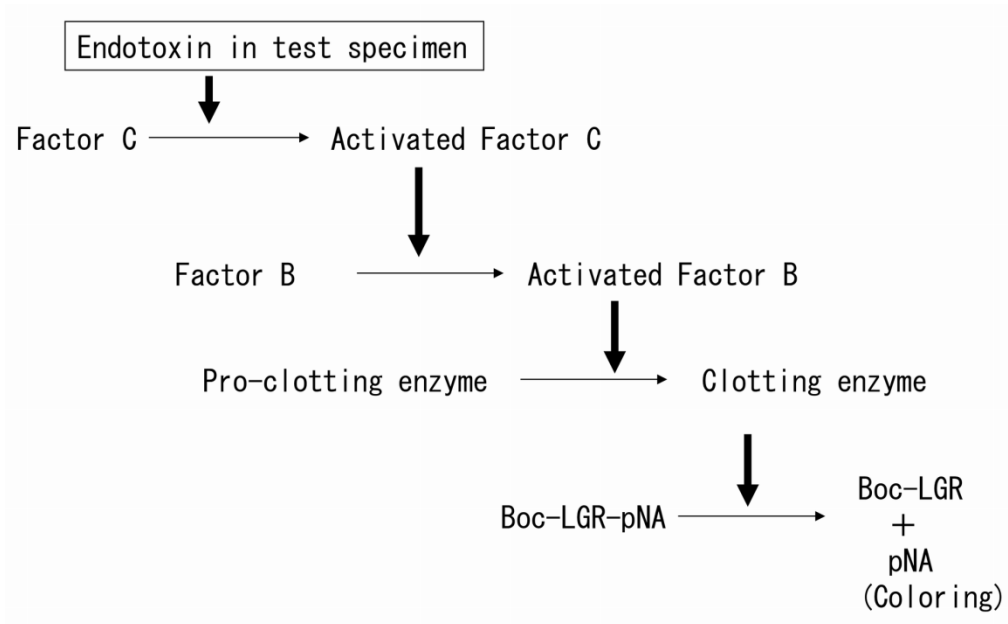
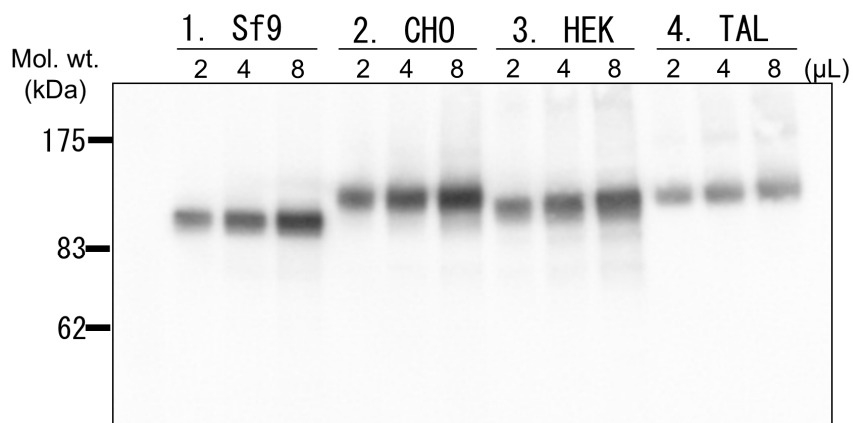


Figures

[Fig. 1]

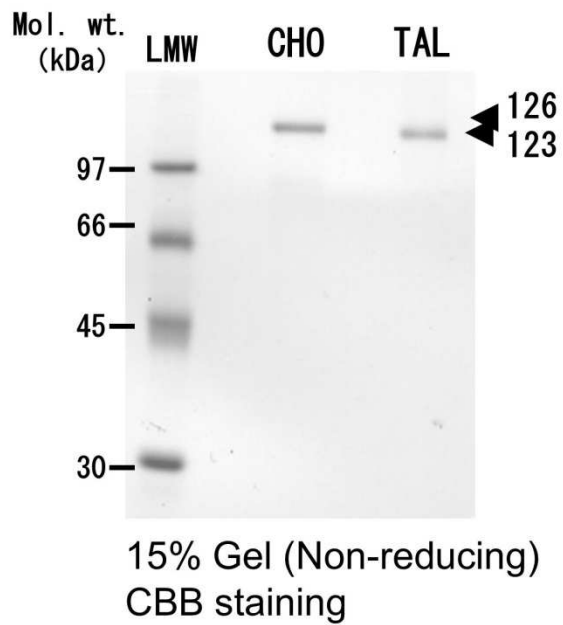


[Fig. 2]

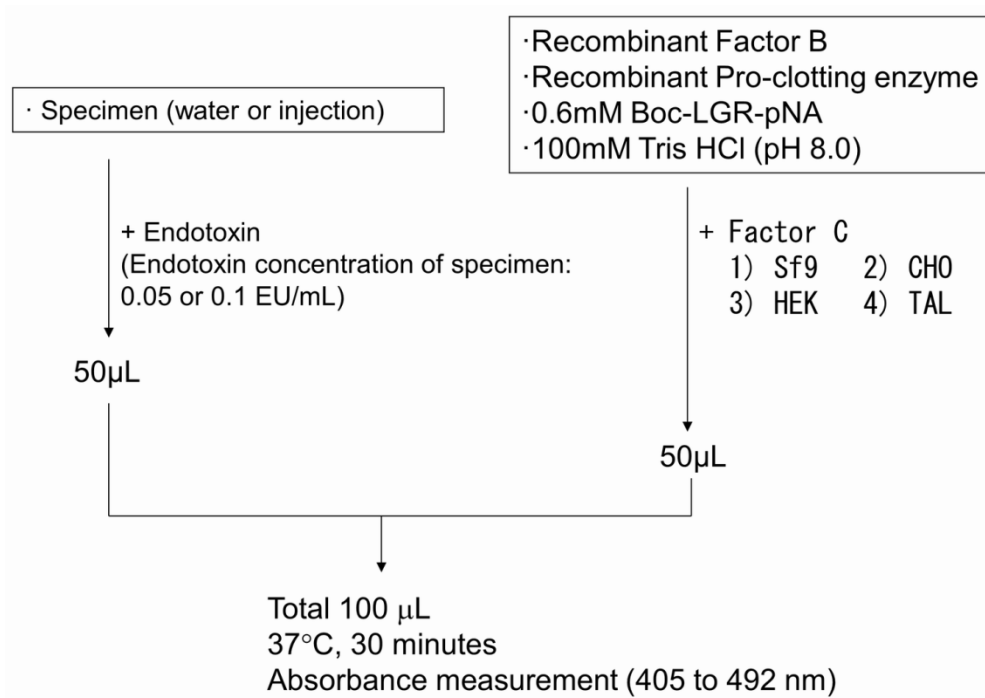


Primary antibody: Anti-factor C monoclonal antibody (2C12)
 Electrophoresis conditions: non-reducing

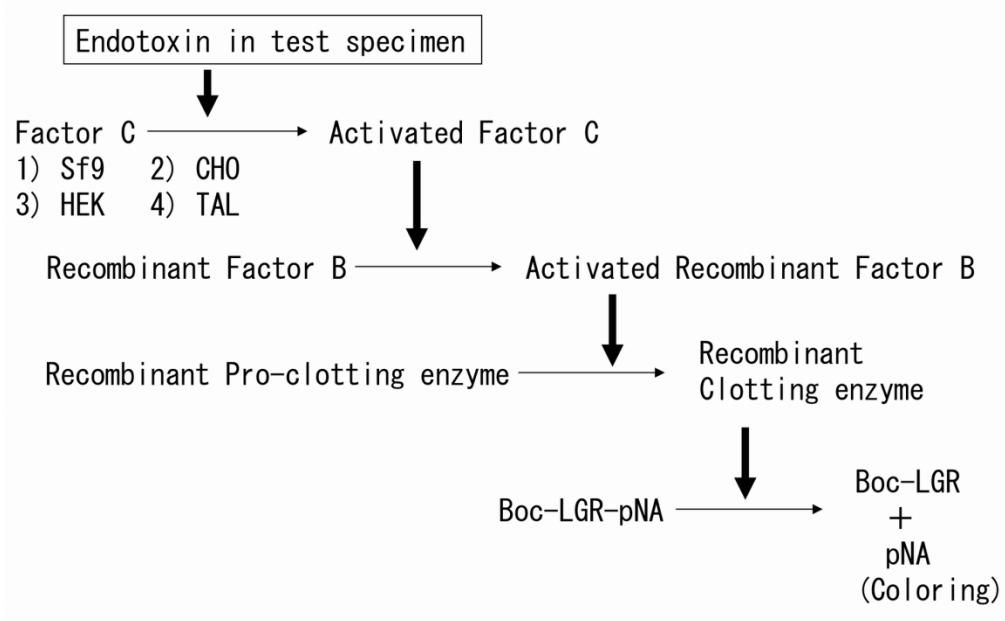
[Fig. 3]



[Fig. 4]



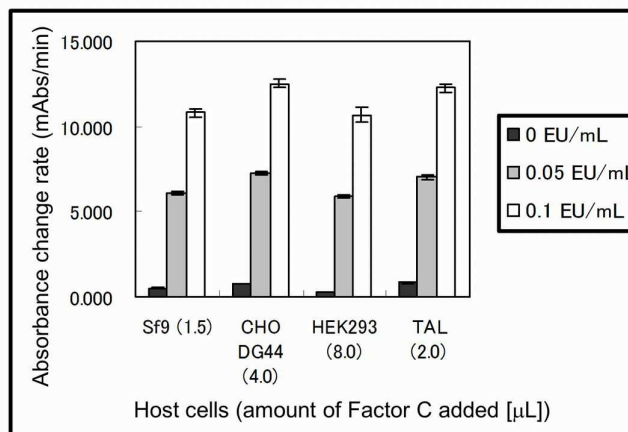
[Fig. 5]



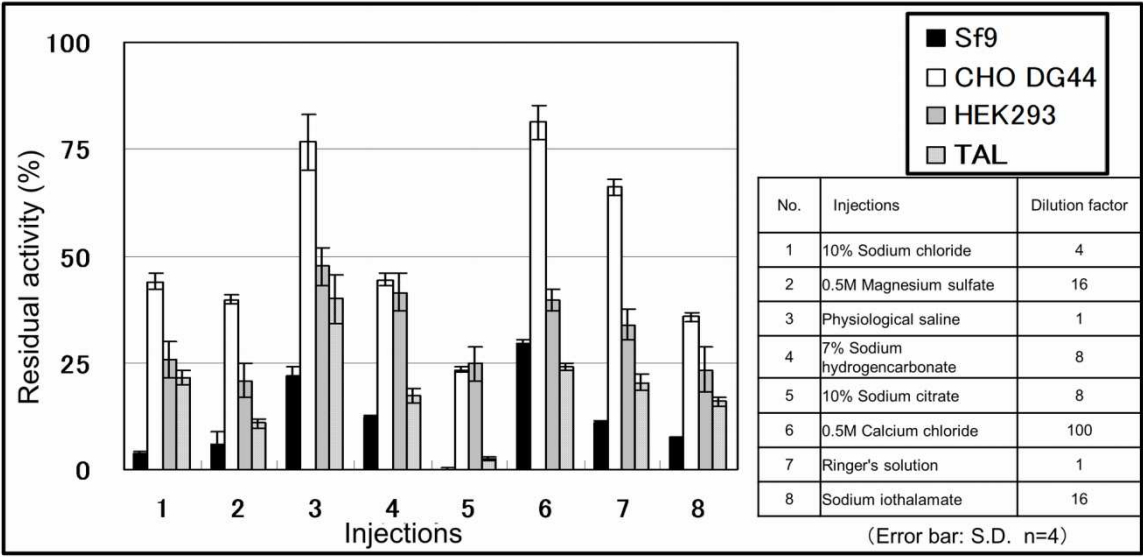
[Fig. 6]

Host cells for Factor C	Amount of Factor C added (μ L)	Endotoxin concentration (EU/mL)	Absorbance change rate (av. $\pm$ S.D.) (mAbs/min)
Sf9	1.5	0	0.520 $\pm$ 0.015
		0.05	6.095 $\pm$ 0.108
		0.1	10.795 $\pm$ 0.246
CHO DG44	4	0	0.770 $\pm$ 0.021
		0.05	7.260 $\pm$ 0.087
		0.1	12.510 $\pm$ 0.255
HEK293	8	0	0.300 $\pm$ 0.017
		0.05	5.885 $\pm$ 0.125
		0.1	10.685 $\pm$ 0.417
TAL	2	0	0.840 $\pm$ 0.055
		0.05	7.030 $\pm$ 0.140
		0.1	12.270 $\pm$ 0.255

n=3



[Fig. 7]



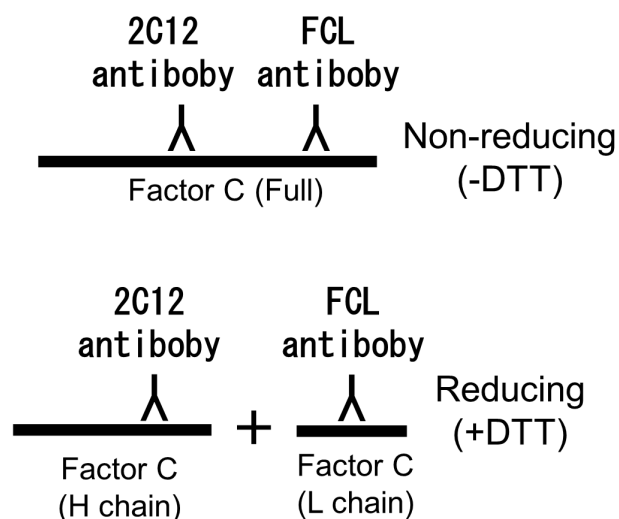
[Fig. 8]

TtFc 834Cr ID4	MVLASFLVSGLVGLILAQQMRPVQSRGVDLGLCDETRFECKCGDPGYVFNVPMKQCTYFY MVLASFLVSGLVGLLLAQKMRPVQSKGVDLGLCDETRFECKCGDPGYVFNIPVKQCTYFY *****:***:*****:*****:*****:***:*****	60
TtFc 834Cr ID4	RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQ RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQ *****	120
TtFc 834Cr ID4	RTGACTCRDRYEGAHCEILKGCPLLPSDSQVQEVNPPDNPQTIDYSCSPGFKLKGVAR RTGACACRDRYEGVHCEILKGCPLLPSDSQVQEVNPPDNPQTIDYSCSPGFKLKGMA *****:*****:*****:*****:*****:***	180
TtFc 834Cr ID4	SCLPNGQWSSFPPKCIRECAKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLT SCLPNGQWSNFPPKCIRECAMVSSPEHGKVNALSGDMIEGATLRFSCDSPYYLIGQETLT *****:*****:*****:*****:*****:***	240
TtFc 834Cr ID4	CQGNQWWSGQIPQCKKLVFCDLDPVNHAHQVKIGVEQKYGQFPQGTEVYTCSGNYFL CQGNQWWSGQIPQCKNLVFCDLDPVNHAHQVKIGVEQKYGQFPQGTEVYTCSGNYFL *****:*****:*****:*****:*****:*****	300
TtFc 834Cr ID4	MGFNTLKCNDPGSWGSGSQPSCKVADREVDCKSAVDFLDDVGEPVRIHCPAGCSLTAGT MGFDTLKCNDPGSWGSGSQPSCKVADREVDCKSAVDFLDDVGEPVRIHCPAGCSLTAGT ***:*****:*****:*****:*****:*****	360
TtFc 834Cr ID4	VWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVNNGPYSDFLGSDLNGIKSEELKSLARS VWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVNNGPYSDFLGSDLNGIKSEELKSLARS *****	420
TtFc 834Cr ID4	FRFDYVSSSTAGRSGCPDGFWEVEENCYVYVTSKQRAWERAQGVCTNMAARLAVLDKDLIP FRFDYVRSSTAGKSGCPDGFWEVDENCYVYVTSKQRAWERAQGVCTNMAARLAVLDKDVIP *****:*****:*****:*****:*****:***	480
TtFc 834Cr ID4	SSLTETLRGKGLTTTWIGLHRLDAEKPFVWELMDRSNVVLNDNLTFWASGEPGNETNCVY NSLTETLRGKGLTTTWIGLHRLDAEKPFVWELMDRSNVVLNDNLTFWASGEPGNETNCVY *****:*****:*****:*****:*****:*****	540
TtFc 834Cr ID4	LDIRDQLQPVWTKSCFPSSFACMMDLSDRNKAKCDDPGPLENGHATLHGQSIDGFYAG MDIQDQLQSVWTKSCFPSSFACMMDLSDRNKAKCDDPGSLENGHATLHGQSIDGFYAG :***:***:*****:*****:*****:*****	600
TtFc 834Cr ID4	SSIRYSCEVLHYLSGTETVTCTTNGTWSAPKPRCIKVITCQNPVPVSYGSVEIKPPSRTN SSIRYSCEVLHYLSGTETVTCTTNGTWSAPKPRCIKVITCQNPVPVSYGSVEIKPPSRTN *****:*****:*****:*****:*****:*****	660

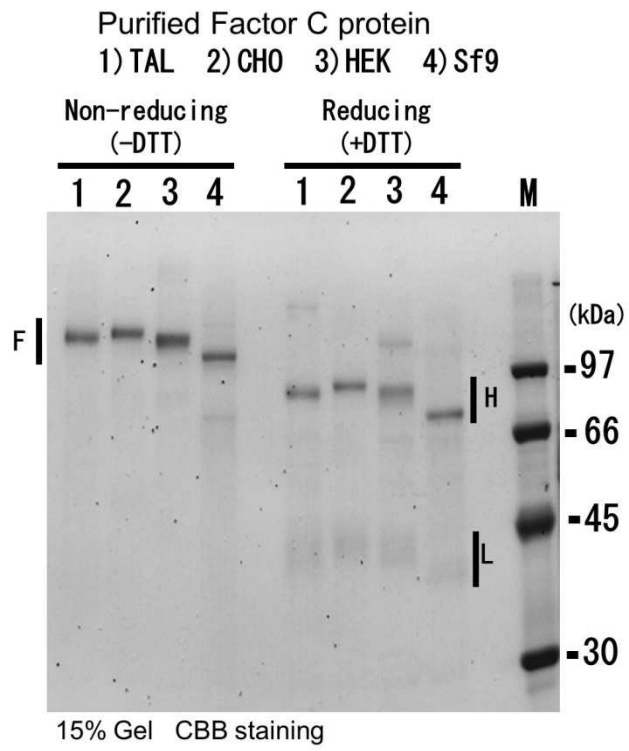
[Fig. 9]

TtFc 834CrID4	SISRVGSPFLRLPRLPLPLARAAPPPKPRSSQPSTVDLASKVKLPEGHYRVGSRAIYTC SISRVGSPFLRLPRLPLPLARAAPPPKPRSSQPSTVDLASKVKLPEGHYRVGSRAIYTC *****	720
TtFc 834CrID4	ESRYEYELLGSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQWPWQAGI ESRYEYELLGSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQWPWQAGI *****	780
TtFc 834CrID4	SRWLADHNMWFLQCGGSLLNEKWIVTAAHCVTYSATAEIIDPSQFKIYLGKYYRDDSRRD SRWLADHNMWFLQCGGSLLNEKWIVTAAHCVTYSATAEIIDPNQFKMYLGKYYRDDSRRD *****	840
TtFc 834CrID4	DYVQVREALEIHVNPNYDPGNLNFIDIALIQLKTPVTLTTRVQPICLPTDITTREHLKEGT DYVQVREALEIHVNPNYDPGNLNFIDIALIQLKTPVTLTTRVQPICLPTDITTREHLKEGT *****	900
TtFc 834CrID4	LAVVTGWGLNENNTYSEMIQQAVALPVVAASTCEEYKEADLPLTVTENMFCAGYKKGRYD LAVVTGWGLNENNTYSETIQQAVLPVVAASTCEEYKEADLPLTVTENMFCAGYKKGRYD *****	960
TtFc 834CrID4	ACSGDSGGPLVFADDSRTERRWVLEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQFI ACSGDSGGPLVFADDSRTERRWVLEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQFI *****	1019

[Fig. 10]

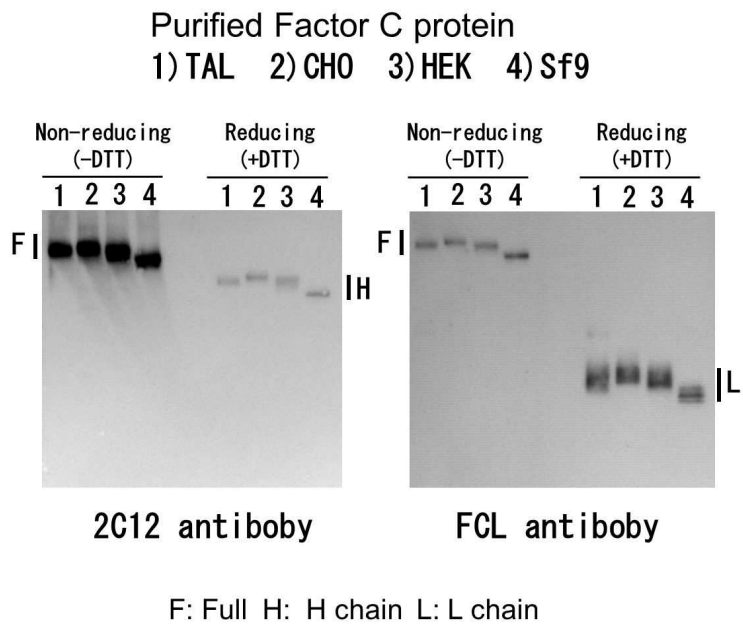


[Fig. 11]

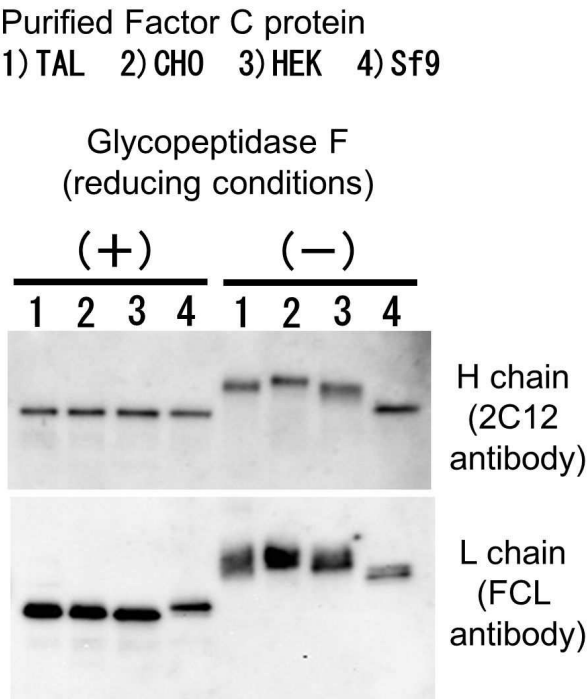


F: Full H: H chain L: L chain

[Fig. 12]



[Fig. 13]



[Fig. 14]

