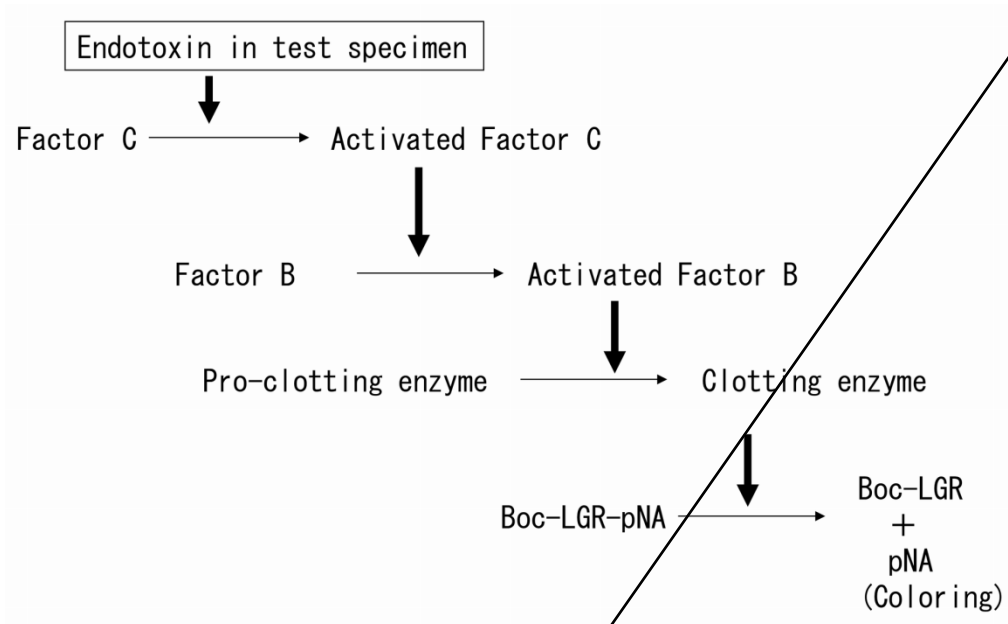
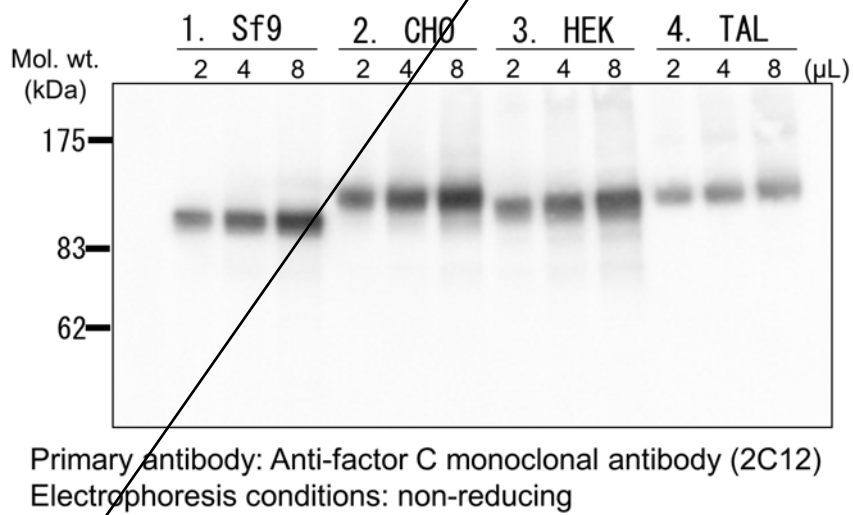


Figures

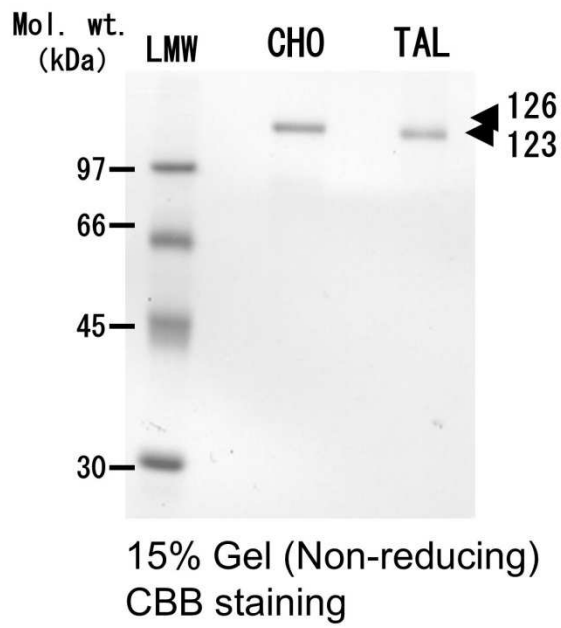
[Fig. 1]



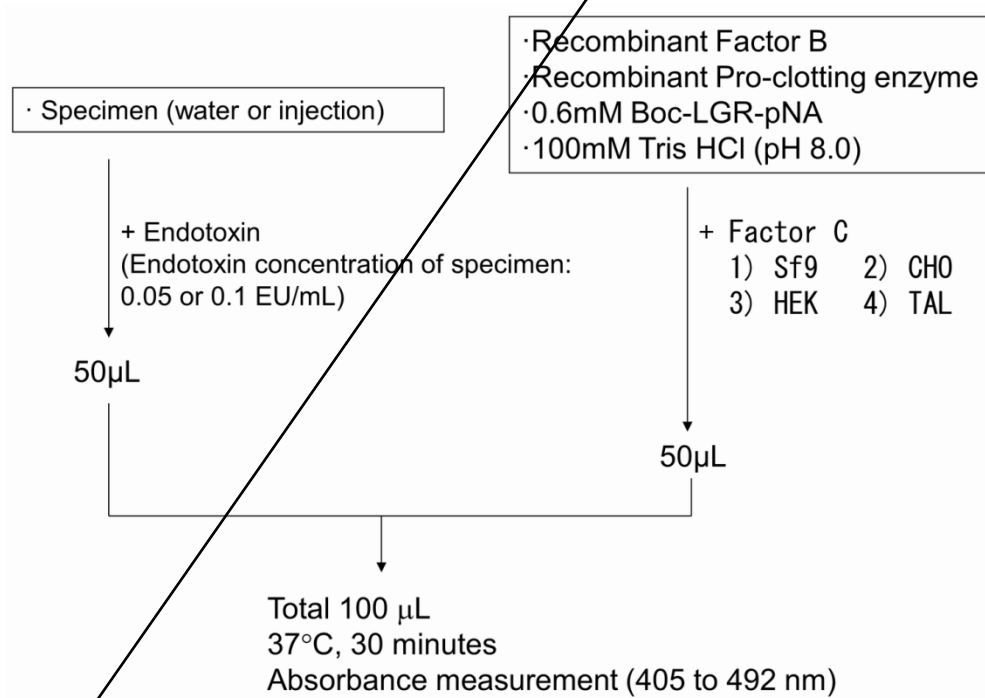
[Fig. 2]



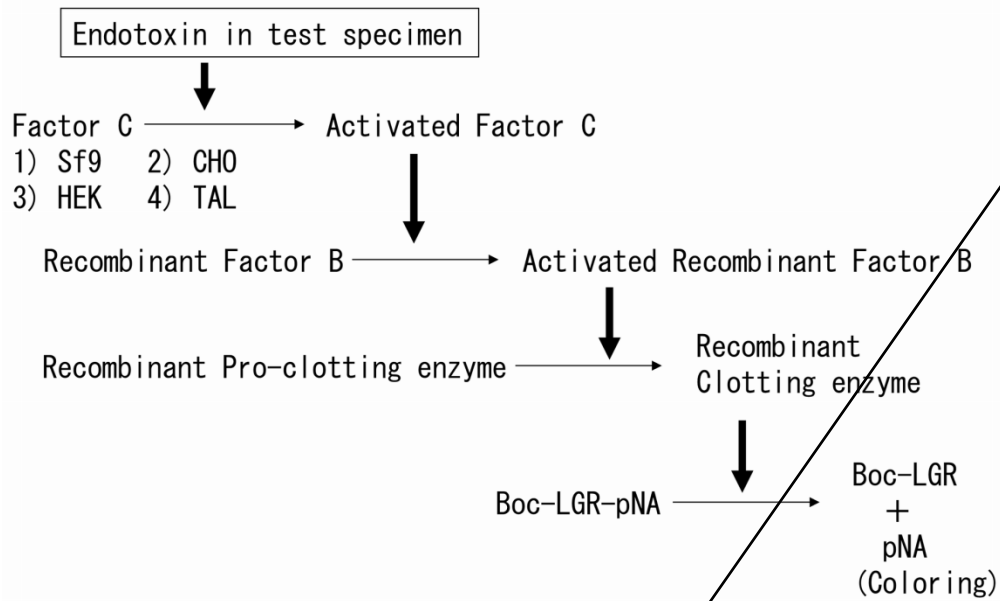
[Fig. 3]



[Fig. 4]



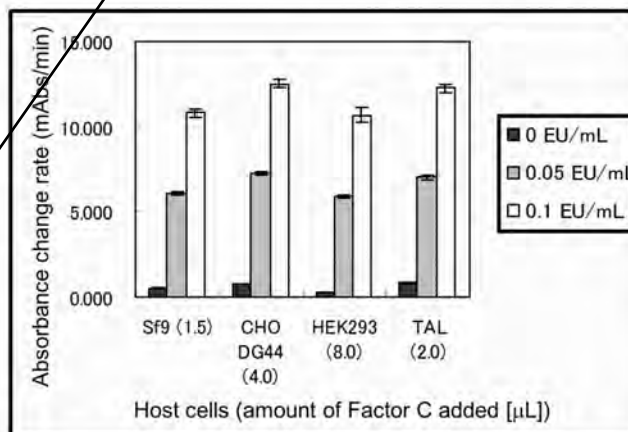
[Fig. 5]



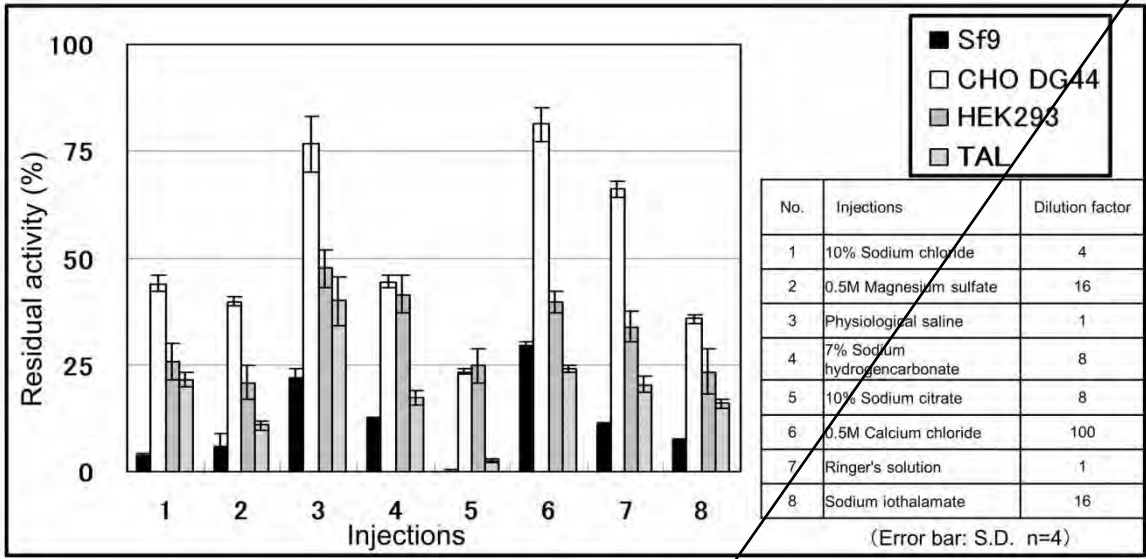
[Fig. 6]

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

n=3



[Fig. 7]



[Fig. 8]

TtFc 834Cr ID4	MVLASFLVSGLVLGILAQQMRPVQSRGVDLGLCDETRFECKCGDPGYVFNVPMKQCTYFY MVLASFLVSGLVLGLLAQKMRPVQSKGVDLGLCDETRFECKCGDPGYVFNIPVKQCTYFY *****.***.*****.*****.*****.***.*****	60
TtFc 834Cr ID4	RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQ RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQ *****	120
TtFc 834Cr ID4	RTGACTCRDRYEGAHCEILKGCPLLPSDSQVQEVNPPDPNPQTIDYSCSPGFKLKGVARL RTGACACRDRYEGVHCEILKGCPLLPSDSQVQEVNPPDPNPQTIDYSCSPGFKLKGMARL *****.*****.*****.*****.*****.*****.***	180
TtFc 834Cr ID4	SCLPNGQWSSFPPKCIRECAKVSSPEHGKVNAPSGNMIEGATLRFSCDSPYYLIGQETLT SCLPNGQWSNFPPKCIRECAMVSSPEHGKVNALSGDMIEGATLRFSCDSPYYLIGQETLT *****.*****.*****.*****.*****.*****	240
TtFc 834Cr ID4	CQGNQWWSGQIPQCKKLVFCDLDPVNHAHQVKIGVEQKYGQFPQGTEVYTTCSGNYFL CQGNQWWSGQIPQCKNLVFCDLDPVNHAHQVKIGVEQKYGQFPQGTEVYTTCSGNYFL *****.*****.*****.*****.*****.*****.*****	300
TtFc 834Cr ID4	MGFNTLKCNPDGSGWSGSPSCVKVADREVDGDSKAVDFLDDVGEPVRIHCPAGCSL TAGT MGFDTLKCNPDGSGWSGSPSCVKVADREVDGDSKAVDFLDDVGEPVRIHCPAGCSL TAGT ***.*****.*****.*****.*****.*****.*****	360
TtFc 834Cr ID4	VWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVNNGPYSDFLGSDLNGIKSEELKSLARS VWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVNNGPYSDFLGSDLNGIKSEELKSLARS *****.*****.*****.*****.*****.*****.*****	420
TtFc 834Cr ID4	FRFDYVSSSTAGRSGCPDGWFVEEENCYVYVTSKQRAWERAQGVCTNMAARLAVLDKDLIP FRFDYVRSSTAGKSGCPDGWFVEEENCYVYVTSKQRAWERAQGVCTNMAARLAVLDKDVIP *****.*****.*****.*****.*****.*****.*****	480
TtFc 834Cr ID4	SSLTETLRGKGLTTTWIGLHRLDAEKPFVWELMDRSNVVLNDNLTFWASGEPGNETNCVY NSLTETLRGKGLTTTWIGLHRLDAEKPFVWELMDRSNVVLNDNLTFWASGEPGNETNCVY *****.*****.*****.*****.*****.*****.*****	540
TtFc 834Cr ID4	LDIRDQLQPVWTKSCFQPSFACMMDLSDRNKAKCDDPGPLENGHATLHGQSIDGFYAG MDIQDQLQSVWTKSCFQPSFACMMDLSDRNKAKCDDPGSLENGHATLHGQSIDGFYAG :***.***.*****.*****.*****.*****.*****	600
TtFc 834Cr ID4	SSIRYSCEVLHYLSGTETVTCTTNGTWSAPKPRCIKVITCQNPVPVSYGSVEIKPPSRTN SSIRYSCEVLHYLSGTETVTCTTNGTWSAPKPRCIKVITCQNPVPVSYGSVEIKPPSRTN *****.*****.*****.*****.*****.*****.*****	660

[Fig. 9]

TtFC	SISRVGSPFLRLPRLPLPLARAAPPPKPRSSQPSTVDLASKVKLPEGHYRVGSRAIYTC	
834CrID4	SISRVGSPFLRLPRLPLPLARAAPPPKPRSSQPSTVDLASKVKLPEGHYRVGSRAIYTC	720

TtFC	ESRYYE ~~LL~~ GSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGN ~~STE~~ IGQWPWQAGI	
834CrID4	ESRYYE ~~LL~~ GSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGN ~~STE~~ IGQWPWQAGI	780

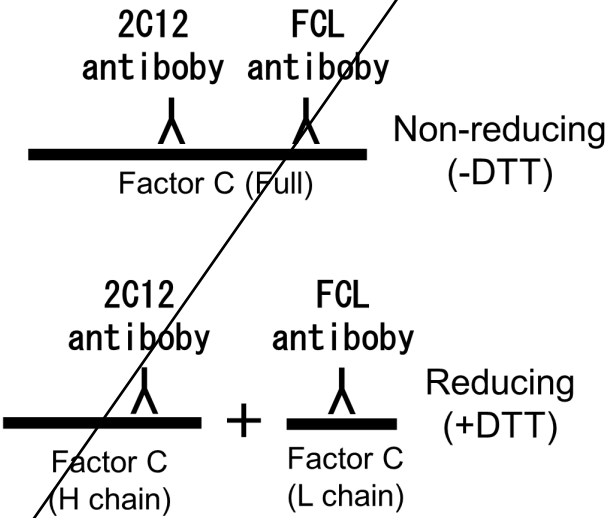
TtFC	SRWLADHNMWFLQCGGSLLNEKWIVTAAHCVTYSATAEIIDPSQFKI ~~Y~~ LGKYYRDDSRRD	
834CrID4	SRWLADHNMWFLQCGGSLLNEKWIVTAAHCVTYSATAEIIDPNQFKMYLGKYYRDDSRRD	840

TtFC	DYVQVREALEIHVNPNYDPGNLNFDIALIQLKTPVTLTTRVQPICLPTDITTREHLKEGT	
834CrID4	DYVQVREALEIHVNPNYDPGNLNFDIALIQLKTPVTLTTRVQPICLPTDITTREHLKEGT	900

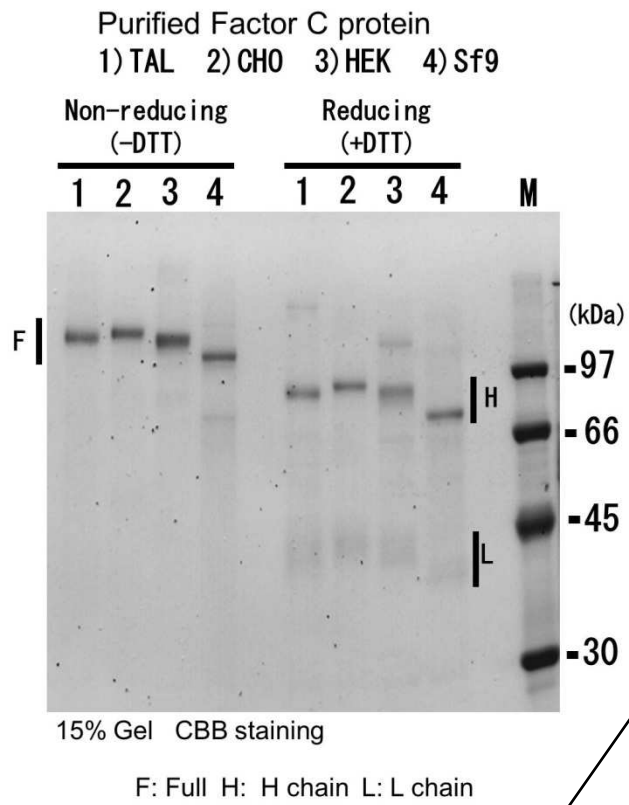
TtFC	LAVVTGWGLNE ~~N~~ NTYSEMIQQAVLPVVAASTCEEYKEADLPLTVTENMFCAGYKKGRYD	
834CrID4	LAVVTGWGLNE ~~N~~ NTYSETIQQAVLPVVAASTCEEYKEADLPLTVTENMFCAGYKKGRYD	960

TtFC	ACSGDSGGPLVFADDSRTERRWVLEGI ~~V~~ SWGSPSGCGKANQYGGFTKVN ~~V~~ FLSWIRQFI	
834CrID4	ACSGDSGGPLVFADDSRTERRWVLEGI ~~V~~ SWGSPSGCGKANQYGGFTKVN ~~V~~ FLSWIRQFI	1019

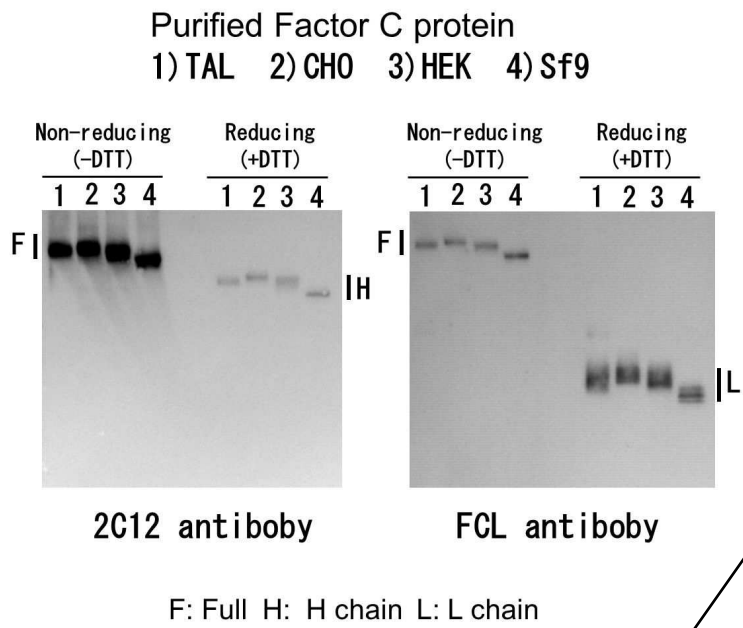
[Fig. 10]



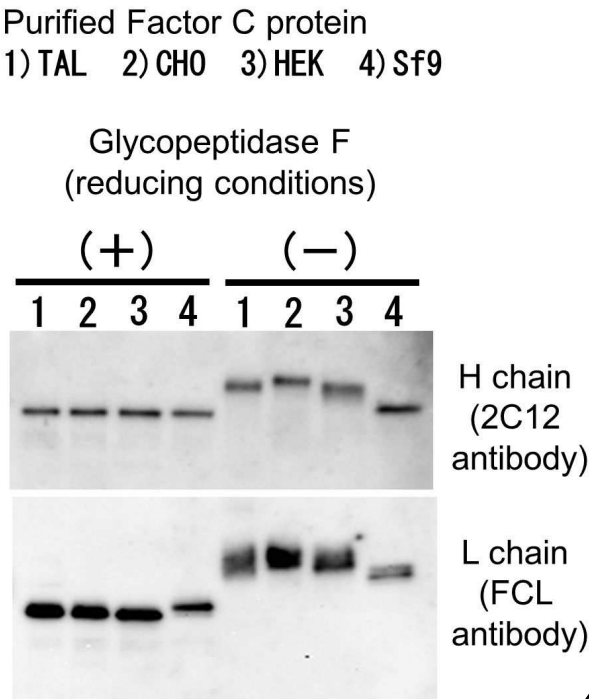
[Fig. 11]



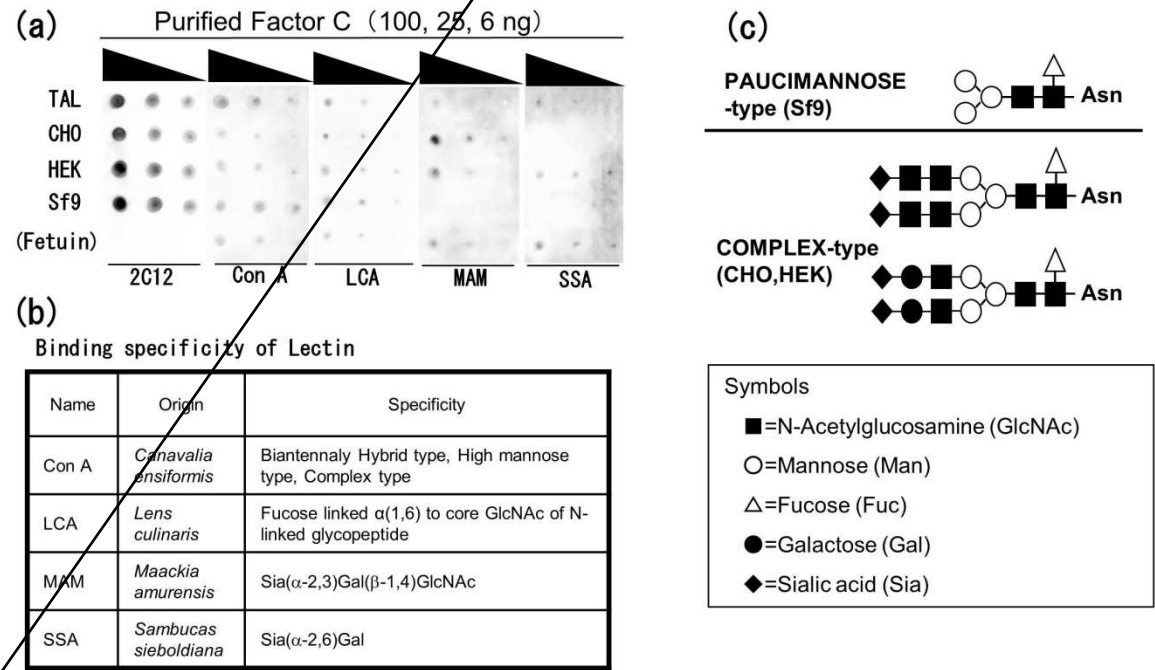
[Fig. 12]



[Fig. 13]

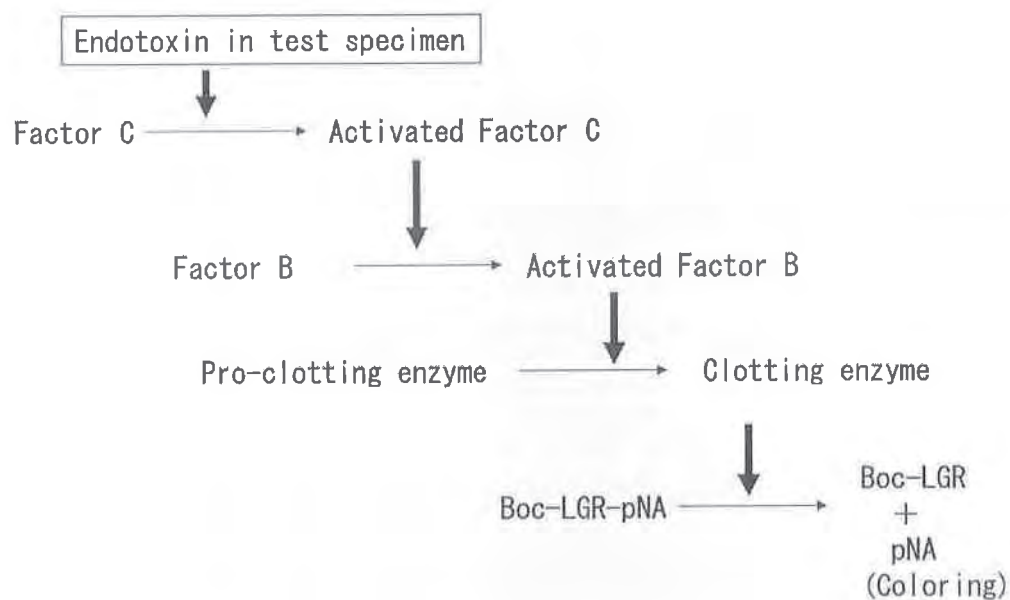


[Fig. 14]



Figures

[Fig. 1]



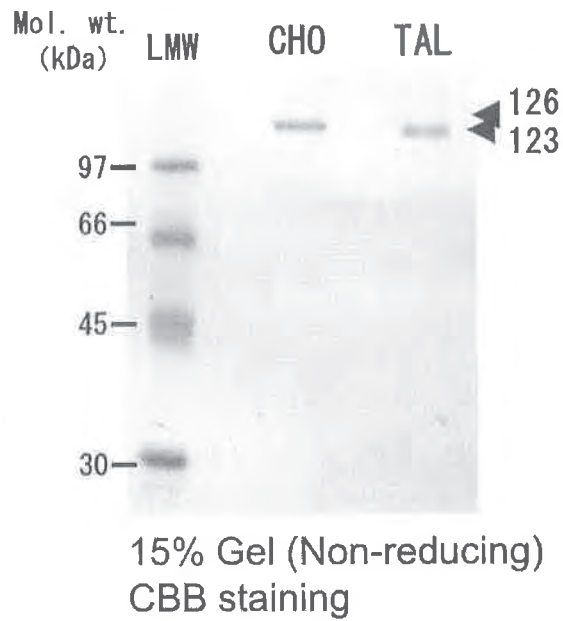
[Fig. 2]



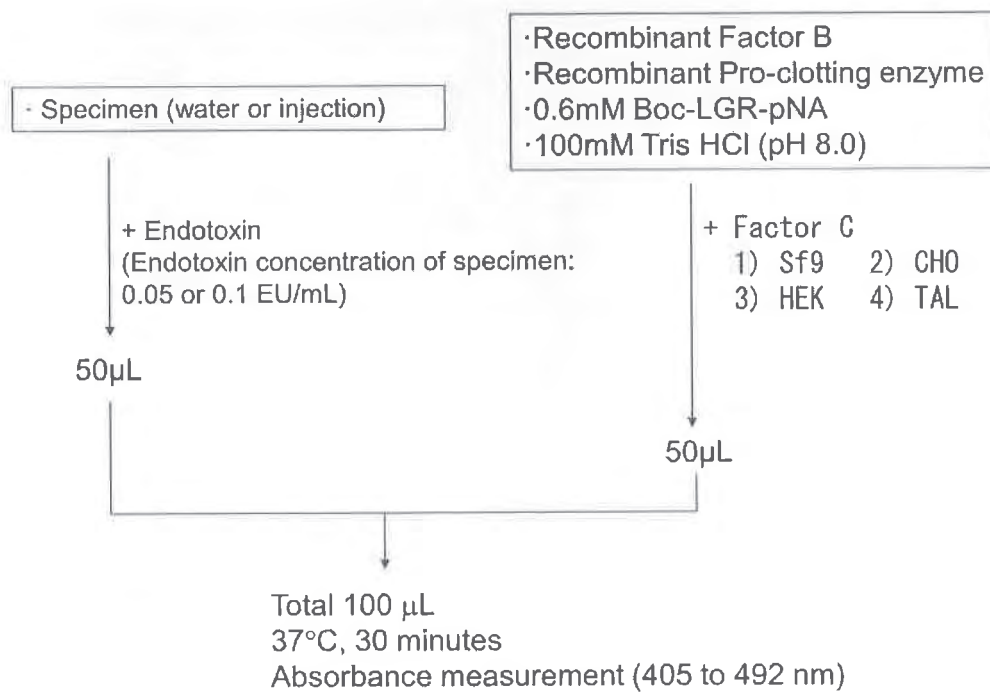
Primary antibody: Anti-factor C monoclonal antibody (2C12)

Electrophoresis conditions: non-reducing

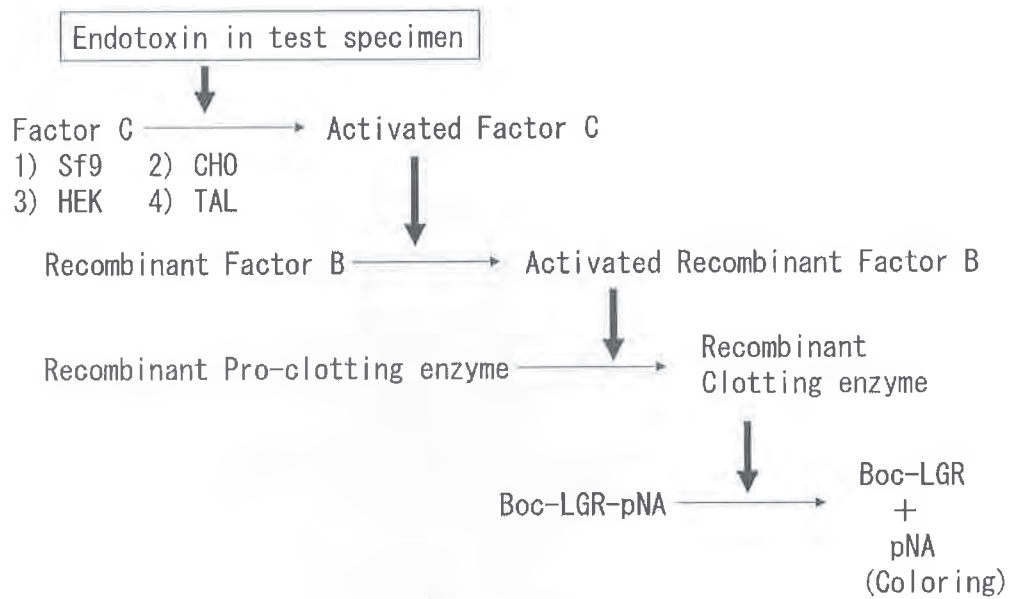
[Fig. 3]



[Fig. 4]



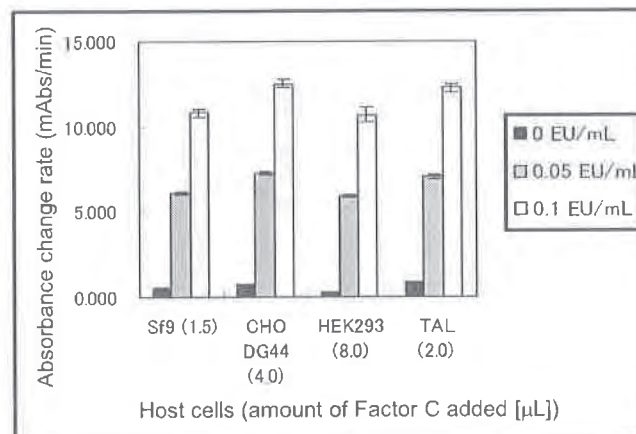
[Fig. 5]



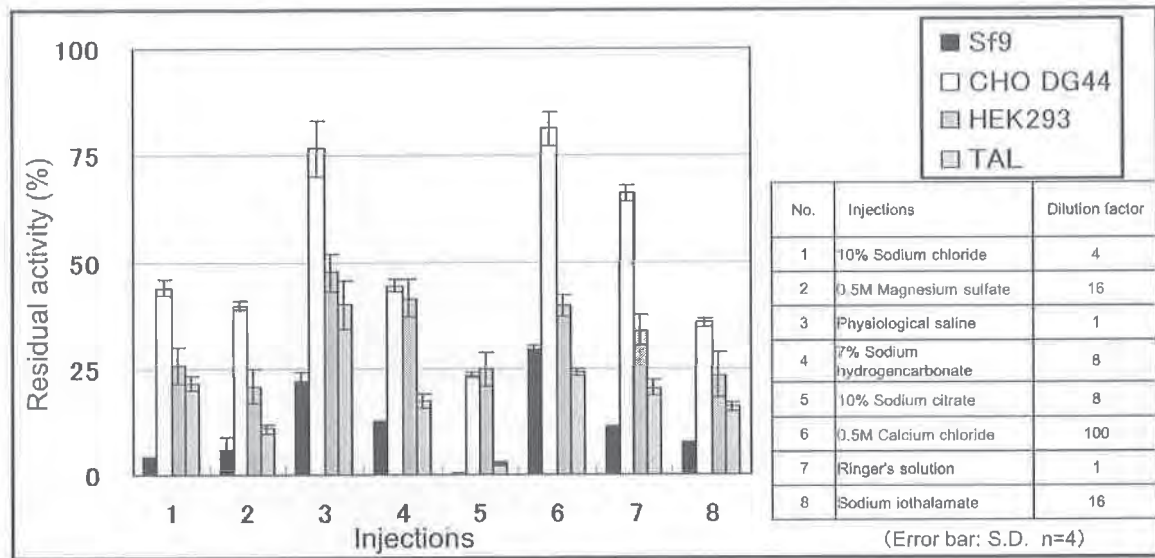
[Fig. 6]

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]



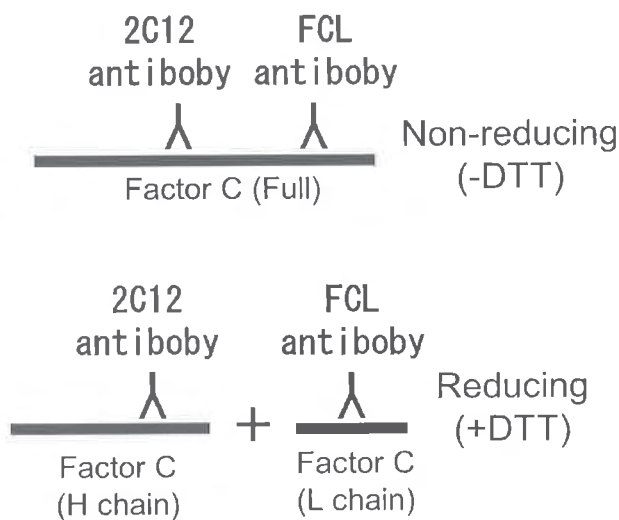
[Fig. 8]

TtFC 834Cr ID4	MVLASFLVSGLVLGILAQQMRPVQSRGVDLGLCDETRFECKCGDPGYVFNVPKQCTYFY MVLASFLVSGLVLGILAQQMRPVQSRGVDLGLCDETRFECKCGDPGYVFNIPVKQCTYFY *****[***:*****:*****:*****:***]	60
TtFC 834Cr ID4	RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQ RWRPYCKPCDDLEAKDICPKYKRCQECKAGLDSCVTCPPNKYGTWCSGECQCKNGGICDQ *****	120
TtFC 834Cr ID4	RTGACTCRDRYEGAHCEILKGCPLLPSDSQVQEVNPPDNPQTIDYSCSPGFKLKGVAR I RTGACACRDRYEGVHCEILKGCPLLPSDSQVQEVNPPDNPQTIDYSCSPGFKLKGMA R I *****:*****:*****:*****:*****:*****:*****:*****:*****	180
TtFC 834Cr ID4	SCLPNGQWSSFPPKCI RECAKVSSPEHGKVNAPSGNMI EGATLRFSCDSPYYLIGQETLT SCLPNGQWSNFPPKCI RECAMVSSPEHGKVNALSGDMIEGATLRFSCDSPYYLIGQETLT *****:*****:*****:*****:*****:*****:*****:*****:*****	240
TtFC 834Cr ID4	CQGNQWWSGQIPQCKKLVFCPLDPVNHAHQVKIGVEQKYQQFPQGTEVYTCSGNYFL CQGNQWWSGQIPQCKKLVFCPLDPVNHAHQVKIGVEQKYQQFPQGTEVYTCSGNYFL *****:*****:*****:*****:*****:*****:*****:*****:*****	300
TtFC 834Cr ID4	MGFNTLKCNPDGSGWSGSPSCVKVADREVD CDSKAVDFLDDVGEPVRIHCPAGCSL TAGT MGFNTLKCNPDGSGWSGSPSCVKVADREVD CDSKAVDFLDDVGEPVRIHCPAGCSL TAGT ***:*****:*****:*****:*****:*****:*****:*****:*****	360
TtFC 834Cr ID4	VWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVNNGPYSDFLGSDLNGIKSEELKSLARS VWGTAIYHELSSVCRAAIHAGKLPNSGGAVHVNNGPYSDFLGSDLNGIKSEELKSLARS *****	420
TtFC 834Cr ID4	FRFDYVSSSTAGRSGCPDGWFEVEENCYVYTSKQRAWERAQGVCTNMAARLAVLDKDLIP FRFDYVRSSTAGKSGCPDGWFEVDENCYVYTSKQRAWERAQGVCTNMAARLAVLDKDVIP *****:*****:*****:*****:*****:*****:*****:*****:*****	480
TtFC 834Cr ID4	SSLTETLRGKGLTTTWIGLHRLDAEKPFVWELMDRSNNVLNDNLTFWASGEPGNETNCVY NSLTETLRGKGLTTTWIGLHRLDAEKPFVWELMDRSNNVLNDNLTFWASGEPGNETNCVY *****:*****:*****:*****:*****:*****:*****:*****:*****	540
TtFC 834Cr ID4	LDIRDQLQPVWKT KSCFQPSSFACMMDLSDRNKAKCDDPGPLENGHATLHGQSIDGFYAG MDIQDQLQSVWKT KSCFQPSSFACMMDLSDRNKAKCDDPGSLENGHATLHGQSIDGFYAG :***:****:*****:*****:*****:*****:*****:*****:*****	600
TtFC 834Cr ID4	SSIRYSCEVLHYLSGTETVTCTTNGTWSAPKPRCIKVITCQNPVPSYGSVEIKPPSRTN SSIRYSCEVLHYLSGTETVTCTTNGTWSAPKPRCIKVITCQNPVPSYGSVEIKPPSRTN *****	660

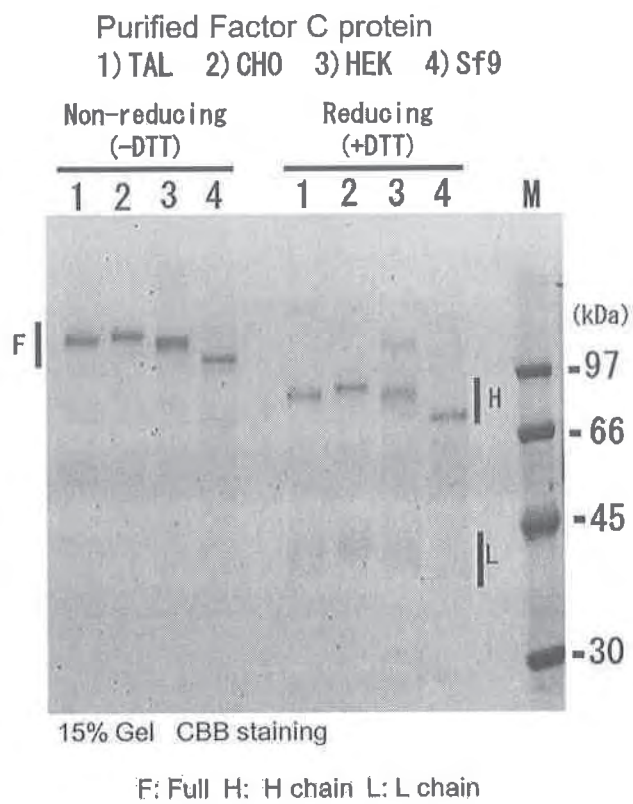
[Fig. 9]

TtFc 834Cr ID4	SISRVGSPFLRLPRLPLPLARAAPPPKPRSSQPSTVDLASKVKLPEGHYRVGSRAIYTC SISRVGSPFLRLPRLPLPLARAAPPPKPRSSQPSTVDLASKVKLPEGHYRVGSRAIYTC *****	720
TtFc 834Cr ID4	ESRYEYELLGSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQWPWQAGI ESRYEYELLGSQGRRCDSNGNWSGRPASCIPVCGRSDSPRSPFIWNGNSTEIGQWPWQAGI *****	780
TtFc 834Cr ID4	SRWLADHNMWFLQCGGSLLNEKWIVTAAHCVTYSATAEIIDPSQFKIYLGKYYRDDS RDD SRWLADHNMWFLQCGGSLLNEKWIVTAAHCVTYSATAEIIDPNQFKMYLGKYYRDDS RDD *****	840
TtFc 834Cr ID4	DYVQVREALEIHVNPNYDPGNLNF DIALIQLKTPVTLTTRVQPICLPTDITTREHLKEGT DYVQVREALEIHVNPNYDPGNLNF DIALIQLKTPVTLTTRVQPICLPTDITTREHLKEGT *****	900
TtFc 834Cr ID4	LAVVTGWGLNENNTYSEMIQQA VLPVVAASTCEEYKEADLPLTVTENMFCAGYKKGRYD LAVVTGWGLNENNTYSEMIQQA VLPVVAASTCEEYKEADLPLTVTENMFCAGYKKGRYD *****	960
TtFc 834Cr ID4	ACSGDSGGPLVFADDSRTERRWVLEGI VSWGSPSGCGKANQYGGFTKVVNVL SWIRQFI ACSGDSGGPLVFADDSRTERRWVLEGI VSWGSPSGCGKANQYGGFTKVVNVL SWIRQFI *****	1019

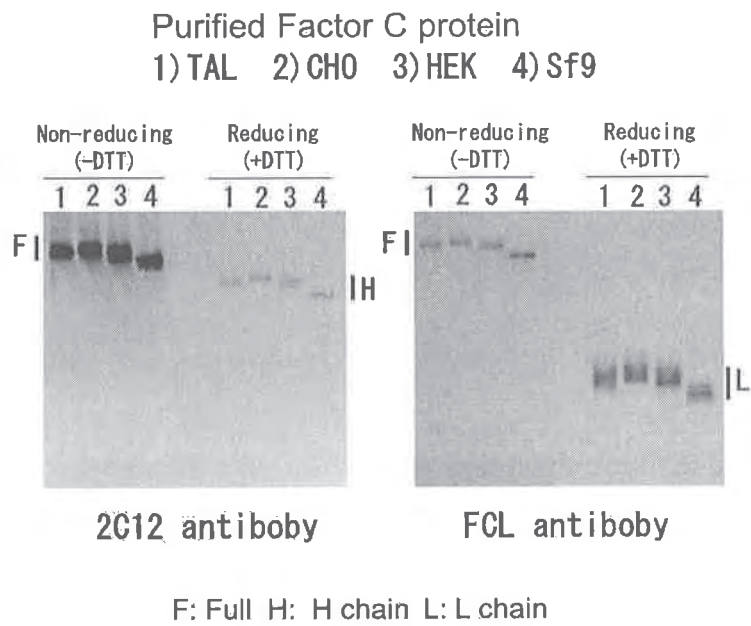
[Fig. 10]



[Fig. 11]



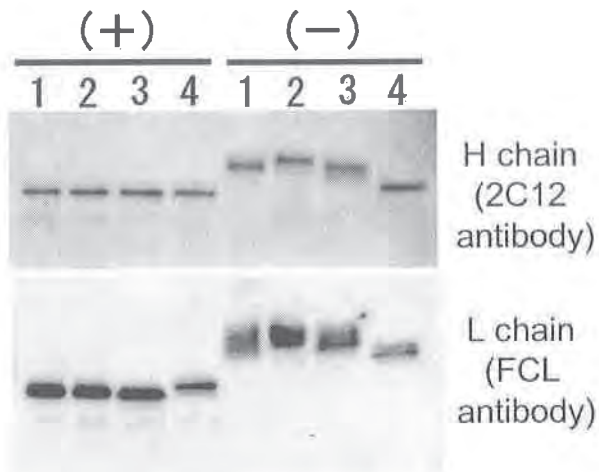
[Fig. 12]



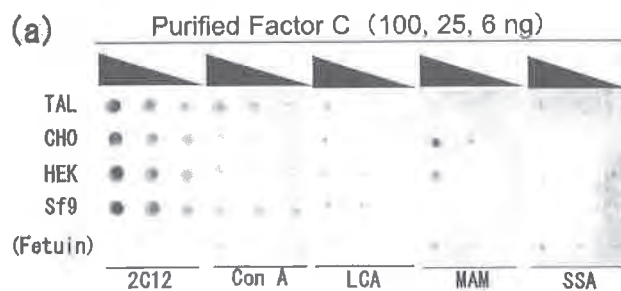
[Fig. 13]

Purified Factor C protein
1) TAL 2) CHO 3) HEK 4) Sf9

Glycopeptidase F
(reducing conditions)

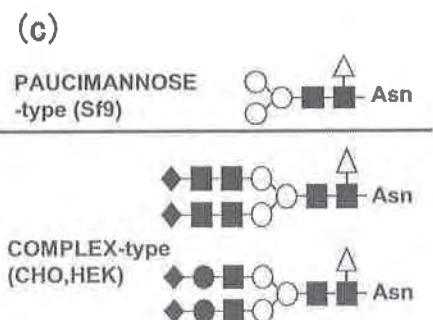


[Fig. 14]



(b)
Binding specificity of Lectin

Name	Origin	Specificity
Con A	<i>Canavalia ensiformis</i>	Biantennary Hybrid type, High mannose type, Complex type
LCA	<i>Lens culinaris</i>	Fucose linked $\alpha(1,6)$ to core GlcNAc of N-linked glycopeptide
MAM	<i>Maackia amurensis</i>	Sia(α -2,3)Gal(β -1,4)GlcNAc
SSA	<i>Sambucus sieboldiana</i>	Sia(α -2,6)Gal



Symbols

- =N-Acetylglucosamine (GlcNAc)
- =Mannose (Man)
- △=Fucose (Fuc)
- =Galactose (Gal)
- ◆=Sialic acid (Sia)