Figure 1

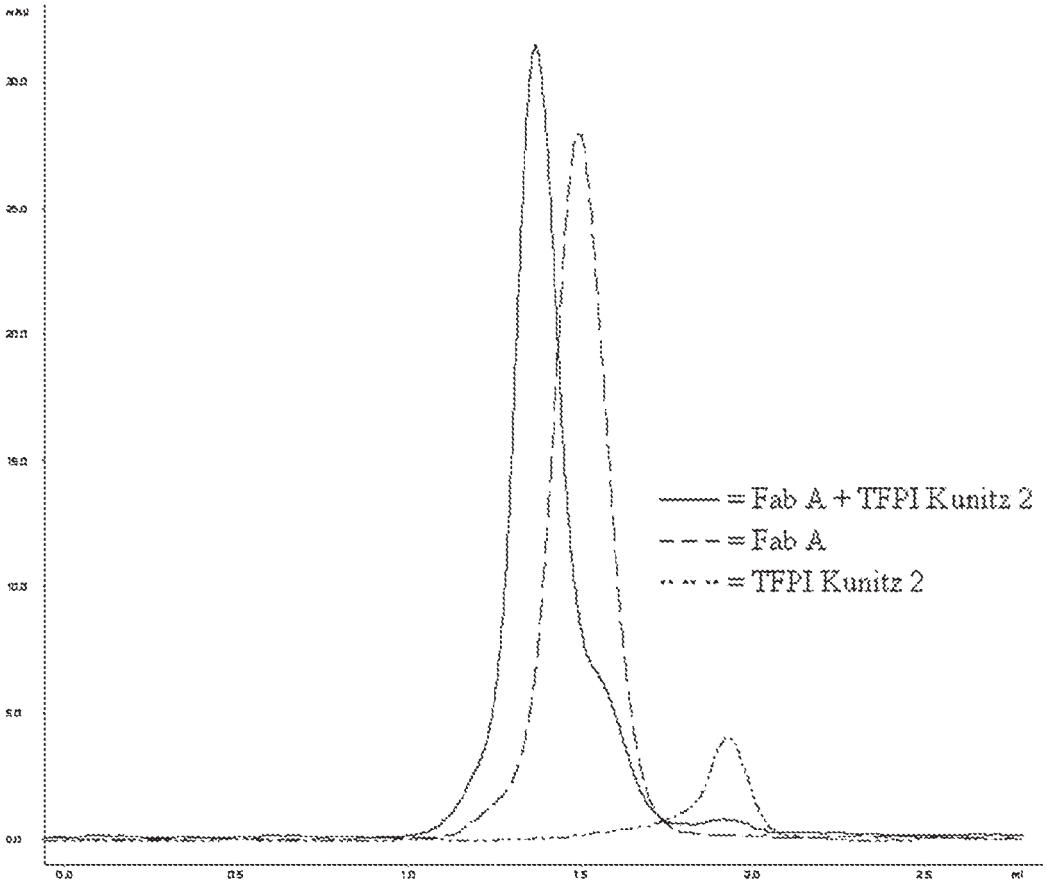


Figure 2

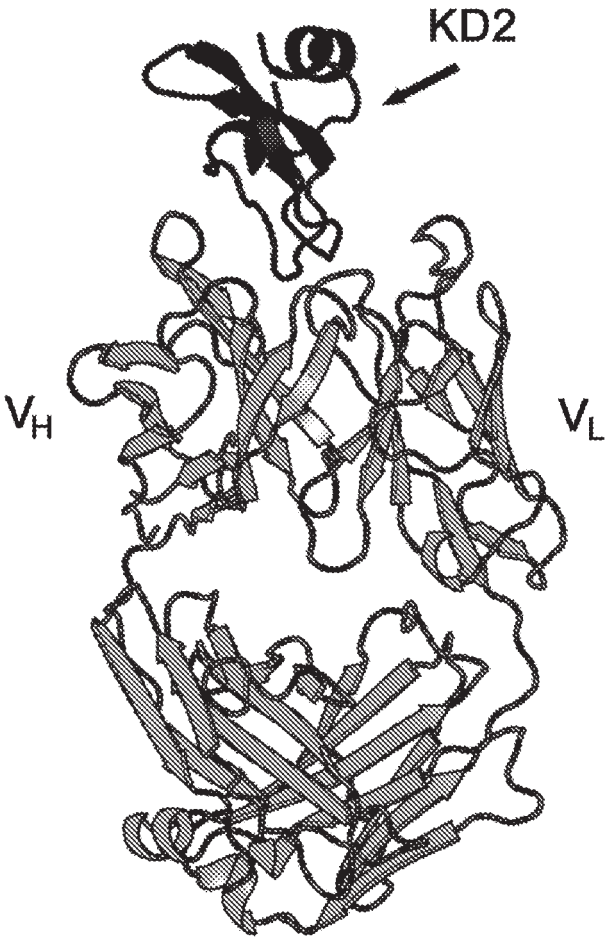


Figure 3

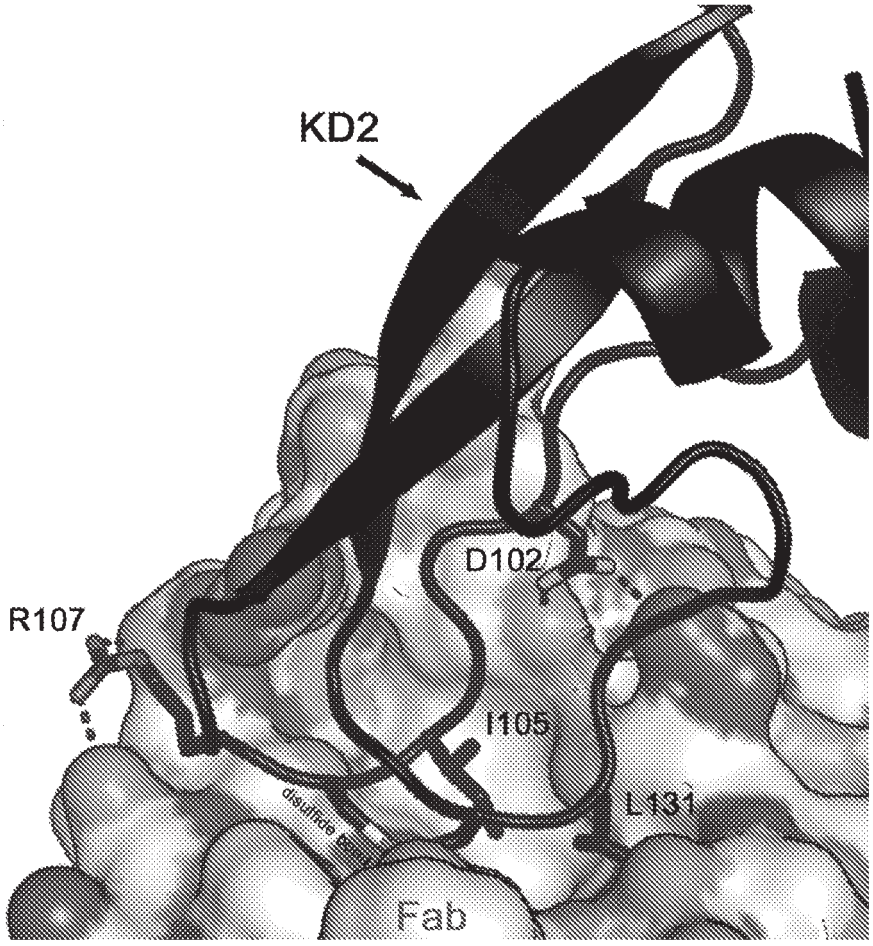


Figure 4

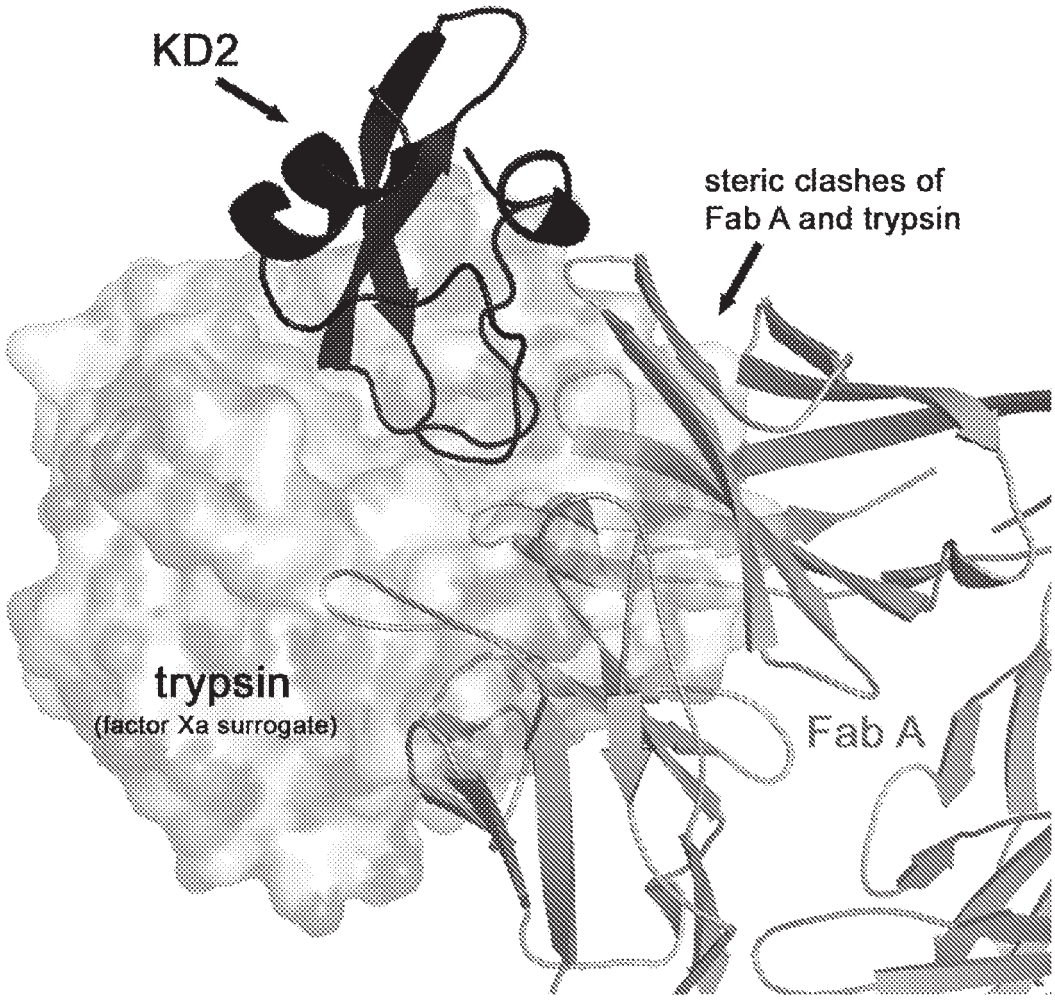

KD2
steric clashes of
Fab A and trypsin
trypsin
(factor Xa surrogate)
Fab A

Figure 5

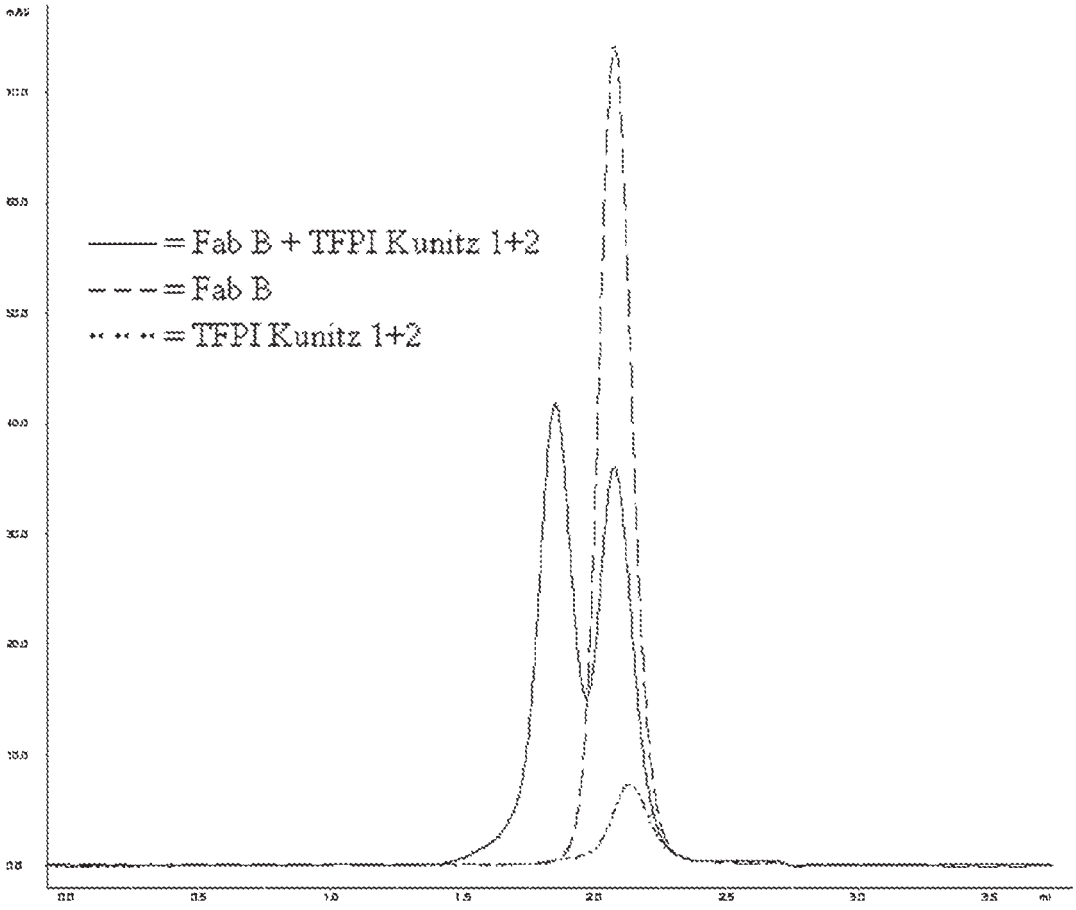


Figure 6

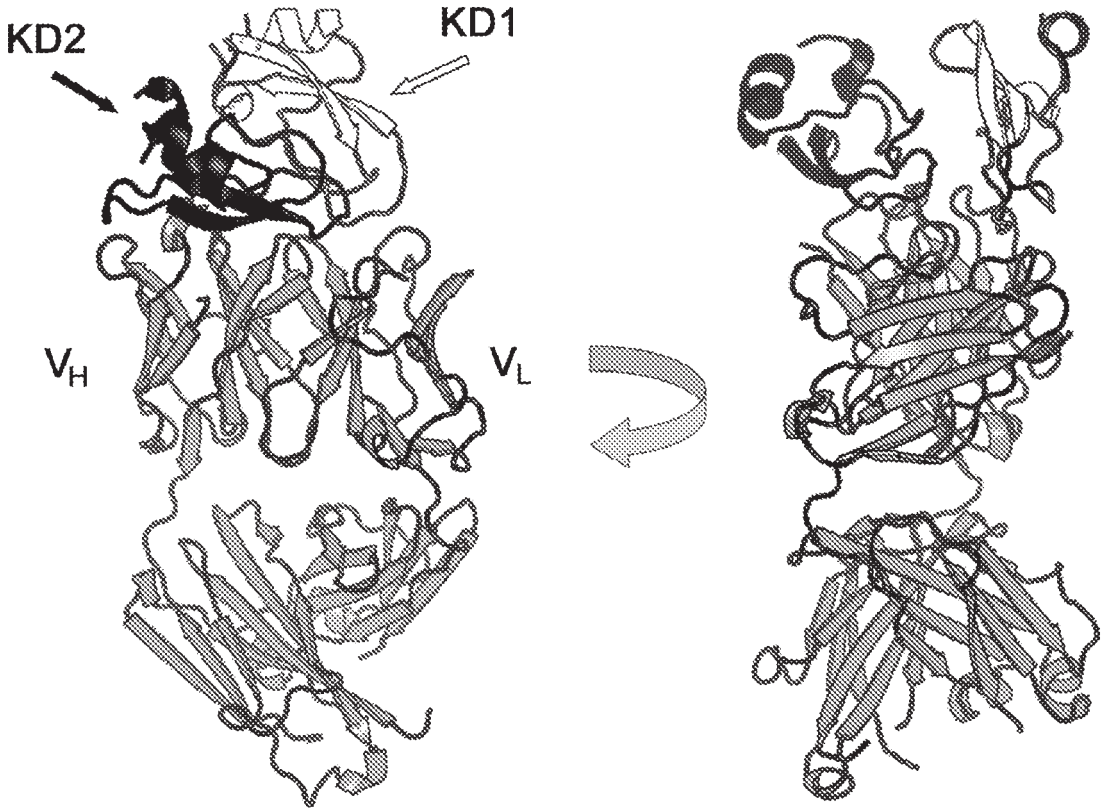


Figure 7

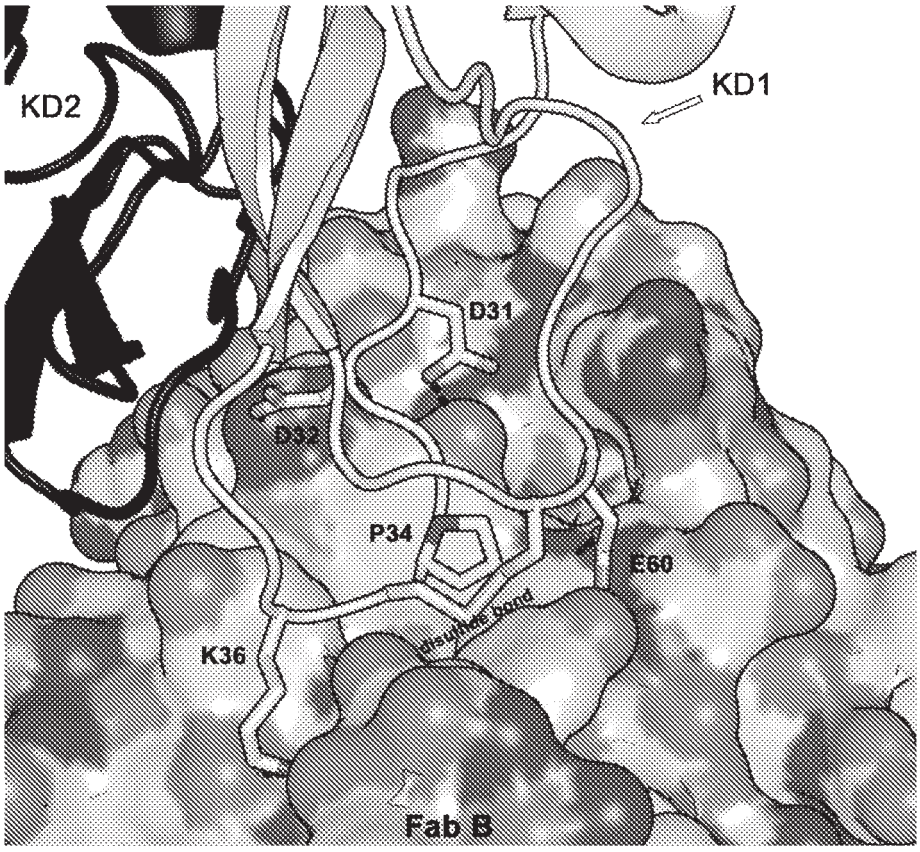


Figure 8

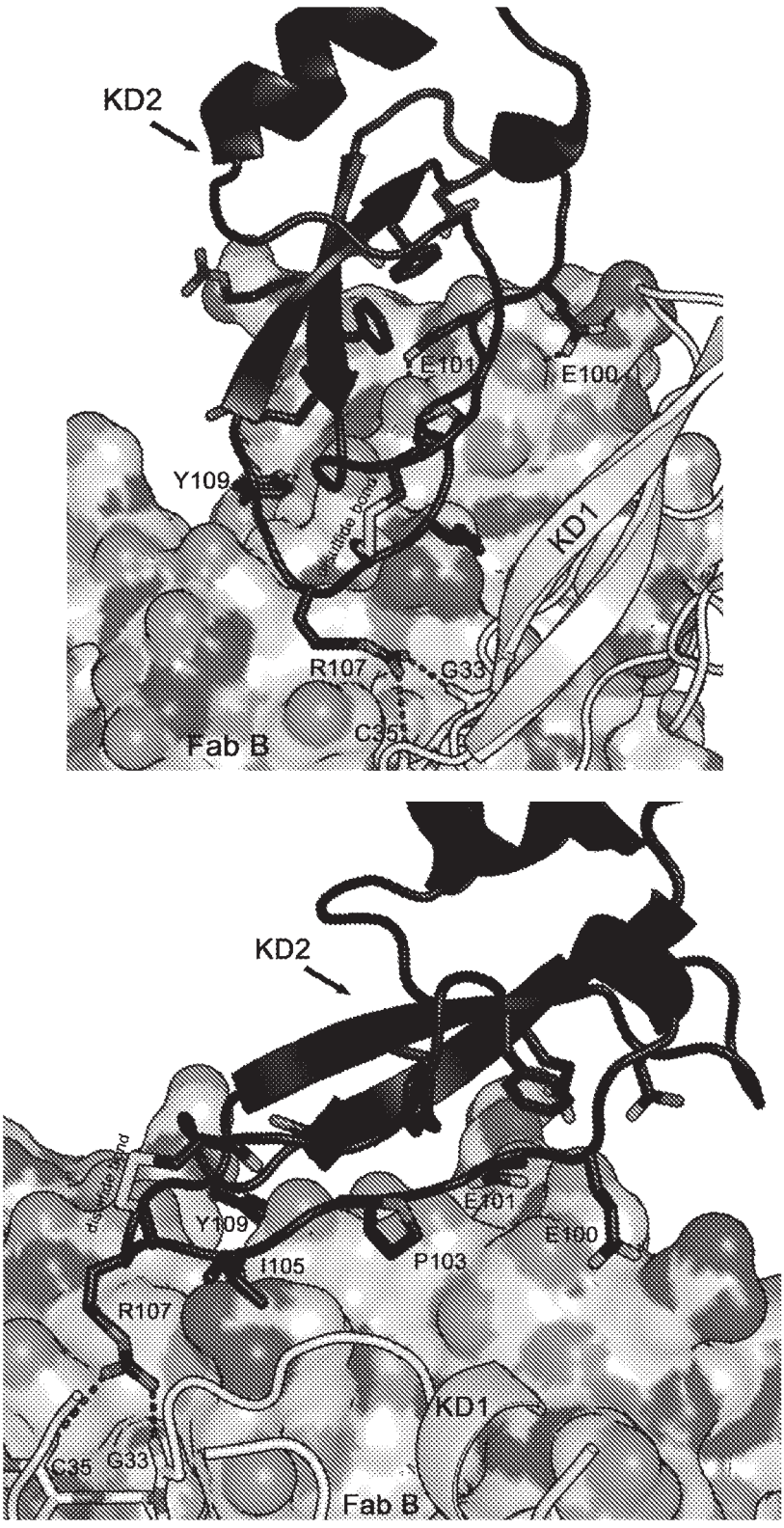

KD2
E101
E100
Y109
KD1
R107
G33
C35
Fab B
KD2
E101
Y109
E100
I105
P103
R107
KD1
C35
G33
Fab B

Figure 9

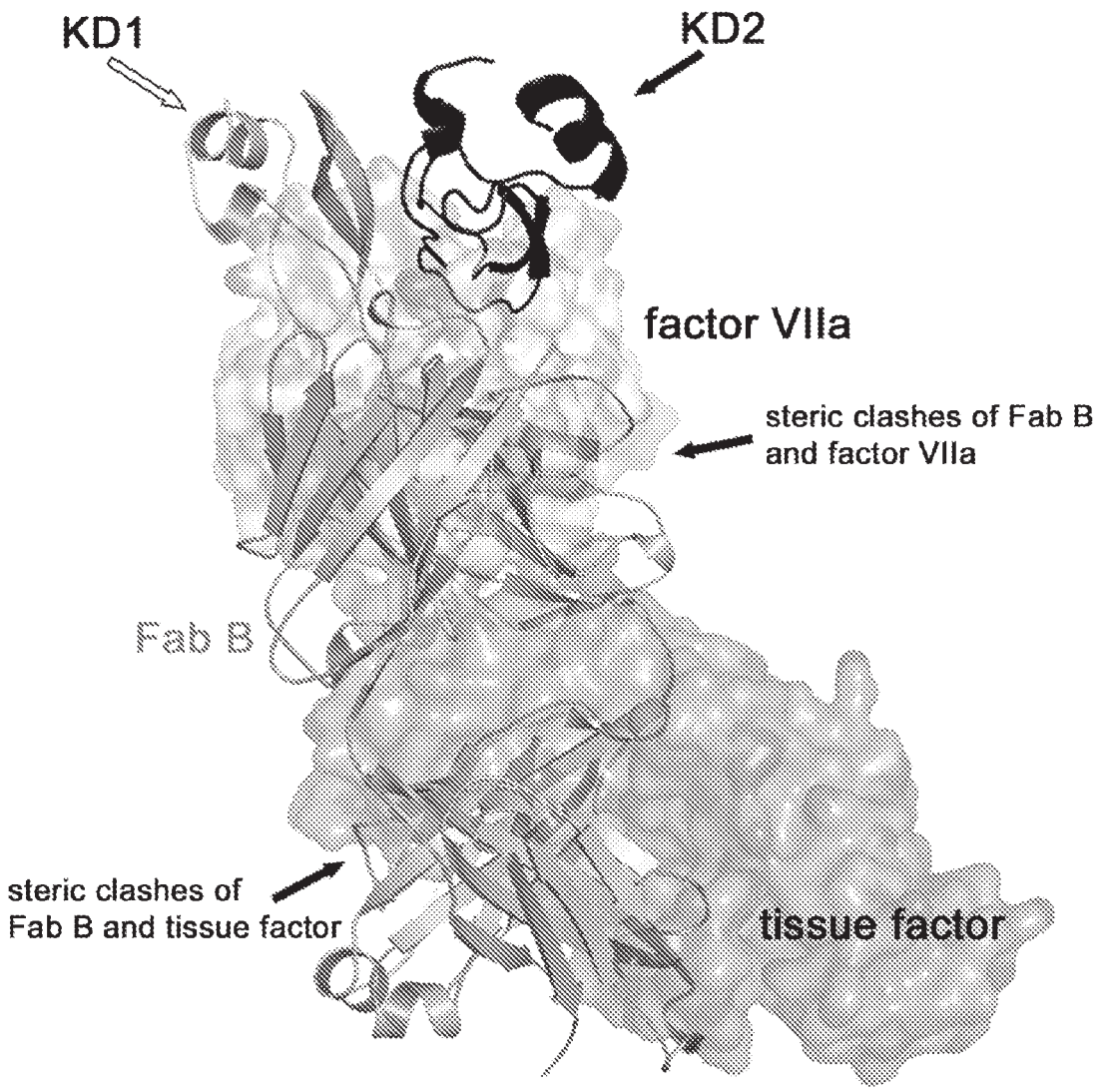

KD1
KD2
factor VIIa
steric clashes of Fab B
and factor VIIa
Fab B
steric clashes of
Fab B and tissue factor
tissue factor

Figure 10

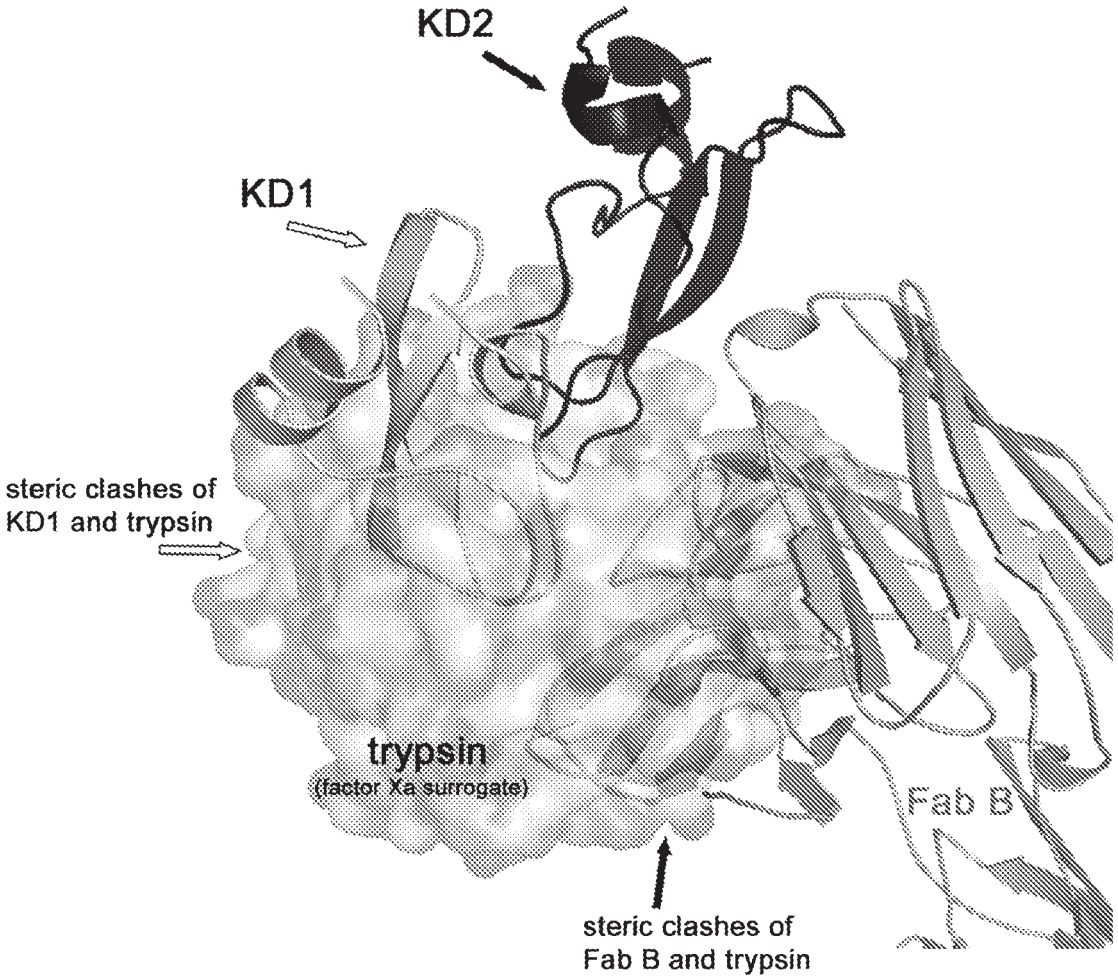

KD2
KD1
steric clashes of
KD1 and trypsin
trypsin
(factor Xa surrogate)
Fab B
steric clashes of
Fab B and trypsin

Figure 11

A

Light Chain:

```
Fab A: 1   DIVMTQSPLSLPVTPGEPASISCRSSQSLVFSDGNTYLNWYLQKPGQSPQLLIYKGSNRA 60
           DIVMTQSPLSLPVTPGEPASISCRSSQSLVF DG TYLNWYLQKPGQSPQLLIYKGSNRA
Fab C: 1   DIVMTQSPLSLPVTPGEPASISCRSSQSLVFRDGITYLNWYLQKPGQSPQLLIYKGSNRA 60

Fab A: 61  SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYDSYPLTFGQGTKVEIKRTVAAPSV 120
           SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYDSYPLTFGQGTKVEIKRTVAAPSV
Fab C: 61  SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCQQYDSYPLTFGQGTKVEIKRTVAAPSV 120

Fab A: 121 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
           FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL
Fab C: 121 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180

Fab A: 181 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 218
           SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE
Fab C: 181 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 218
```

Heavy Chain:

```
                                          *
Fab A: 1   QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWSWIRQSPGRGLEWLGIIYKRSKWY 60
           QVQLQQSGPGLVKPSQTLSLTCAISGDSVSS SAAWSWIRQSP RGLEWLGIIY RSKWY
Fab C: 1   QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSPSAAWSWIRQSPSRGLEWLGIIYYRSKWY 60

Fab A: 61  NRYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARWHSDKHWGFDYWGQGTLVT 120
           NRYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARWHSDKHWGFD WGQGTLVT
Fab C: 61  NRYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARWHSDKHWGFDDWGQGTLVT 120

Fab A: 121 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
           VSSASTKGPSVFPLAP S+STS  TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
Fab C: 121 VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180

Fab A: 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK 224
           QSSGLYSLSSVVTVPSS+ GTQTY CNV+HKPSNTKVDK VE K
Fab C: 181 QSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERK 224
```

Figure 11

B

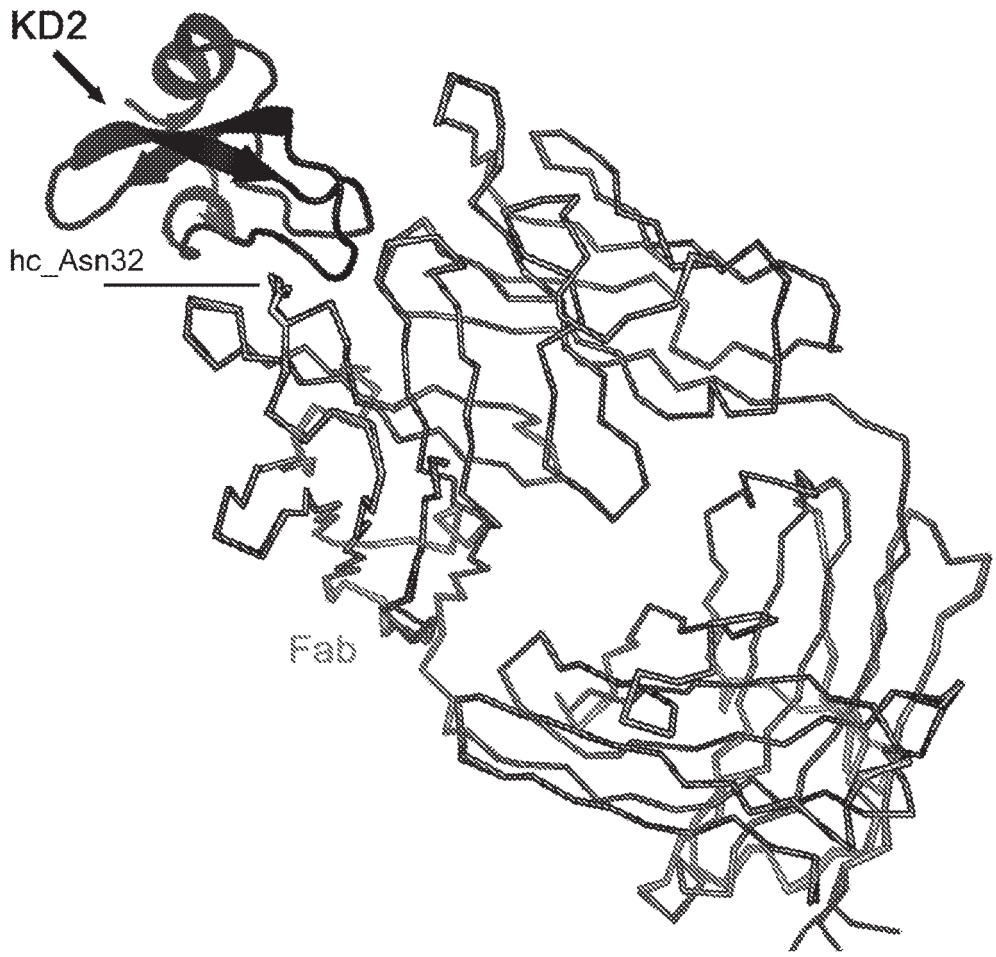


Figure 12

A

Light Chain:

```
                                        **                  *
Fab B: 1   DIELTQPPSVSVAPGQTARISCSGDNLRNYYAHWYQQKPGQAPVVVIYYDNNRPSGIPER 60
             ELTQPPSVSV+PGQTARI+CSGDNL YYAHWYQQKPGQAPVVVI+YD NRPSGIPER
Fab D: 1   SYELTQPPSVSVSPGQTARITCSGDNLPKYYAHWYQQKPGQAPVVVIFYDVNRPSGIPER 60

                                           **
Fab B: 61  FSGSNSGNTATLTISGTQAEDEADYYCQSWDDGVPVFGGGTKLTVLGQPKAAPSVTLFPP 120
           FSGSNSGNTATLTISGTQA DEADYYCQ+W   PVFGGGTKLTVLGQPKAAPSVTLFPP
Fab D: 61  FSGSNSGNTATLTISGTQAMDEADYYCQAWWSSTPVFGGGTKLTVLGQPKAAPSVTLFPP 120

Fab B: 121 SSEELQANKATLVCLISDFYPGAVTVAWKGDSSPVKAGVETTTPSKQSNNKYAASSYLSL 180
           SSEELQANKATLVCLISDFYPGAVTVAWK DSSPVKAGVETTTPSKQSNNKYAASSYLSL
Fab D: 121 SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSL 180

Fab B: 181 TPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 212
           TPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
Fab D: 181 TPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 212
```

Heavy Chain:

```
           *                                *
Fab B: 1   QVELVESGGGLVQPGGSLRLSCAASGFTFRSYGMSWVRQAPGKGLEWVSSIRGSSSSTYY 60
           +V+LVESGGGLVQPGGSLRLSCAASGFTF SYGM WVRQAPGKGLEWVSSIRGS  STYY
Fab D: 1   EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYGMDWVRQAPGKGLEWVSSIRGSRGSTYY 60

Fab B: 61  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLYRYWFDYWGQGTLVTVSSAST 120
           ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLYRYWFDYWGQGTLVTVSSAST
Fab D: 61  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLYRYWFDYWGQGTLVTVSSAST 120

Fab B: 121 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180
           KGPSVFPLAP S+STS  TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
Fab D: 121 KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 180

Fab B: 181 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC 220
           SLSSVVTVPSS+ GTQTY CNV+HKPSNTKVDK VE K C
Fab D: 181 SLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCC 220
```

Figure 12

B

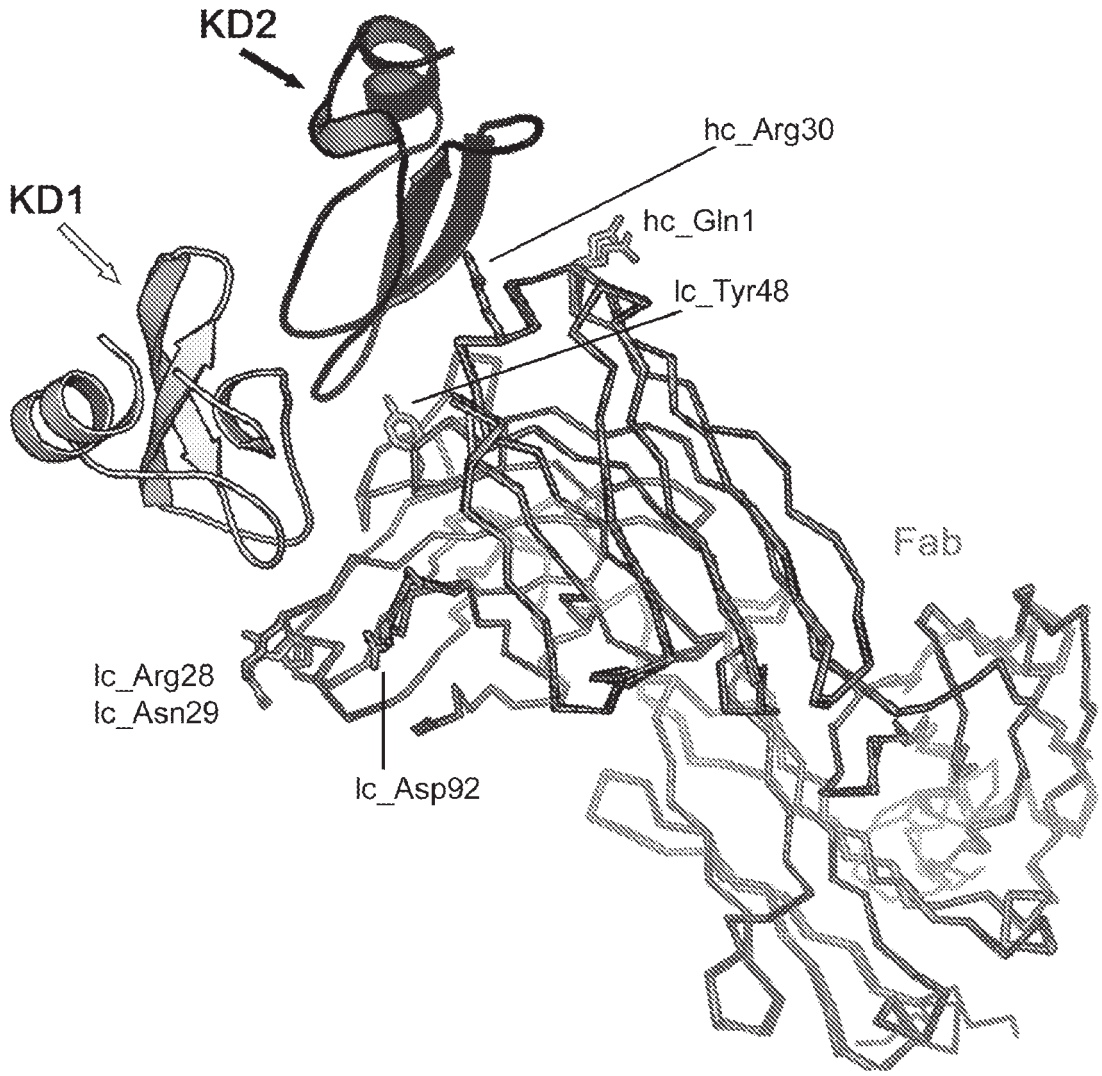
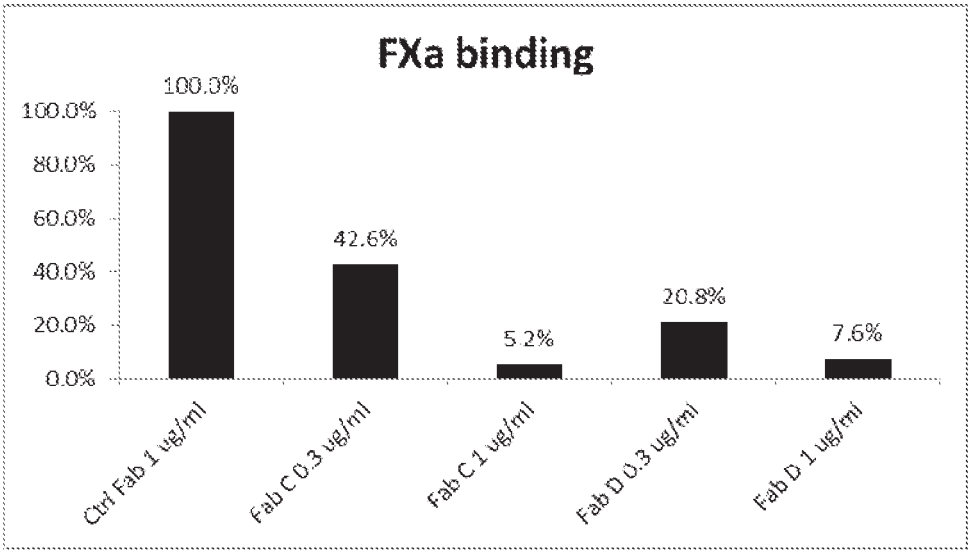
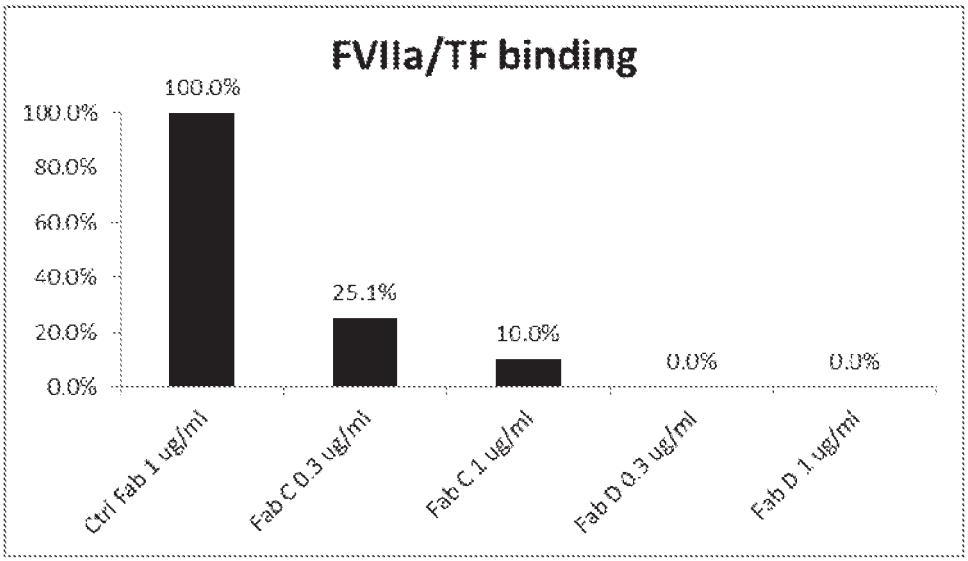

KD2
KD1
hc_Arg30
hc_Gln1
lc_Tyr48
Fab
lc_Arg28
lc_Asn29
lc_Asp92

Figure 13

A


FXa binding
100.0%
80.0%
60.0%
40.0%
20.0%
0.0%
100.0%
42.6%
5.2%
20.8%
7.6%
Ctrl Fab 1 ug/ml
Fab C 0.3 ug/ml
Fab C 1 ug/ml
Fab D 0.3 ug/ml
Fab D 1 ug/ml

B


FVIIa/TF binding
100.0%
80.0%
60.0%
40.0%
20.0%
0.0%
100.0%
25.1%
10.0%
0.0%
0.0%
Ctrl Fab 1 ug/ml
Fab C 0.3 ug/ml
Fab C 1 ug/ml
Fab D 0.3 ug/ml
Fab D 1 ug/ml