

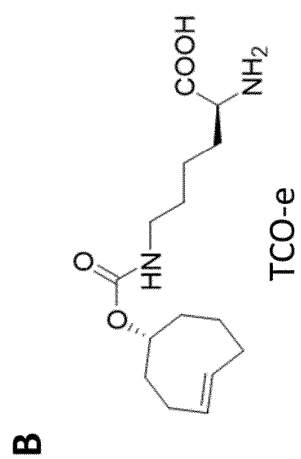
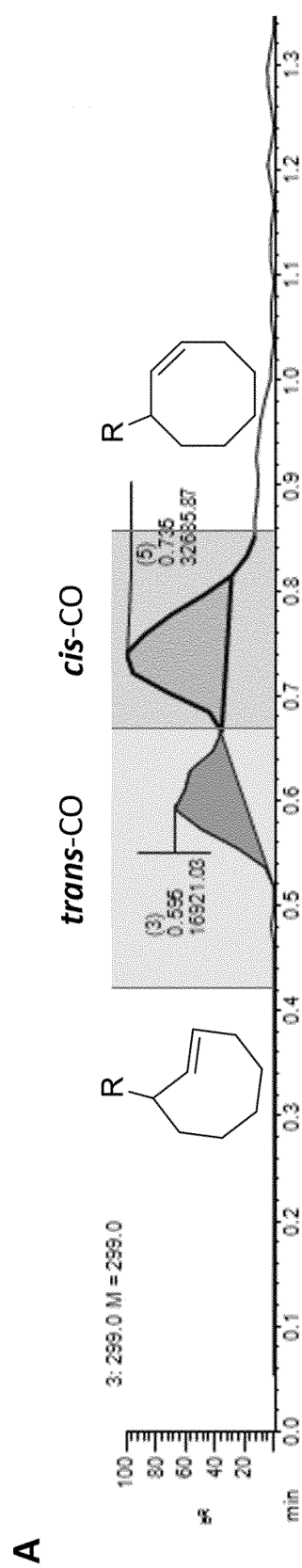


Fig. 1

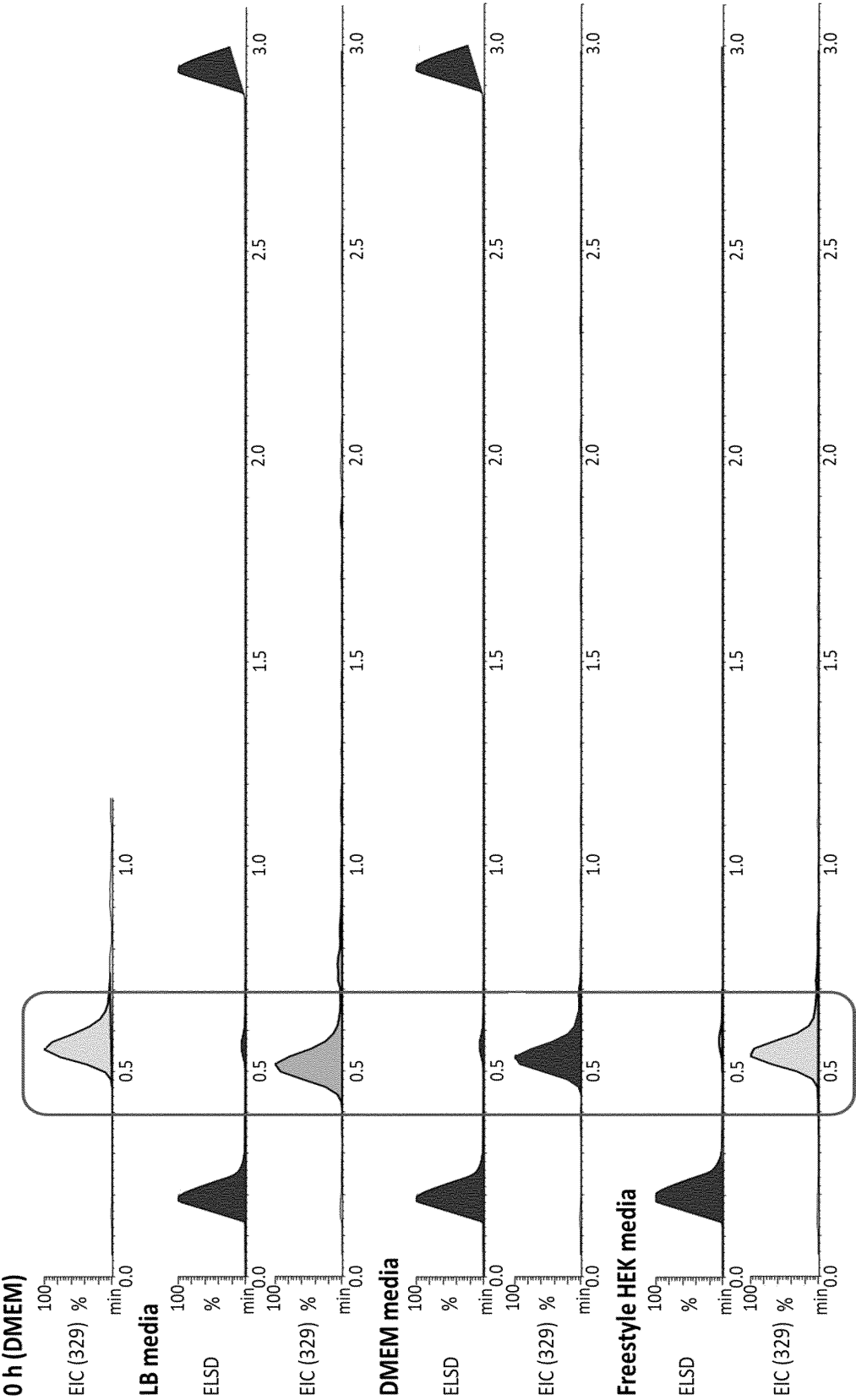


Fig.2

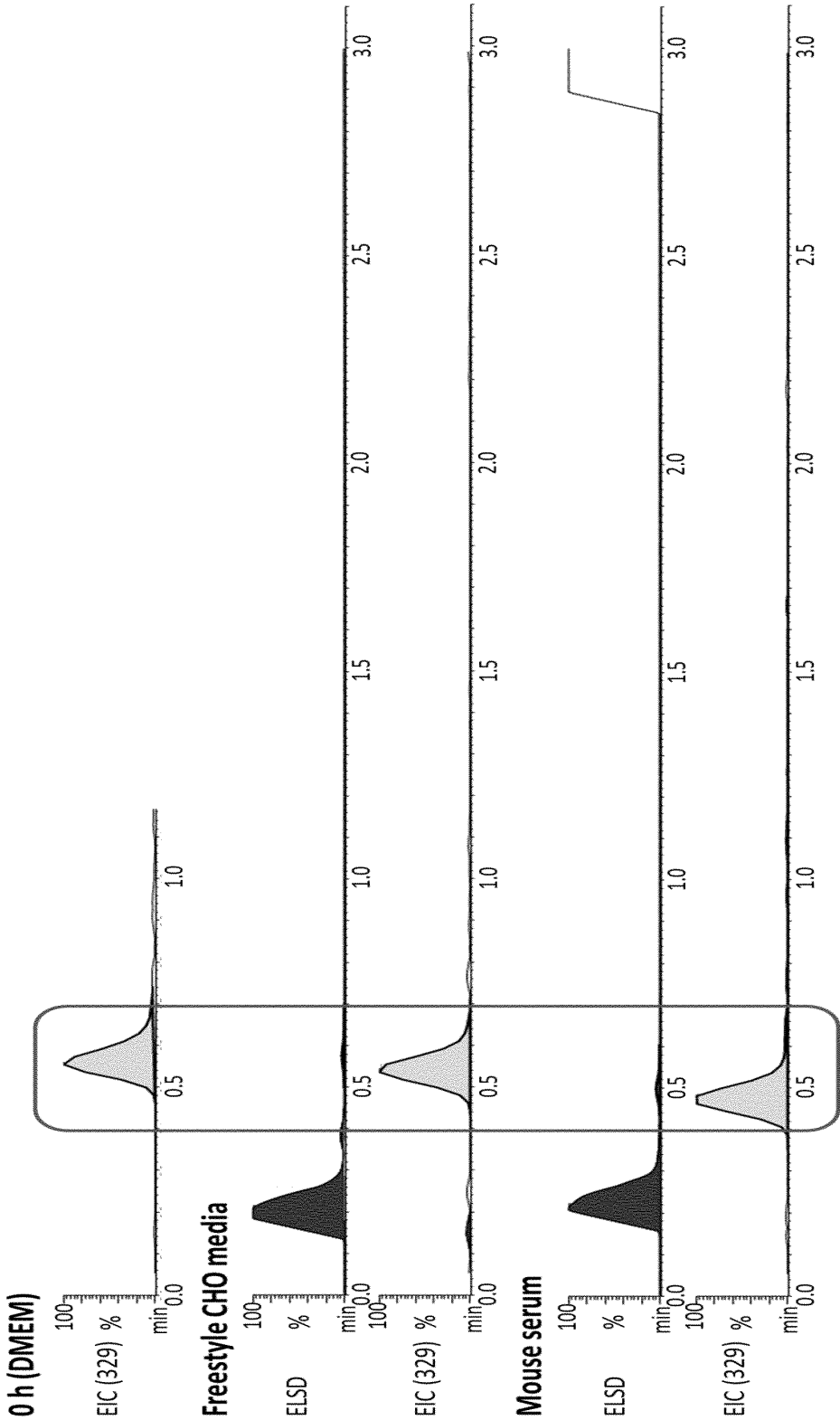


Fig.2 (continued)

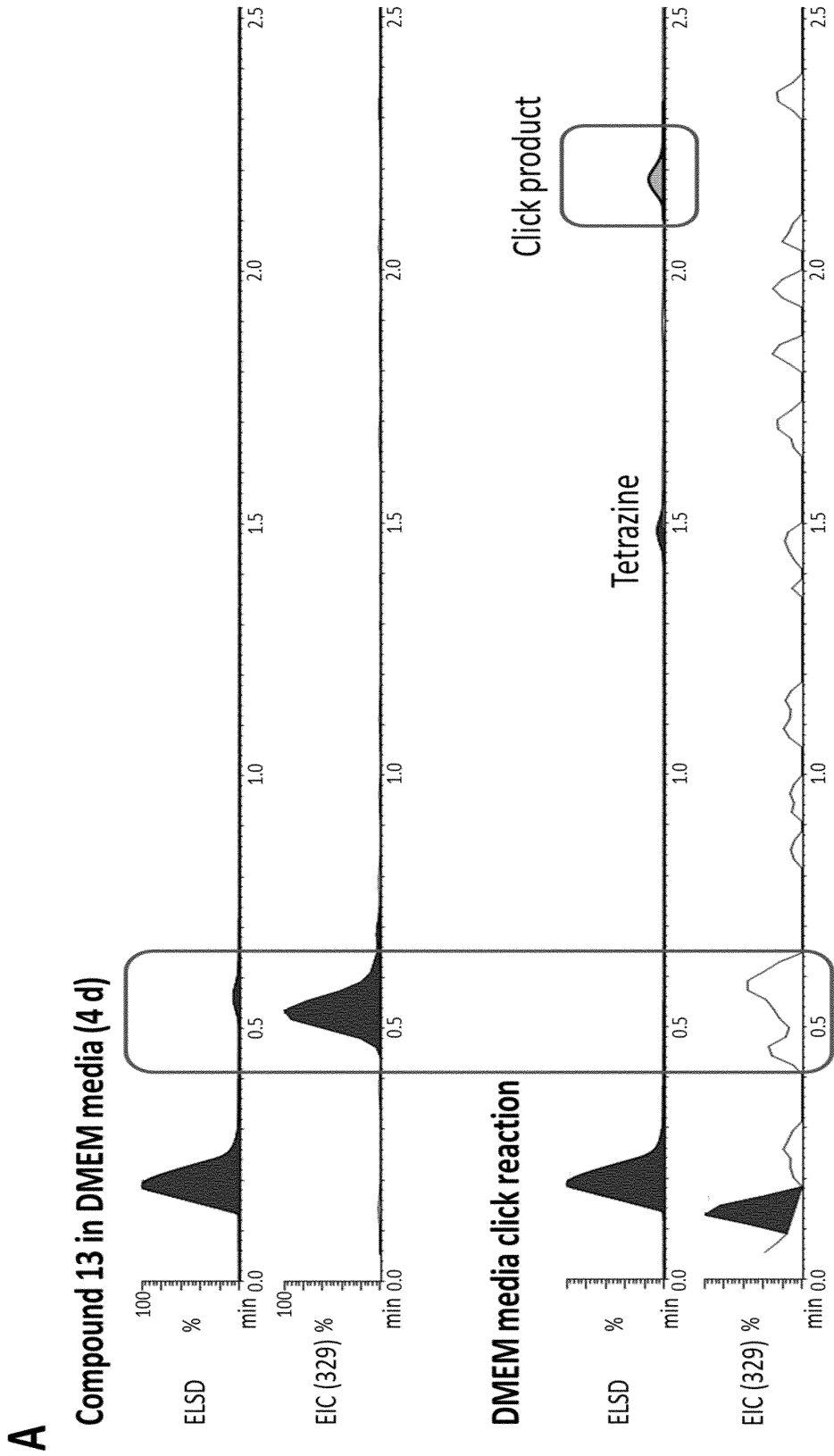
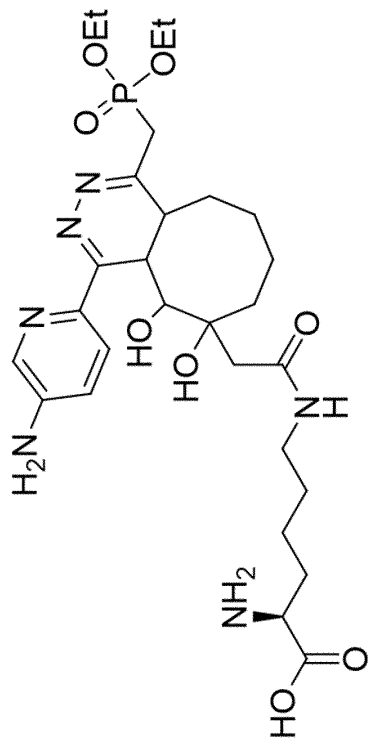


Fig.3

B



Molecular Weight: 624,68

MS TIC +

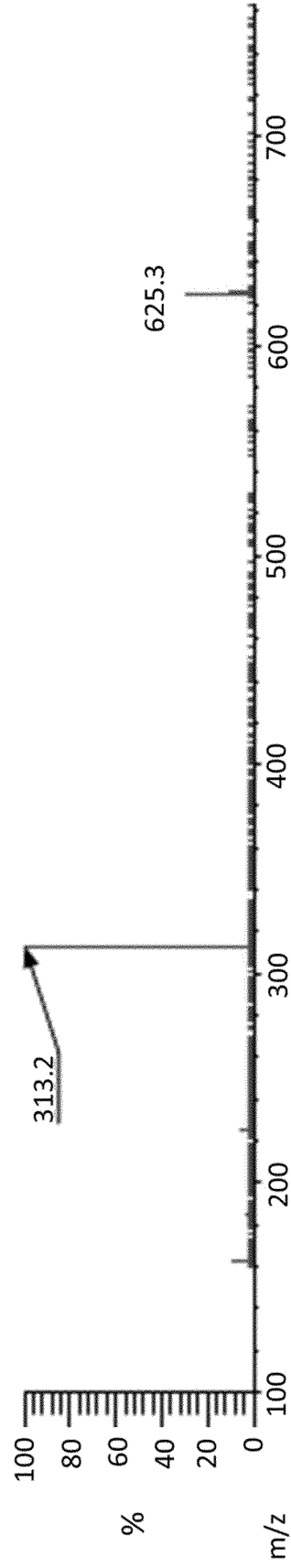


Fig.3 (continued)

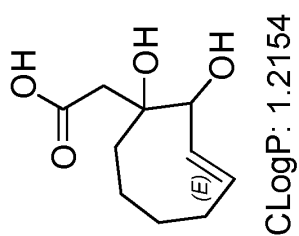
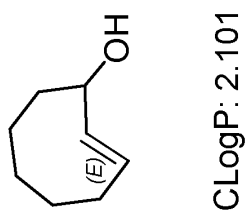
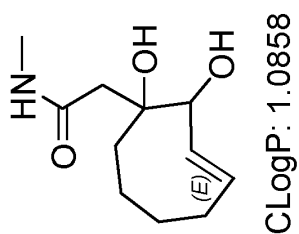
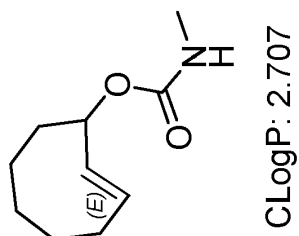


Fig.4

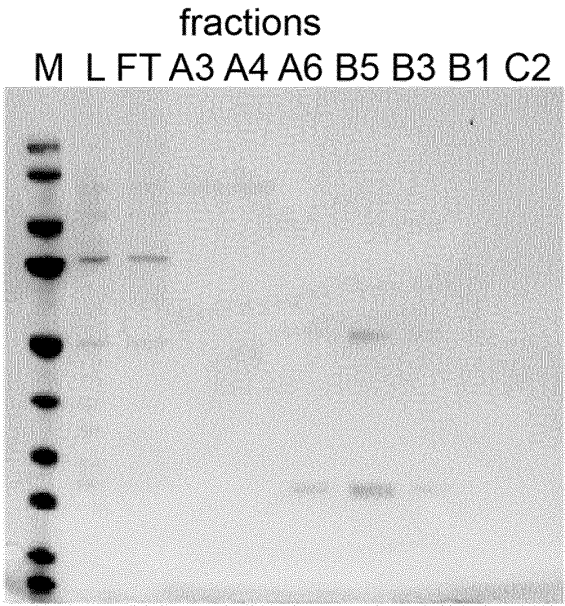
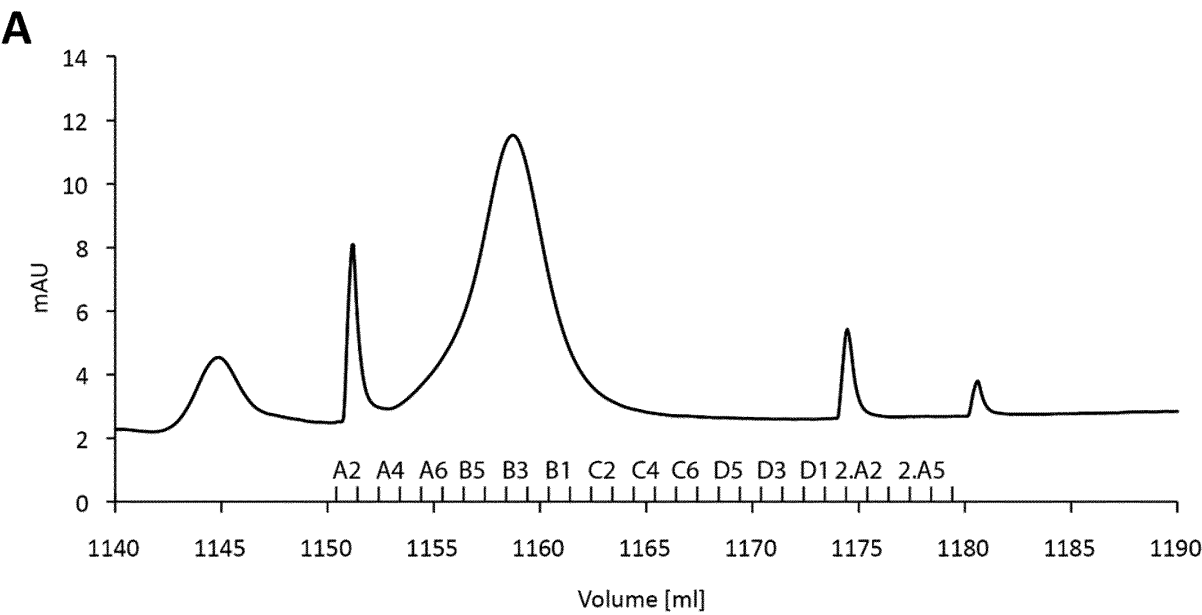
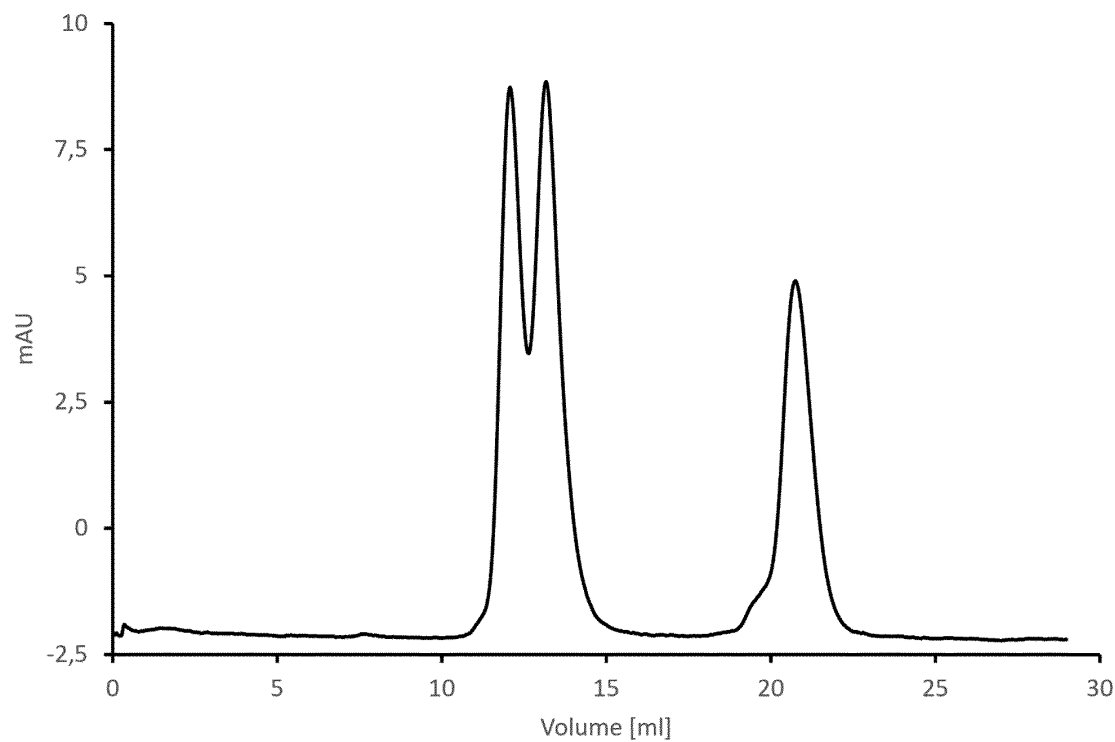


Fig.5

B



fractions
M Inj A6 B6 B5 B4 B3 B2 B1 C1

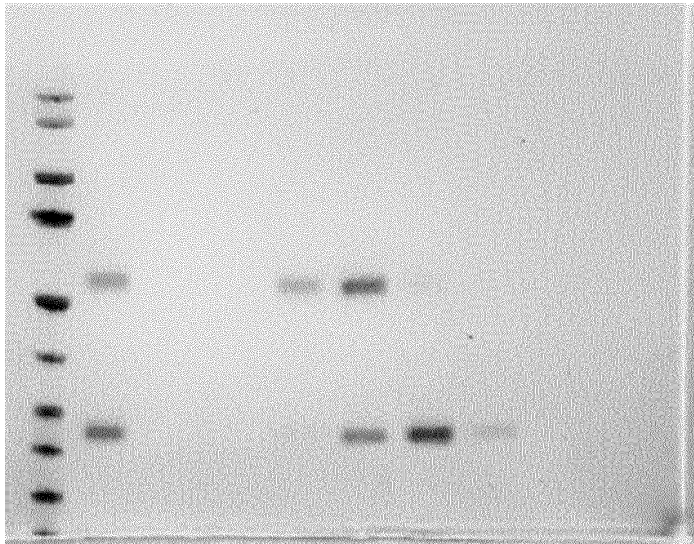


Fig.5 (continued)

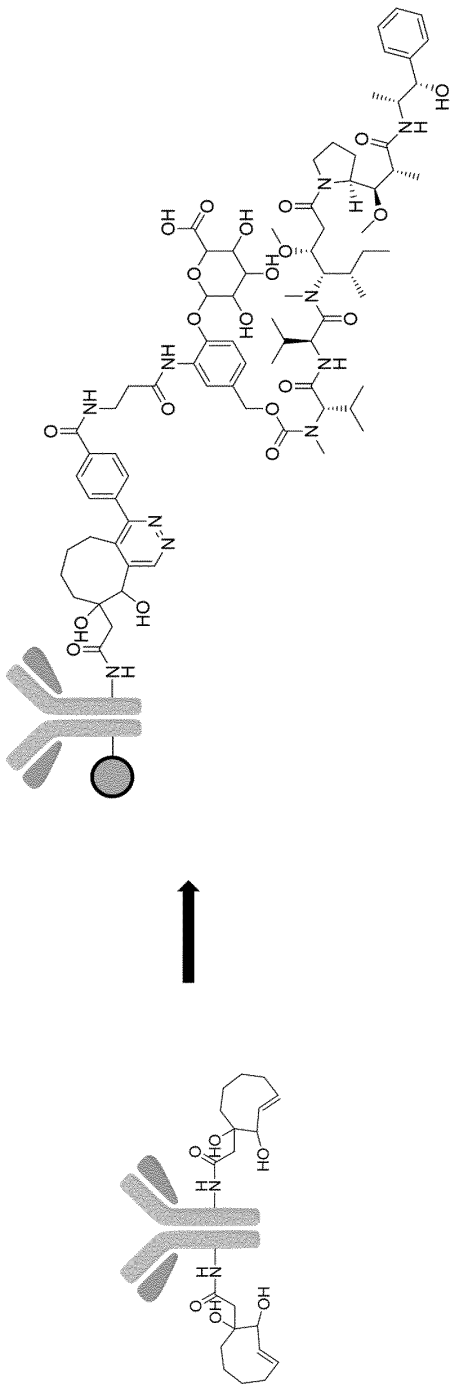
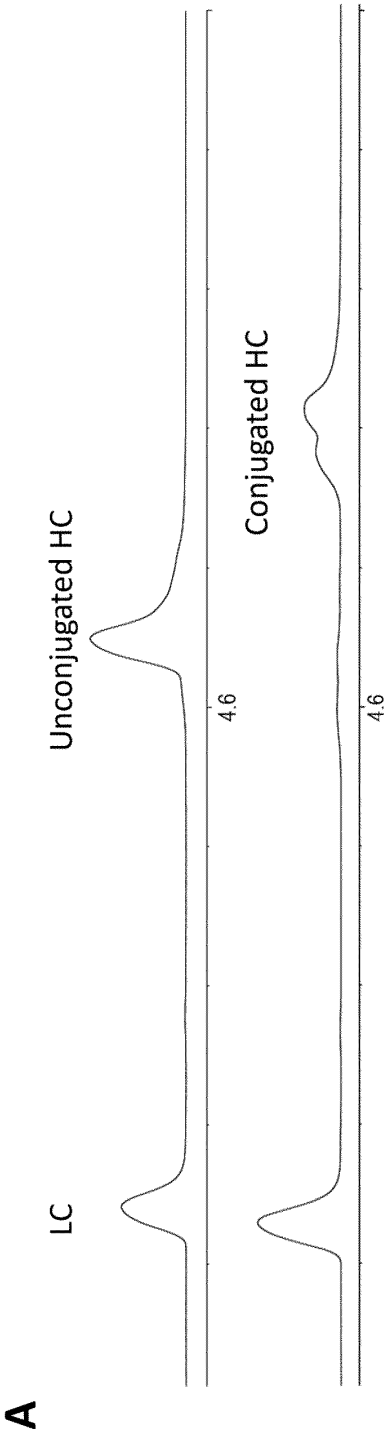


Fig.6

B

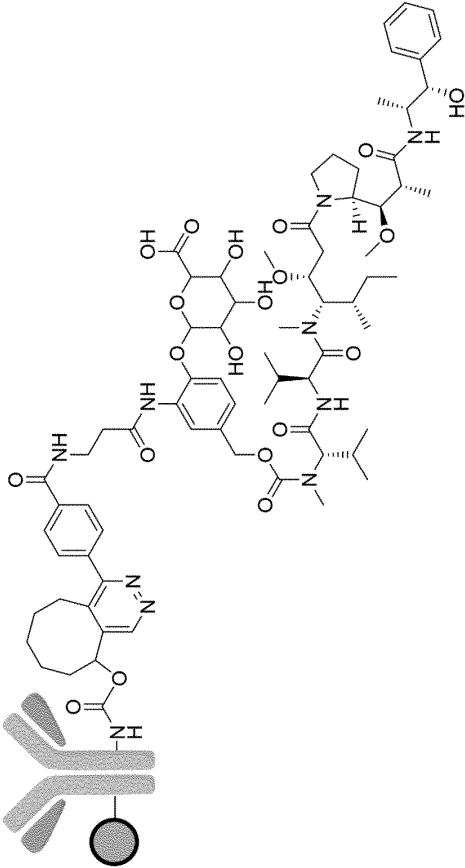
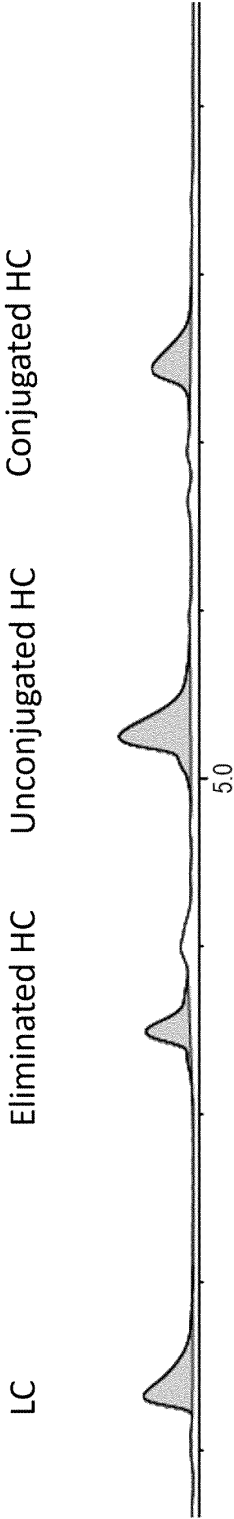


Fig.6 (continued)

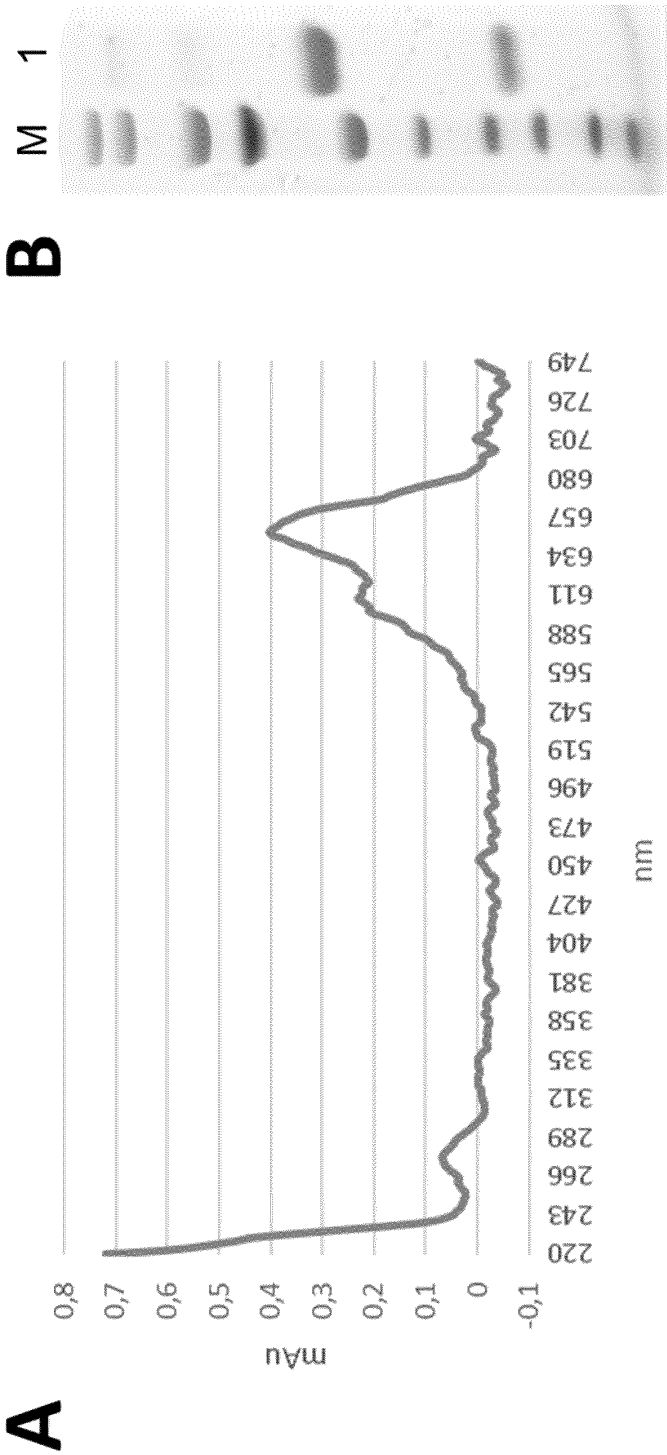


Fig.7

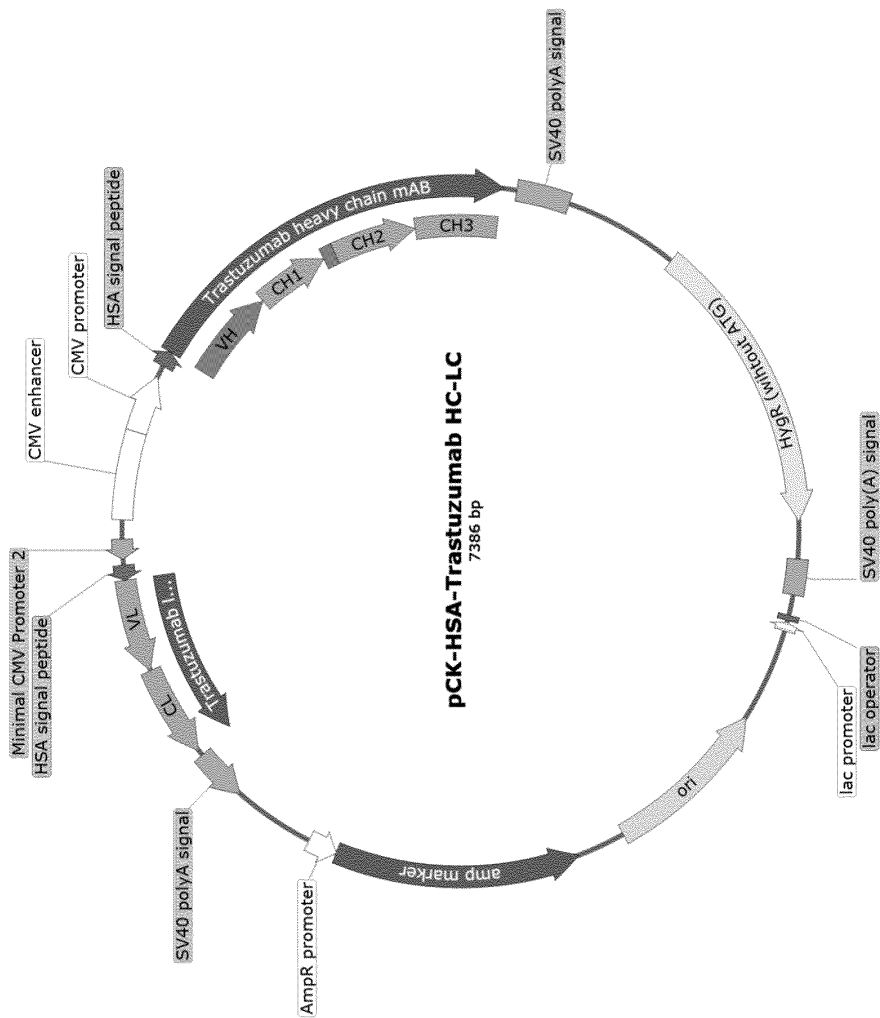


Fig.8

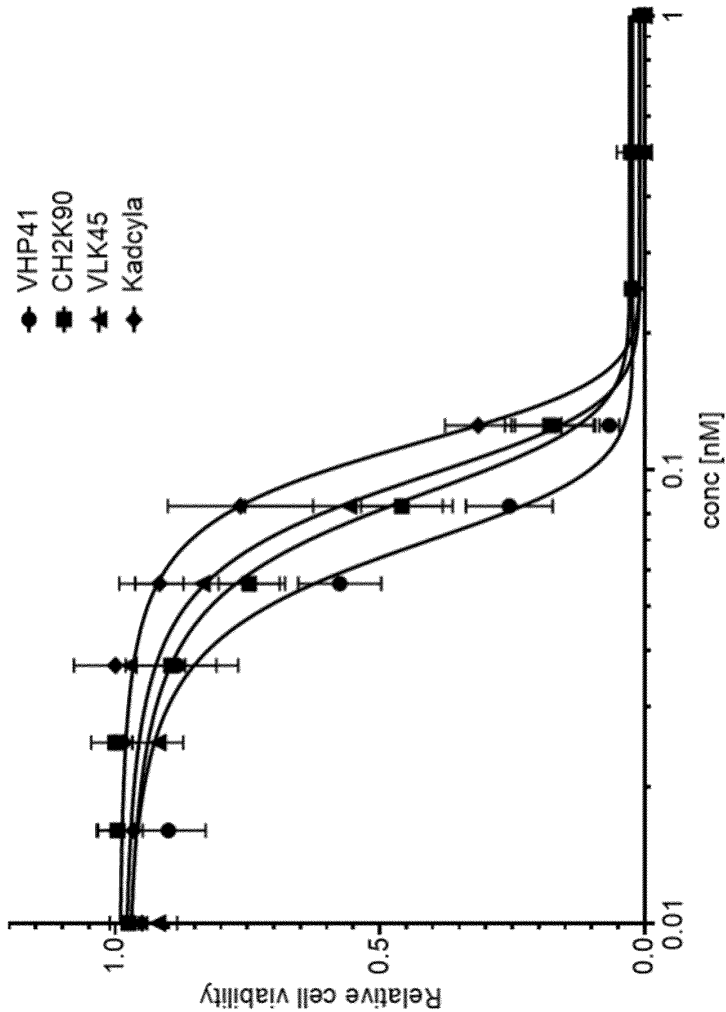


Fig.9

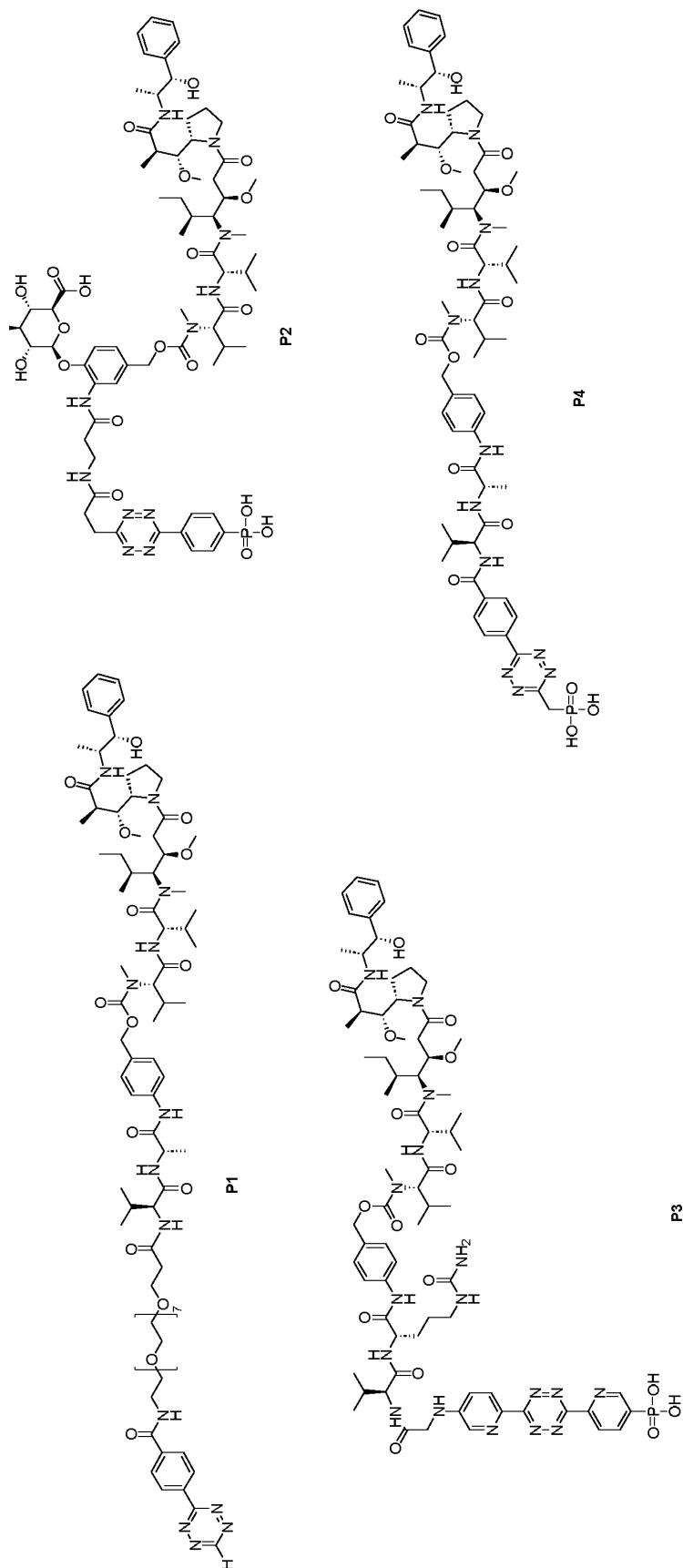


Fig.10

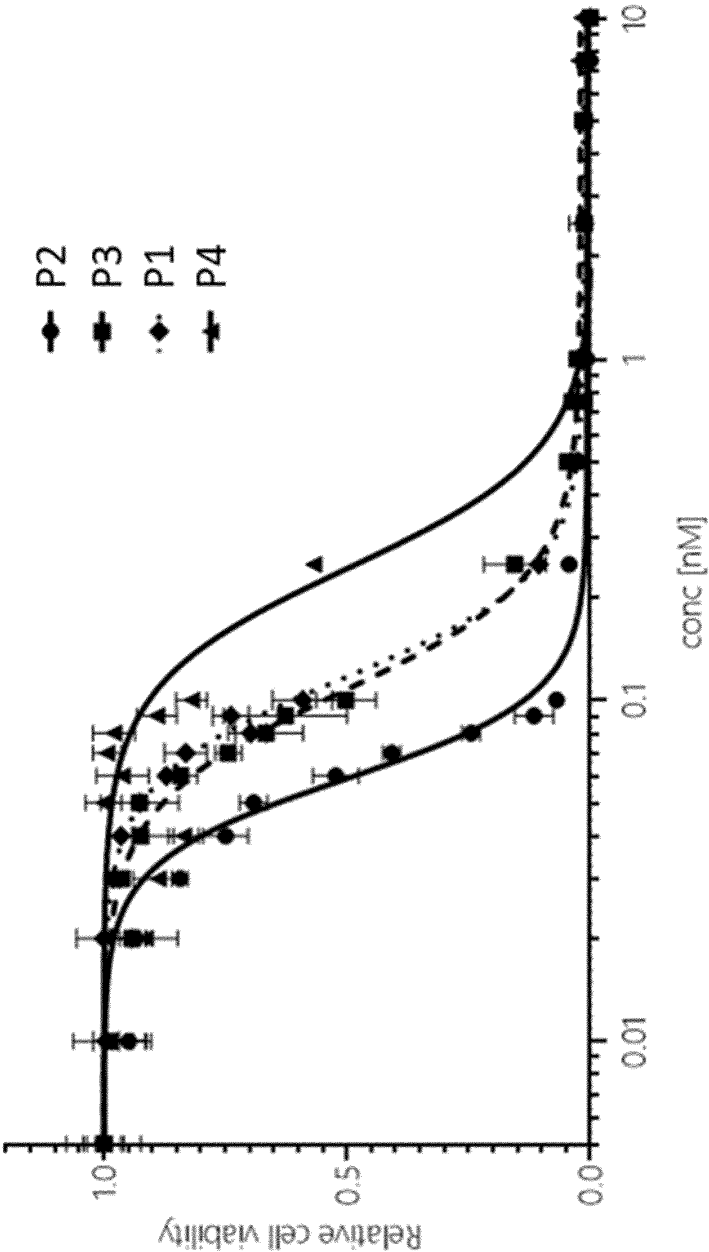


Fig.11

Protein sequences with regions marked

(taken from WO2023/094525)

Trastuzumab heavy chain (SEQ ID NO:1):

EVQLVESGGGLVQPGGSLRLSCAAS**GFNIKDTY**IHWVRQAP**G**KGLEWV**ARIYPTNGYTRY**ADSVKGRFT
 ISADTSKNTAYLQMNSLRAEDTAVYYC**SRWGGDGFYAMDY**WGQGTLVTVSSASTKGPSVFPLAPSSKSTS
 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKP
 SNTKVDKK**VEPKSCDKTHTCPPCP**APPELLGGPSVFLFPP**KpK**DTLMISRTPEVTCVVVDVSHEDPEVKF
 NWYVDGVEVHNA**K**TKPREEQYNSTYRVVSVLTVTLHQDWLNG**KeyK**CKVSNKALPAPIEKTISKAKGQP
 REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVD
 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Mutation positions enlarged

VH domainCH1 domainHinge regionCH2 domainCH3 domain**CDR domains are in bold****Trastuzumab light chain (SEQ ID NO:2):**

DIQMTQSPSSLSASVGDRVTITCRAS**QDVNTA**VAWYQQK**P**GKAP**KLLIYsAs**FLYSGVP**S**SRFSGSRSG
 TDFLTITSSLPEDFATYYC**QOHY****TTPPT**FGQGTKVEIKRTV**A**APSVFIFPPSDEQLKSGTASVVCLLNN
 FYPREAKVQWKVDNALQSGNSQESVTEQDS**K**DSTYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKS
 FNRGEC

Mutation positions enlarged

V-Kappa (VL) domainC-Kappa: constant domain light chain**CDR domains**

Fig.12