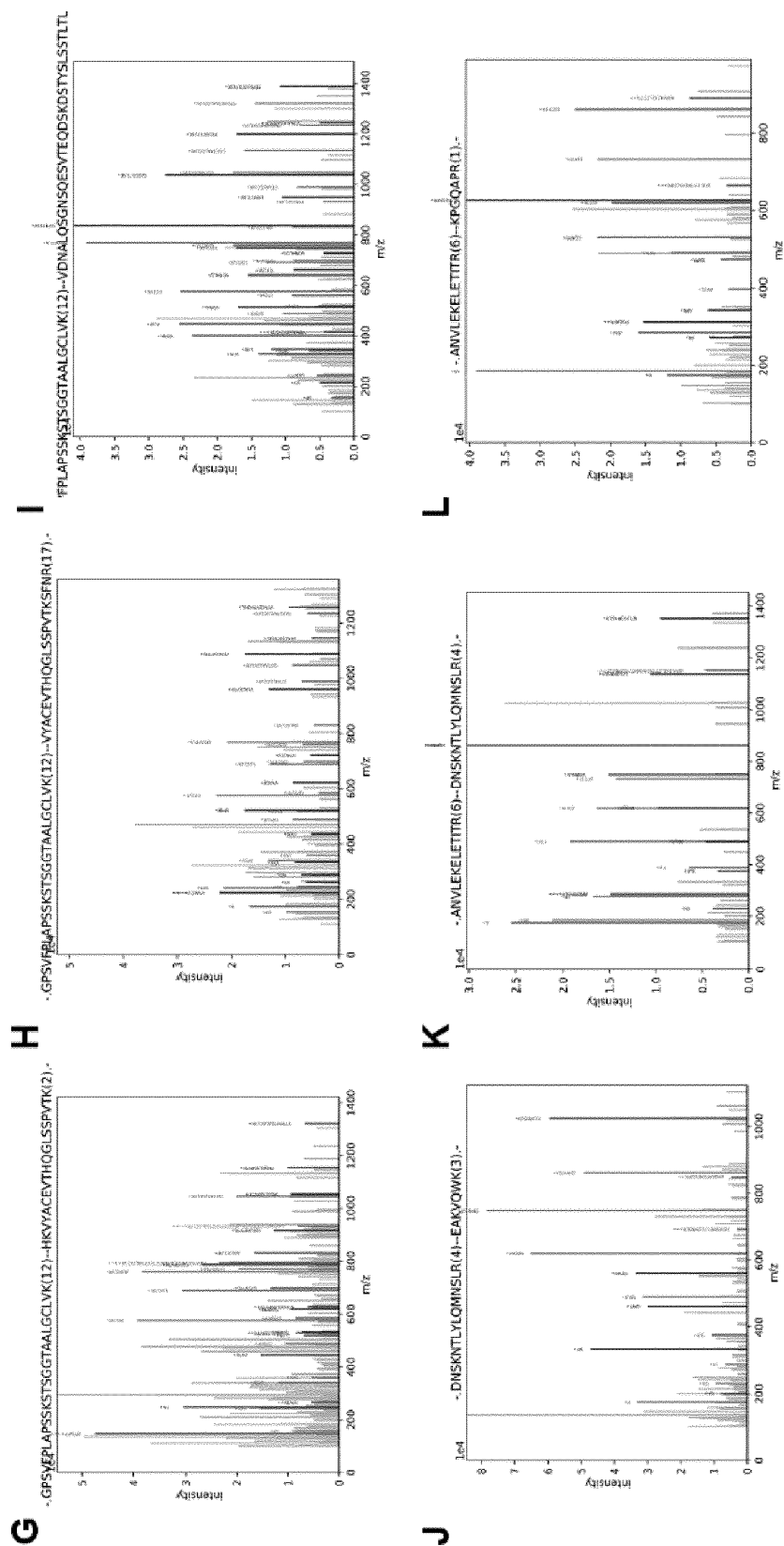


Figure 37

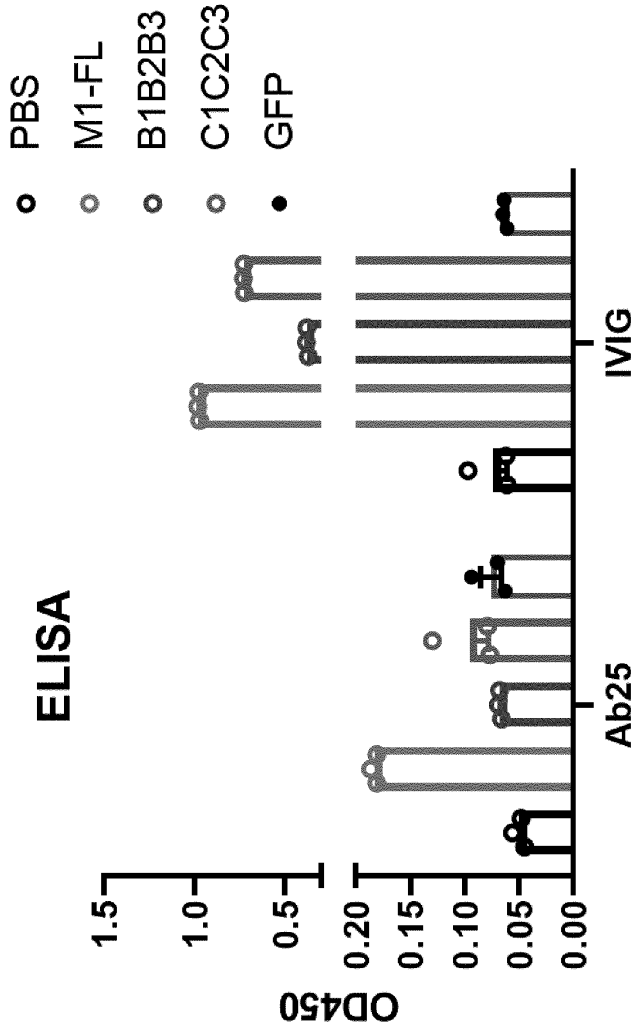


Figure 38

M1_B1B2B3	-----ATALEKELEKKEALELAIDQASRDYHRATALE	33
M1_C1C2C3	-----	0
M1_FL	MDGNPREVIEDLAANNPAIONIHRLRYENKDLKARLENAMVAGROFKAEELEKAKQALEDORKDLETKKELQODYDLAKESTSWDRORLEKELEKKEALELAIDQASRDYHRATALE	120
M1_B1B2B3	KELEKKEKALELAIDQASODYNPRANVIEKELE-----	65
M1_C1C2C3	-----AKLEEEKQISDASRQSLRRDLDSREAKKQVEKDLANLTAELDKVKEDKQISDA	54
M1_FL	KELEKKEKALELAIDQASQDYNPRANVIERELETITREQFINRNLLGNAKLELDQASSEKEQLTIEKAKLEEEKQISDASRQSLRRDLDSREAKKQVEKDLANLTAELDKVKEDKQISDA	240
M1_B1B2B3	-----	65
M1_C1C2C3	SROGLRRDLDSREAKKQVEKDLANLTAELDKVKEEKQISDASRQGLRRDLDSREAKKQVEKALE-----	120
M1_FL	SROGLRRDLDSREAKKQVEKDLANLTAELDKVKEEKQISDASRQGLRRDLDSREAKKQVEKALEEANSKLALEKLNKELEESKLTETERKALELQAKLEAEAKALKEQLAKQAEELAK	360
M1_B1B2B3	-----	65
M1_C1C2C3	-----	120
M1_FL	LRAGKASDSQTPDTKFGNKAVPGKGQAPQAGTKPNONKAPMKETKROLFSTGETANPFTTAAALTVMATAGVAVVVKKEEN	442