

Figure 1

Figure 1A

IGKV1-39 (SEQ ID NO: 99)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYSTP

Figure 1B

IGKV1-39/jk1 (SEQ ID NO: 16)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYSTPPTFGQGTKVEIK

Figure 1C

IGKV1-39/jk5 (SEQ ID NO: 100)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYSTPPITFGQGTRLEIK

Figure 2

Figure 2A

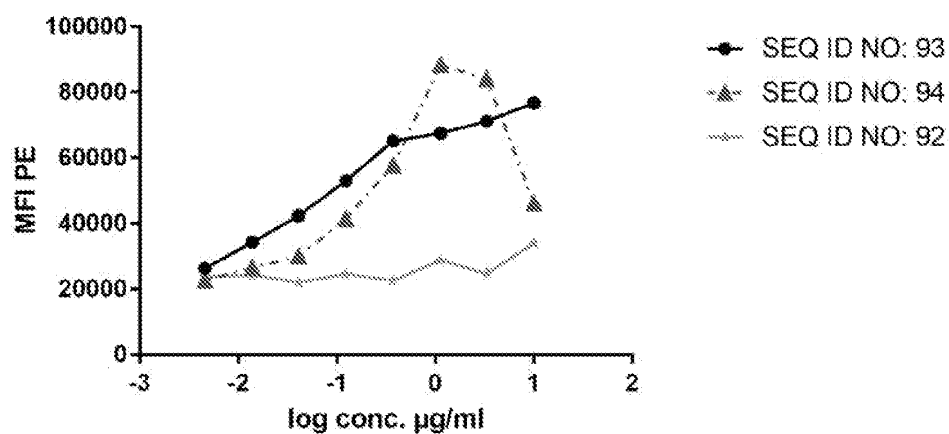


Figure 2B

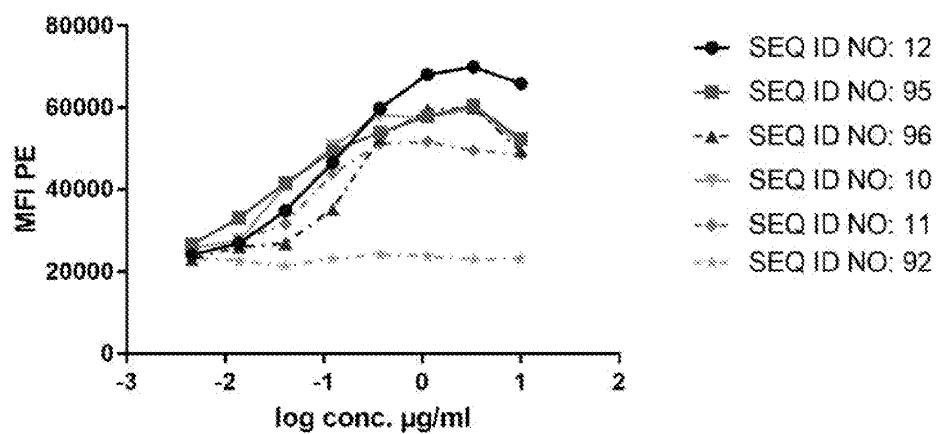


Figure 3

Figure 3A

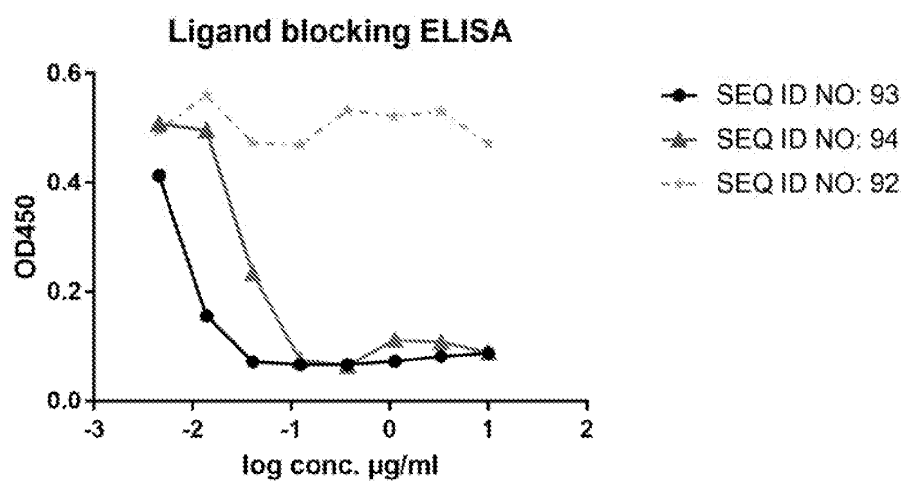


Figure 3B

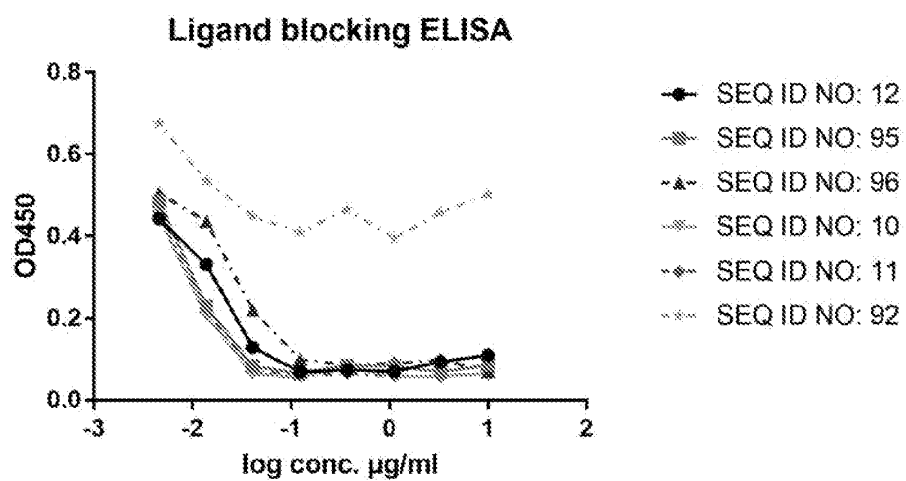


Figure 4

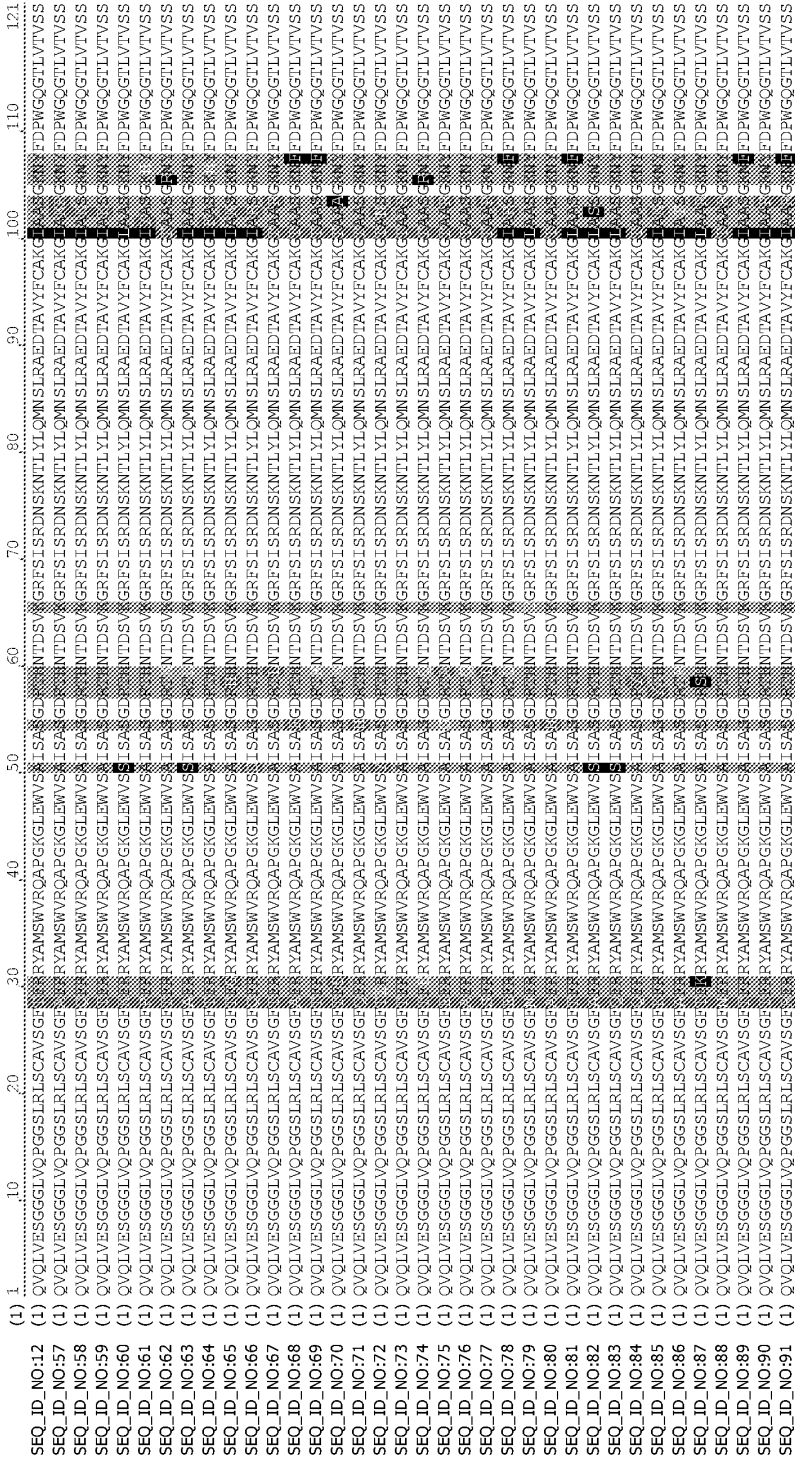


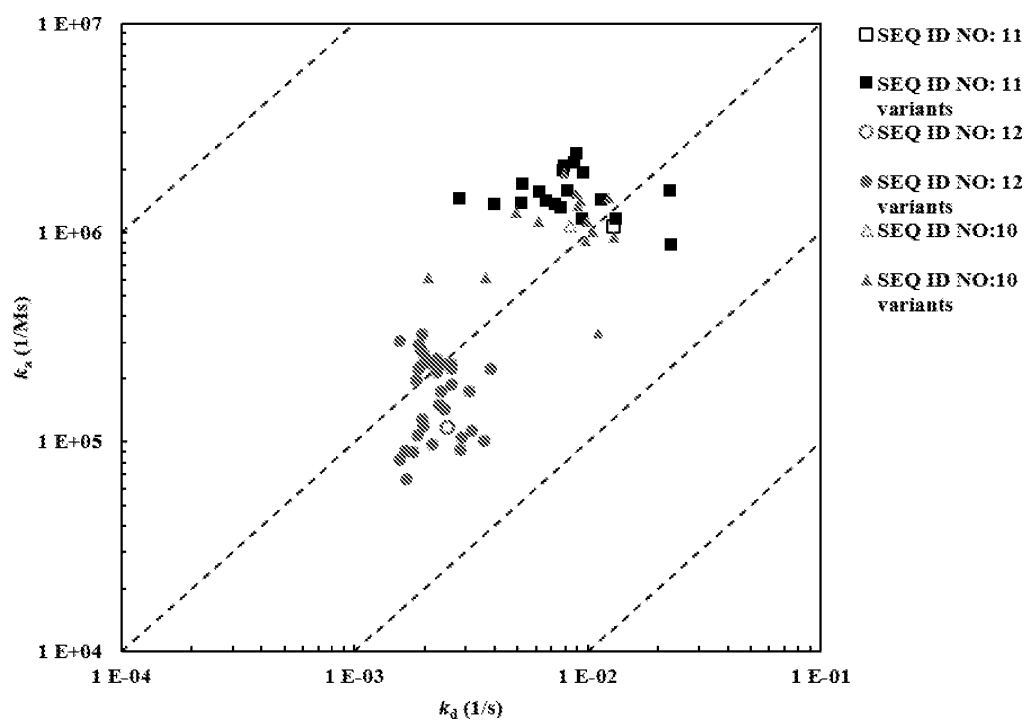
Figure 5

Figure 6

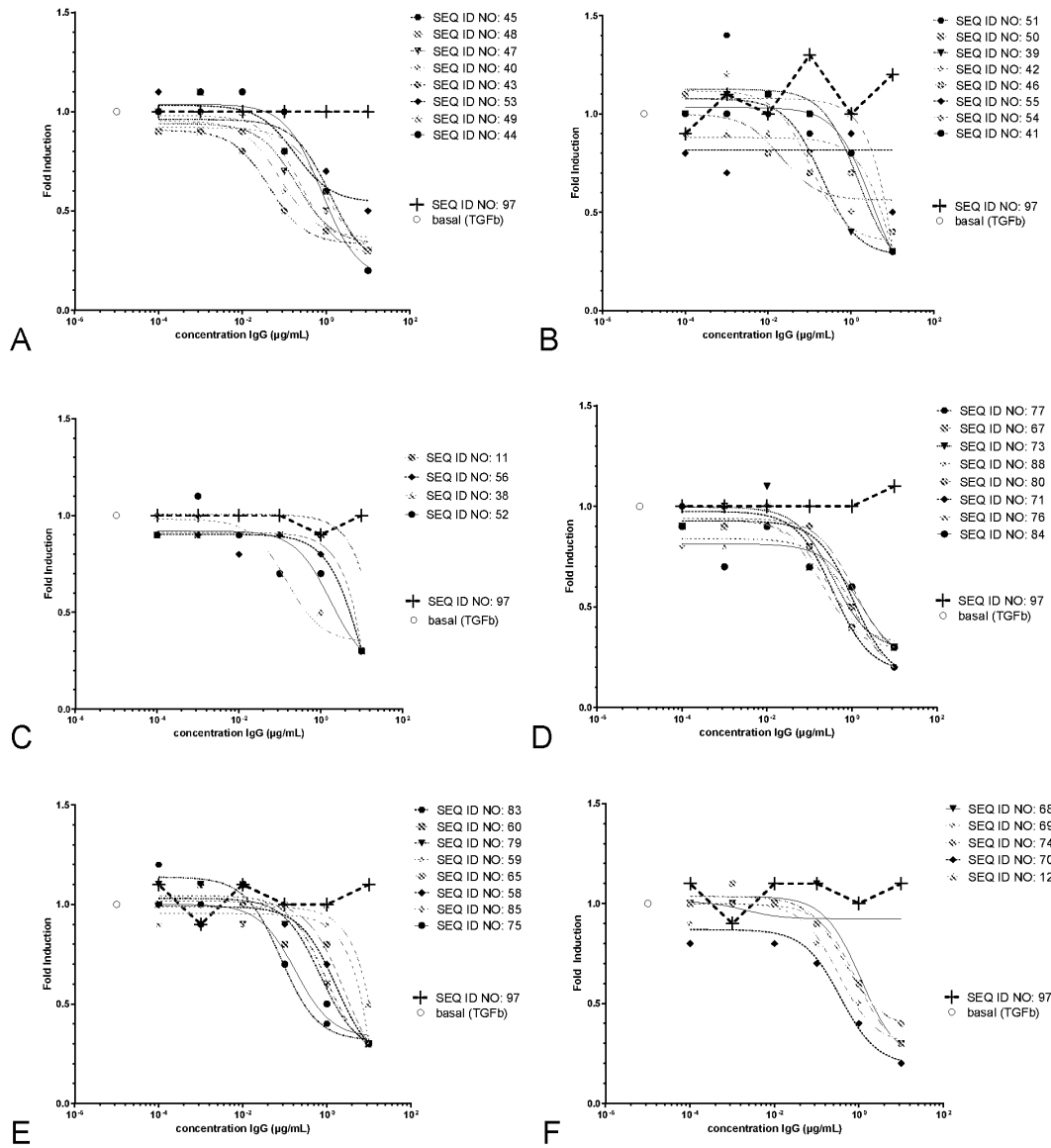


Figure 6 continued

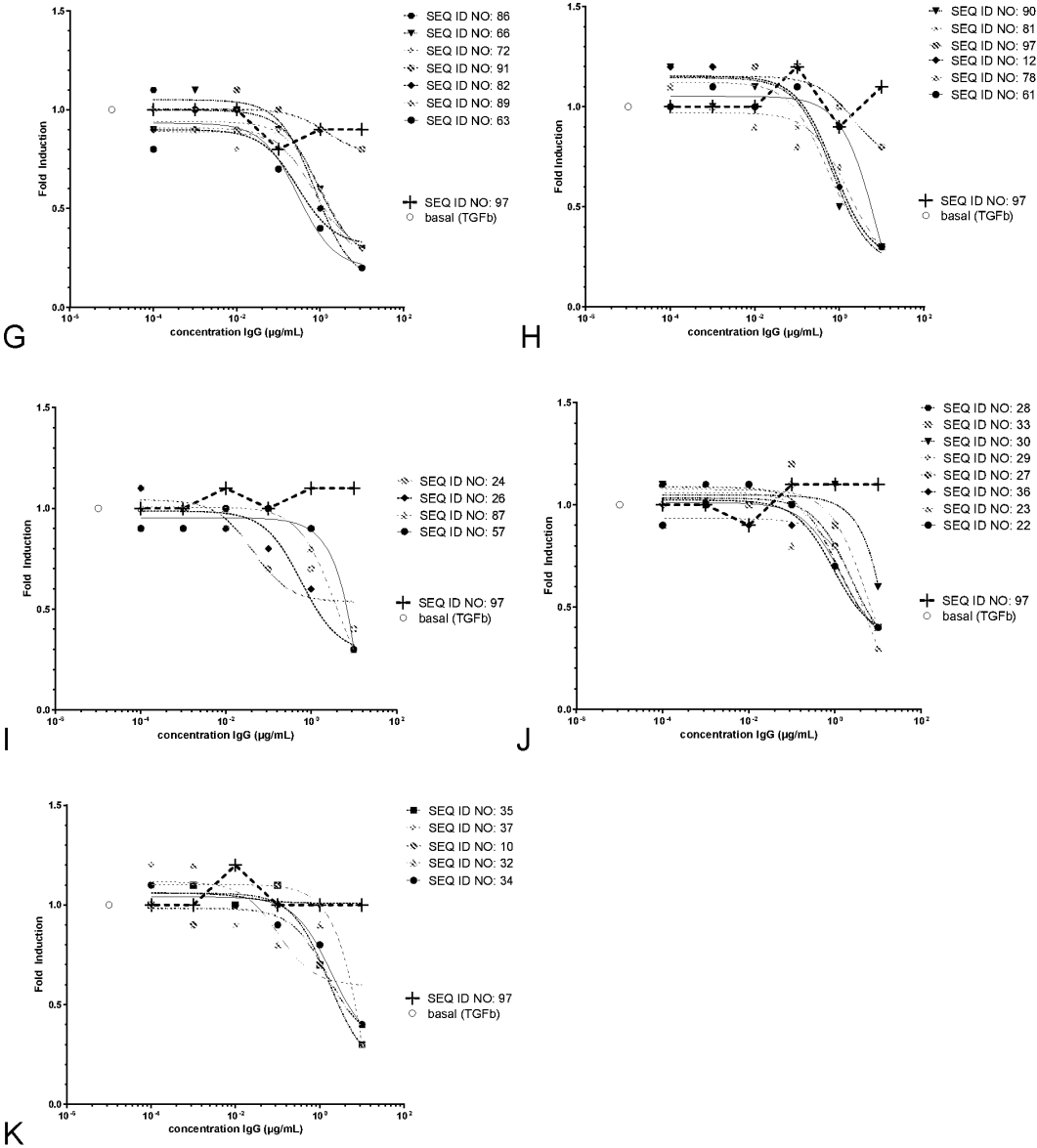


Figure 7

Figure 7A

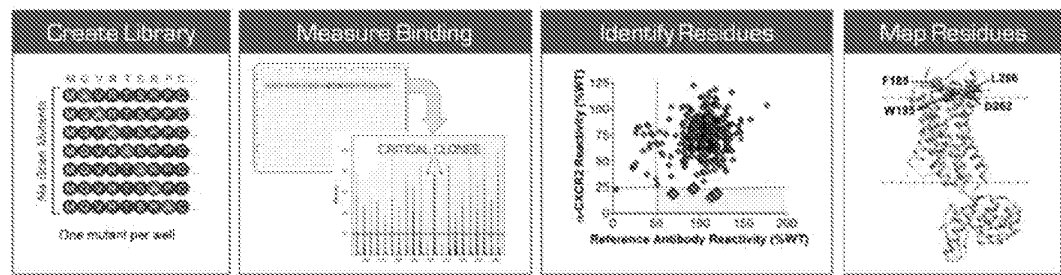


Figure 7B

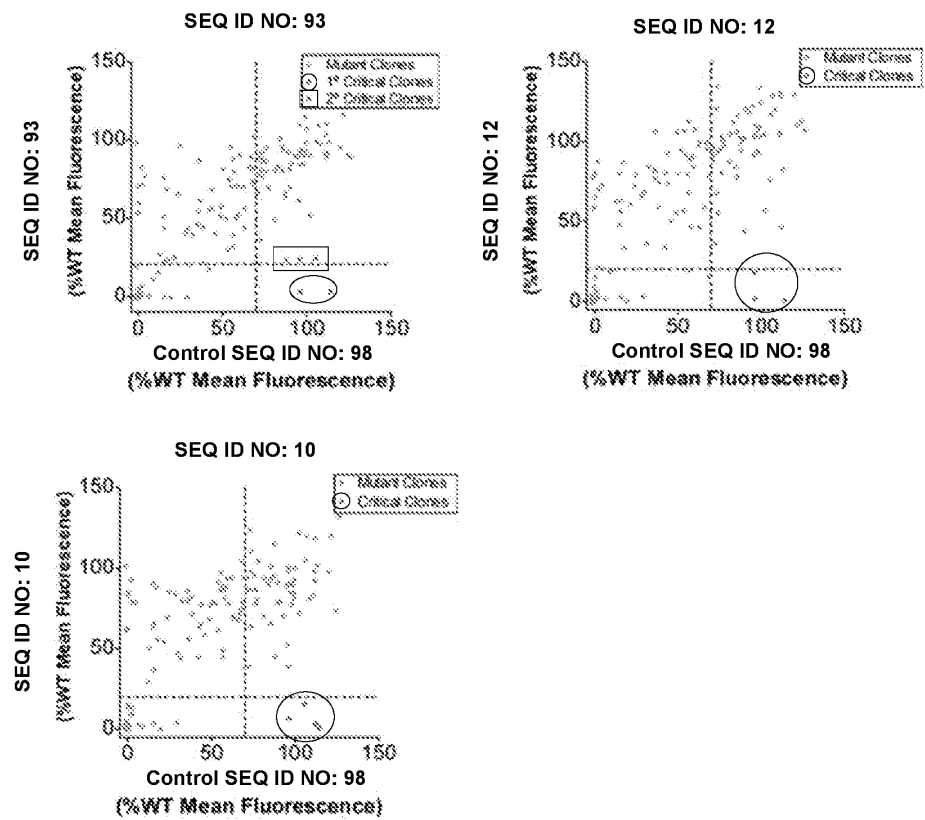


Figure 7 continued

Figure 7C

Binding Reactivity (% WT)				
Mutation	SEQ ID NO: 93	SEQ ID NO: 12	SEQ ID NO: 10	SEQ ID NO: 98
F25A	2.28 (0)	1.5 (0)	6.6 (1)	96.3 (41)
L28A	22.8 (2)	94.2 (10)	44.9 (2)	88.1 (11)
T52A	23.4 (9)	17.9 (13)	38.6 (13)	96.1 (13)
I54A	24 (0)	75.9 (28)	15.4 (3)	105.5 (22)
D119A	2.8 (3)	1 (1)	0.6 (0)	114.3 (14)
E120A	91.5 (9)	46.6 (2)	2.9 (1)	112.3 (6)

Figure 7D

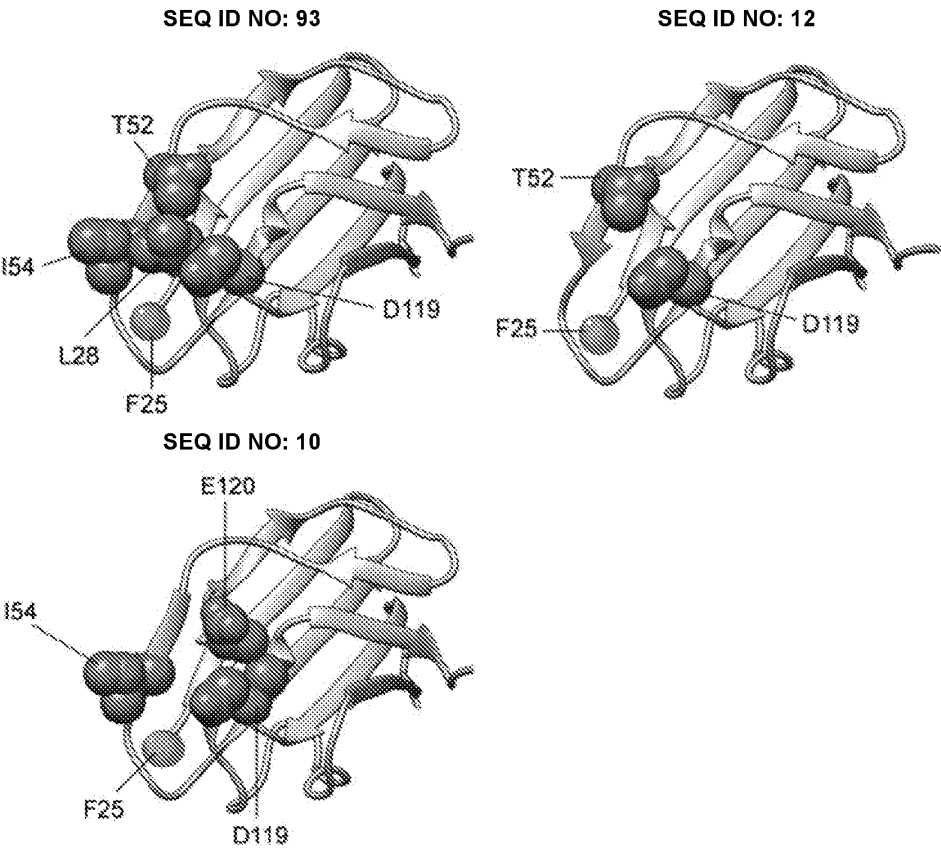


Figure 8

