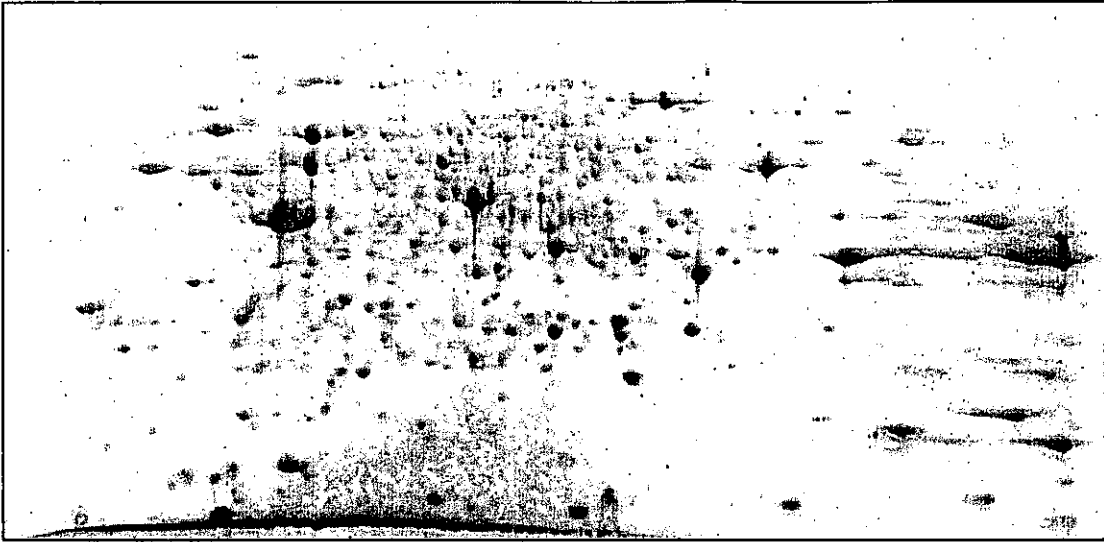
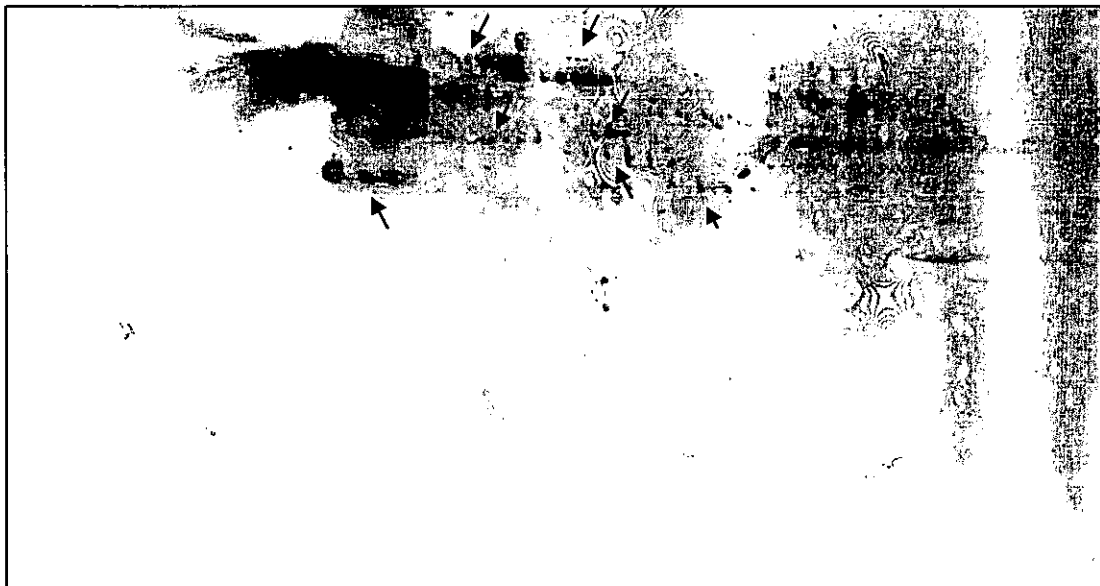


**Fig. 19 Peak area ratio of oligosaccharides from CHO and CHOIII membrane**

**(A) 2D-PAGE**

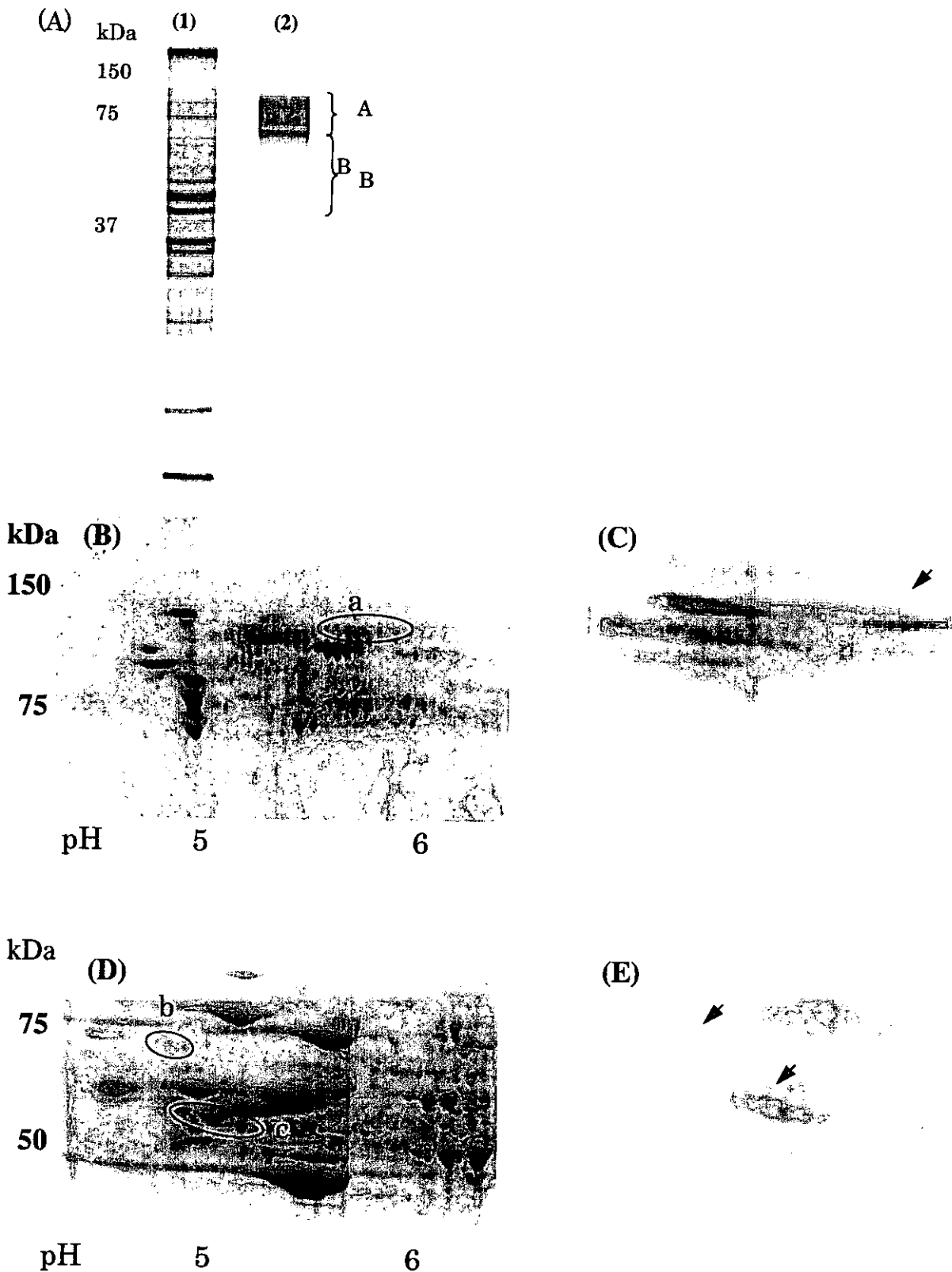


**(B) Lectin blot**



**Fig. 20 2D-GE of CHO-III membrane proteins**

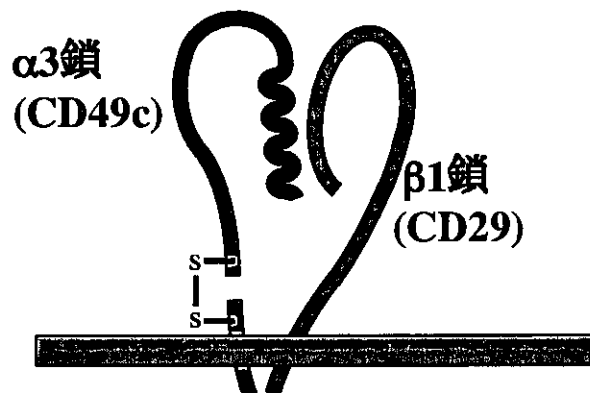
**(A) Sypro Orange, (B) Lectin blot**



**Fig. 21 (A) SDS-PAGE of CHO-III membrane  
 (B) 2D-GE of band A, (c) Lectin blot of Band A  
 (D) 2D-GE of band B, (D) Lectin blot of Band B**

分布：上皮細胞  
 リガンド： ラミニン, フィブロネクチン,  
 コラーゲン  
 臨床：腫瘍細胞での発現異常

細胞接着の制御



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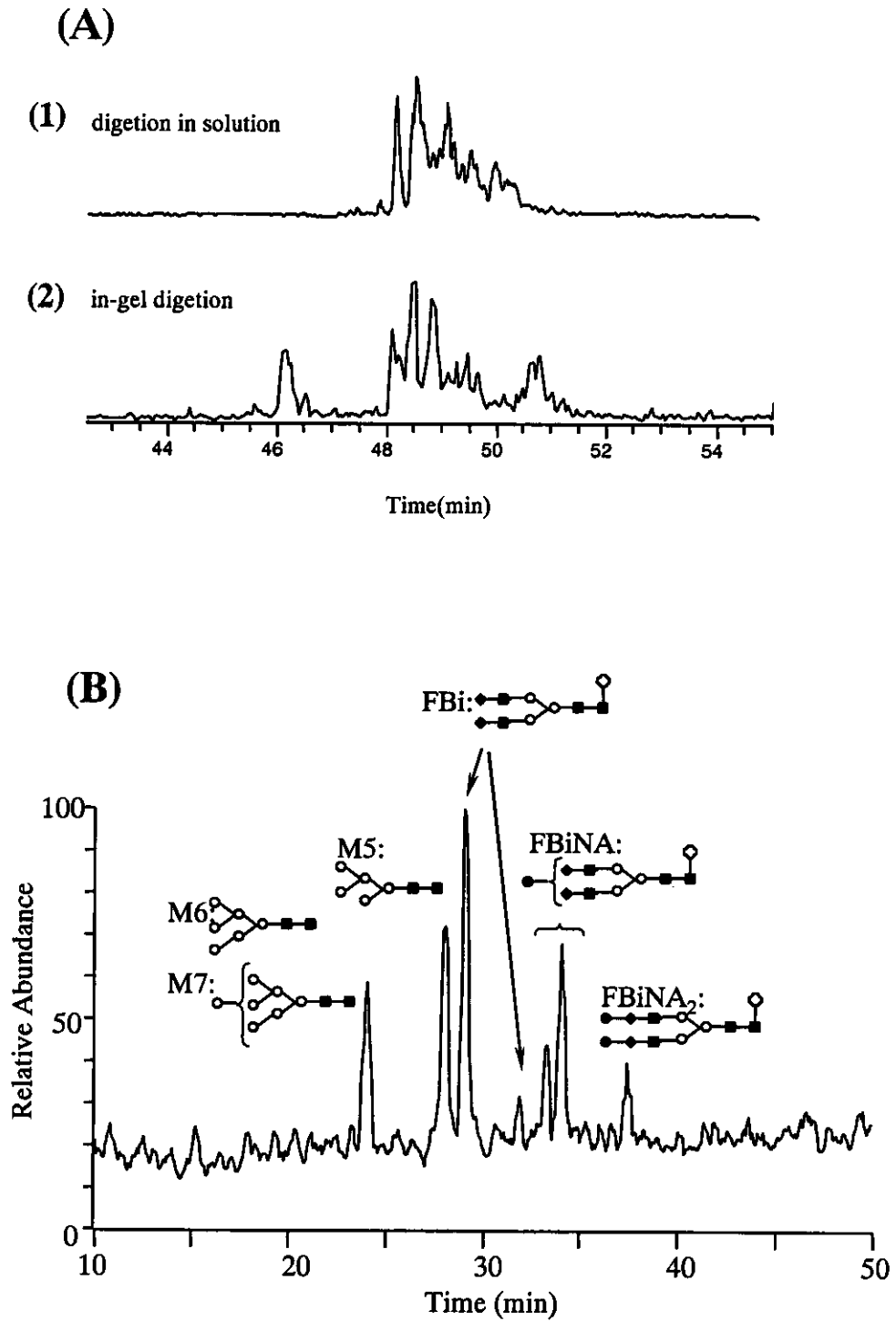
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61  qterqqryll lagaprdlsv adgytNrtga vylcpltalk ddcermdis ksdpdhhiie
121 dmwlgvtvas qgpagrvlc ahrytqvlws gmedqrrmvg keyvrgndiq ldpग्द्धwqty
181 hnemcnsntd yltqgmcdlg tsggftqntv yfgapgaynw kgnsymiqrk dwdlseysyk
241 gsedqgnlyi gytvqvsav lhptyitvva gaprhqhmgga vflsqesgg dlkrkqvleg
301 tqvgayfgsa ialadlnndg wqdlvgapy yferkeevgg avyvfmnqag tsfpdqsll
361 lhgpsrsafg isiasigdin qdgfdiavg apfeglgkvy iyhsssgll rqpqqivhgd
421 klglpglstf gyslsgkmdv ddnsypdll gslsdhivll rarpvinilq rtilvarpavl
481 dpslcptsc vqvelcfayN qsagnpsyrr Nitlaytlea drdrppplr farsqsavfh
541 gflmpethc qilelllmdn vrdklrpi vi amNyslplrm pdrklgmrs ldaypvlnga
601 qaleNhtevh fqkecgpdnk cdsnlqmraa fvseqlqpis rlqysrdtkk lfliNvltnt
661 psrerageda healltlevp palllssvrp sgtcqaNeti lcelgnpfr nqrmelliaf
721 evigvilhtr dikaqlqst sshqdnlqpm tlilqdytl qaslsmlthr lqsffggtvm
781 geagmktved vgsplkyefq vspvgdglaa lgtivlglew pyevtngkwl lypteiihs
841 Neswpcppg nlvnplnil sdpgdkphsp qrrrr
                                     qldpg gdqgsppvll aaakkakset
901 vltcasgrar cvwlecpipd tsNvtNvtvk arvWnstfie dyrdfdrvrv dgwatflfrrt
961 siptinmeNk ttwfsvids elveelpaei elwlvlvavs agllllglii illwkcggfk
1021 ptryyrimpk yhavrireee rypppgstlp tkkhvvtswq irdryy
  
```

Heavy chain  
(33~872)

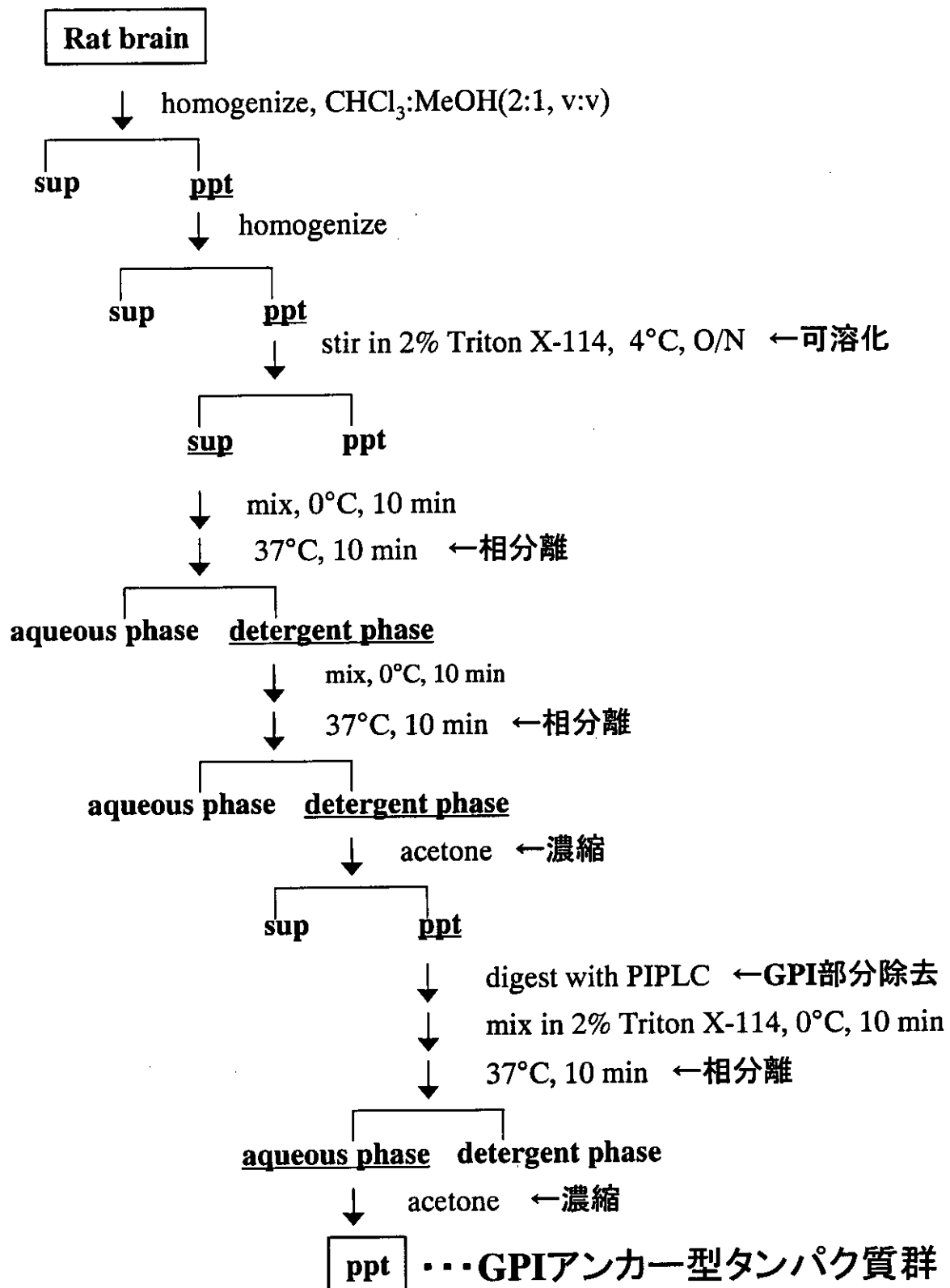
Light chain  
(876~1066)

Under line : Calcium binding region, N: Glycosylation site

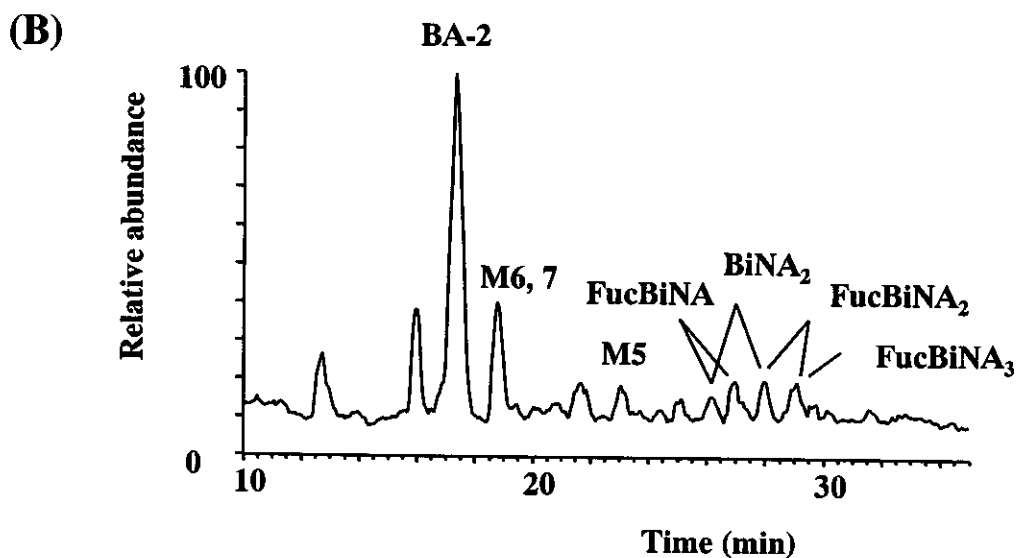
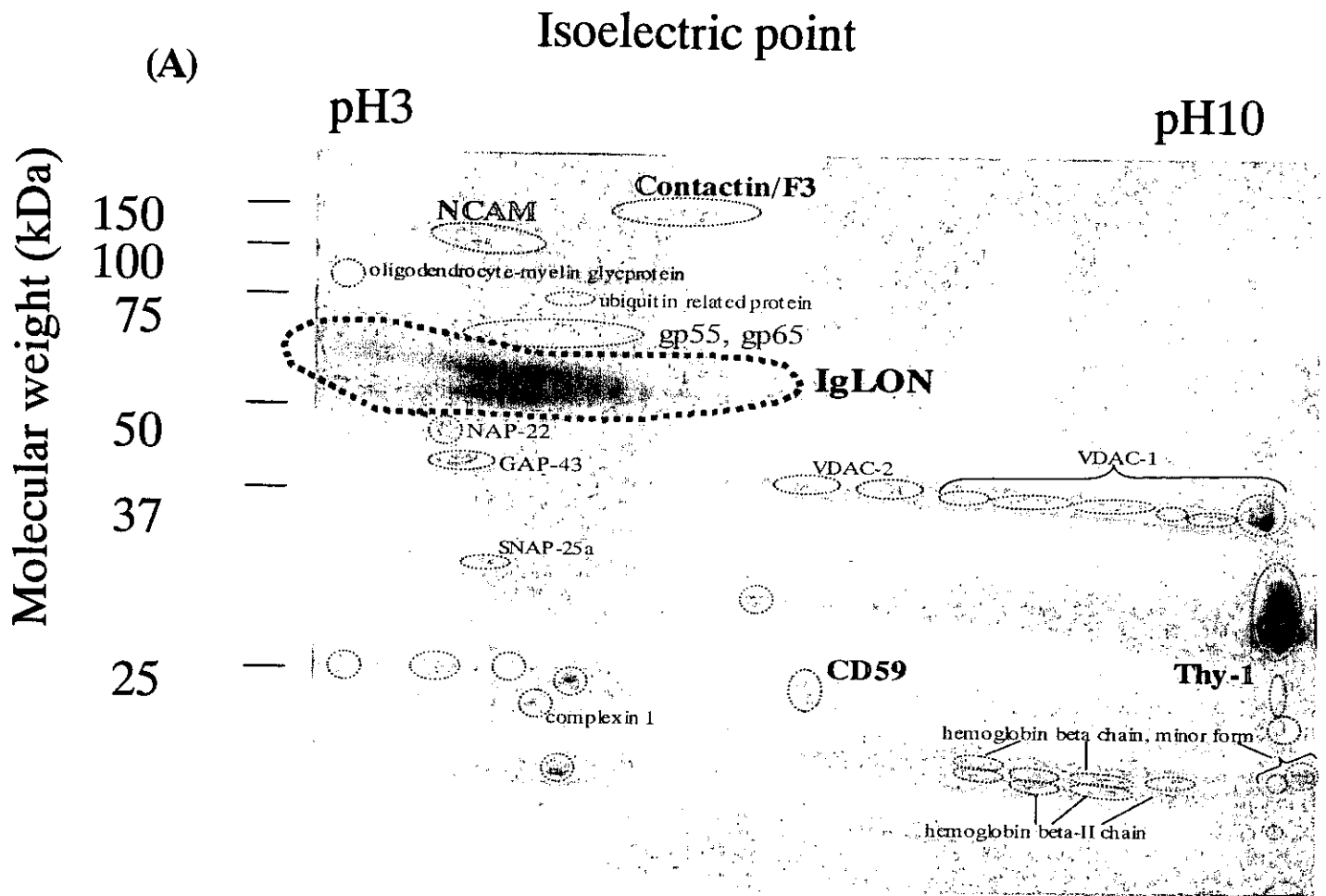
Fig. 22 Amino acid sequence and N-linked glycosylation sites of Integrin  $\alpha$ -3 (CD49c)



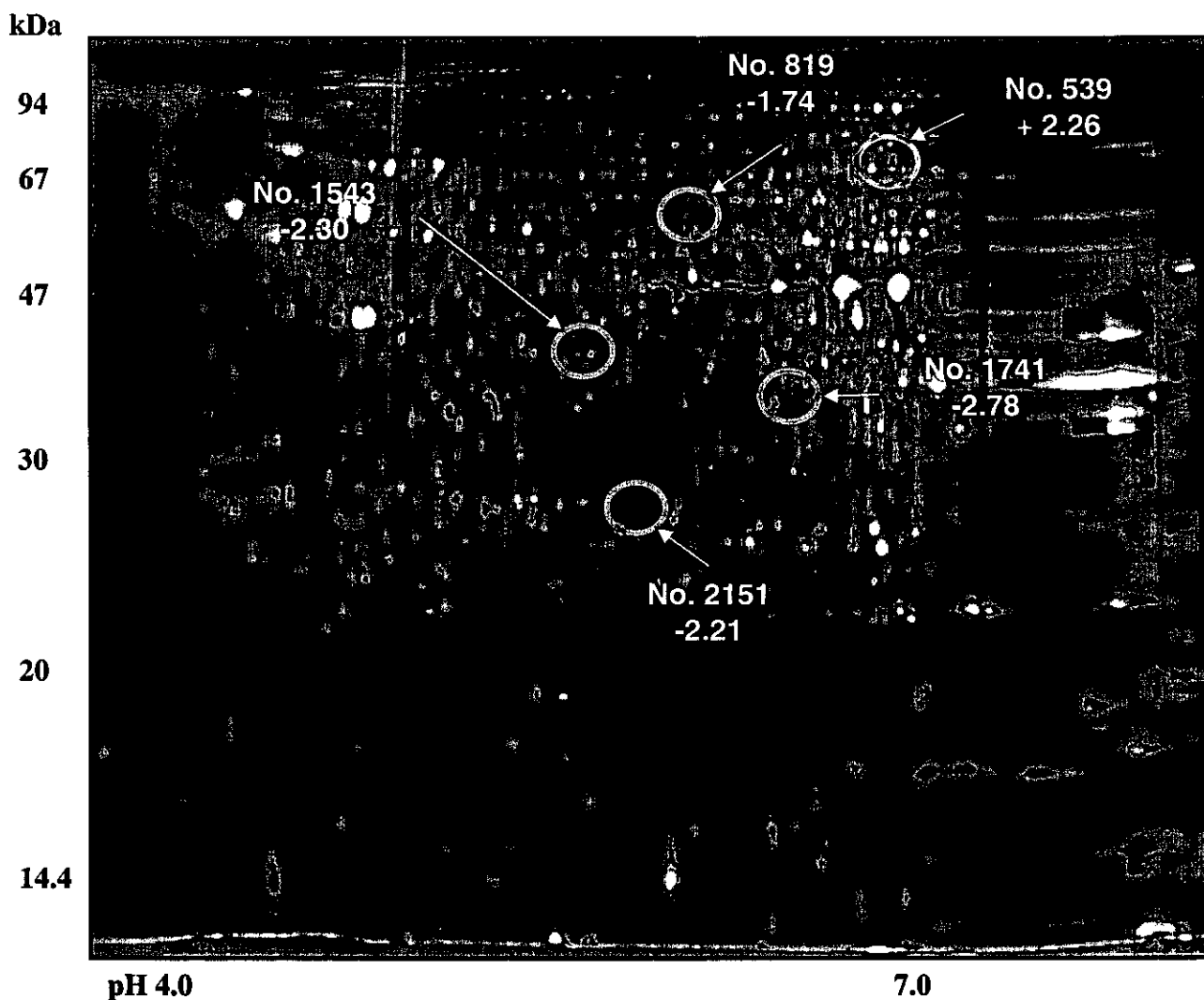
**Fig. 23 Oligosaccharide profiling of gel separated proteins  
(A) Erythropoietin, (B) t-PA**



**Fig. 24 Preparation of lipid-free GPI-anchored proteins from rat brain**



**Fig. 25 (A) 2D-GE of lipid-free GPI-anchored proteins from 3-week old rat brain, (B) Oligosaccharide profiling of gel separated Kilon**



**Fig.5 2D-DIGE images of Cy3 labeled HepG2 (A) and Cy5 labeled HepG2III (B) membrane fraction.**

**Fig. 26 2D-DIGE images of Cy3 labeled HepG2 and Cy5 labeled HepG2III membrane fraction**



Table 4 Glycosylation analysis of alpha-fetoprotein

Retention time (min)	m/z	Charge	M.W.	Peptide Sequences	M.W.	Oligosaccharide Structures	M.W.
23	1013.43	+3	3037.3	K/vnftfeiqk/I	977.5	[HexNAc]4[Hex]5[Neu5Ac]1[Fuc]1	2077.8
23	1519.67	+2	3037.3	K/vnftfeiqk/I	977.5	[HexNAc]4[Hex]5[Neu5Ac]1[Fuc]1	2077.8
23	1081.29	+3	3240.9	K/vnftfeiqk/I	977.5	[HexNAc]5[Hex]5[Neu5Ac]1[Fuc]1	2281.4
23	1621.44	+2	3240.9	K/vnftfeiqk/I	977.5	[HexNAc]5[Hex]5[Neu5Ac]1[Fuc]1	2281.4
23	1446.62	+2	2891.2	K/vnftfeiqk/I	977.5	[HexNAc]4[Hex]5[Neu5Ac]1	1931.8
23	1118.67	+2	2235.3	K/vnftfeiqk/I	977.5	[HexNAc]3[Hex]4	1275.9
23	1264.05	2	2526.1	K/vnftfeiqk/I	977.5	[HexNAc]3[Hex]4[Neu5Ac]1	1566.6
	1110.48	3	2526.1	K/vnftfeiqk/I	977.5	[HexNAc]3[Hex]4[Neu5Ac]1	1566.6
24	1665.44	+2	3328.9	K/vnftfeiqk/I	977.5	[HexNAc]4[Hex]5[Neu5Ac]2[Fuc]1	2369.4
24	1178.33	+3	3532.0	K/vnftfeiqk/I	977.5	[HexNAc]5[Hex]5[Neu5Ac]2[Fuc]1	2572.5
24	1061.78	3	3182.3	K/vnftfeiqk/I	977.5	[HexNAc]4[Hex]5[Neu5Ac]2	2222.9
25	1592.17	2	3182.3	K/vnftfeiqk/I	977.5	[HexNAc]4[Hex]5[Neu5Ac]2	2222.9
27	1236.04	+3	3705.1	K/ttkvnftfeiqk/I	1353.7	[HexNAc]4[Hex]5[Neu5Ac]2[Fuc]1	2369.4
27	1853.29	+2	3704.6	K/ttkvnftfeiqk/I	1353.7	[HexNAc]4[Hex]5[Neu5Ac]2	2222.8
27	1187.17	+3	3558.5	K/ttkvnftfeiqk/I	1353.7	[HexNAc]4[Hex]5[Neu5Ac]2	2222.8
28	1780.23	+2	3558.5	K/ttkvnftfeiqk/I	1353.7	[HexNAc]4[Hex]5[Neu5Ac]2	2222.8
28	1303.56	+3	3907.7	K/ttkvnftfeiqk/I	1353.7	[HexNAc]5[Hex]5[Neu5Ac]2[Fuc]1	2572.0
28	1138.84	+3	3413.5	K/ttkvnftfeiqk/I	1353.7	[HexNAc]4[Hex]5[Neu5Ac]1[Fuc]1	2077.8
28	1206.52	+3	3616.6	K/ttkvnftfeiqk/I	1353.7	[HexNAc]5[Hex]5[Neu5Ac]1[Fuc]1	2280.9
28	1090.14	+3	3267.4	K/ttkvnftfeiqk/I	1353.7	[HexNAc]4[Hex]5[Neu5Ac]1	1931.7
28	1322.75	+3	3965.3	K/ttkvnftfeiqk/I	1353.7	[HexNAc]6[Hex]5[Neu5Ac]2	2629.6

**Table 5 Glycosylation analysis of ceruloplasmin**

Retention time (min)	m/z	Charge	M.W.	Peptide Sequences	M.W.	Oligosaccharide Structures	M.W.
24	1025.17	+4	4096.7	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]4[Hex]5[Neu5Ac]2	2222.9
24	1366.54	+3	4096.6	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]4[Hex]5[Neu5Ac]2+Na	2244.9
24	1373.88	+3	4118.6	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]4[Hex]5[Neu5Ac]2[Fuc]1	2368.9
24	1061.67	+4	4242.7	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]5[Hex]5[Neu5Ac]3[Fuc]2	3171.2
25	1415.23	+3	4242.7	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]5[Hex]6[Neu5Ac]3	2879.1
25	1262.24	+4	5045.0	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]5[Hex]5[Neu5Ac]3[Fuc]2	3171.2
25	1682.65	+3	5045.0	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]5[Hex]5[Neu5Ac]3[Fuc]2	3171.2
25	1189.21	+4	4752.8	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]5[Hex]6[Neu5Ac]3	2879.1
25	1585.27	+3	4752.8	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]5[Hex]6[Neu5Ac]3[Fuc]1	3025.1
25	1225.72	+4	4898.9	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]5[Hex]6[Neu5Ac]3[Fuc]1	3025.1
25	1633.96	+3	4898.9	EHEGAIYPDNTTDFQR	1891.8	[HexNAc]5[Hex]6[Neu5Ac]3[Fuc]1	3025.1
27	1093.95	+4	4371.8	ELHHLQEQNVSN AFLDK	2021.0	[HexNAc]4[Hex]5[Neu5Ac]2[Fuc]1	2368.8
27	1458.27	+3	4371.8	ELHHLQEQNVSN AFLDK	2021.0	[HexNAc]4[Hex]5[Neu5Ac]2[Fuc]1	2368.8
27	1057.43	+4	4225.7	ELHHLQEQNVSN AFLDK	2021.0	[HexNAc]4[Hex]5[Neu5Ac]2	2222.7
27	1409.57	+3	4225.7	ELHHLQEQNVSN AFLDK	2021.0	[HexNAc]5[Hex]6[Neu5Ac]3[Fuc]1	3025.0
28	1257.99	+4	5028.0	ELHHLQEQNVSN AFLDK	2021.0	[HexNAc]5[Hex]6[Neu5Ac]3[Fuc]1	3025.0
28	1677.01	+3	5028.0	ELHHLQEQNVSN AFLDK	2021.0	[HexNAc]5[Hex]6[Neu5Ac]3[Fuc]1	3025.0
28	1221.48	+4	4881.9	ELHHLQEQNVSN AFLDK	2021.0	[HexNAc]5[Hex]6[Neu5Ac]3	2878.9
28	1628.30	+3	4881.9	ELHHLQEQNVSN AFLDK	2021.0	[HexNAc]5[Hex]6[Neu5Ac]3	2878.9
33	1347.54	+3	4039.6	ENLTAPGSDSAVFFEQGTTR	2126.0	[HexNAc]4[Hex]5[Neu5Ac]1	1931.6
34	1450.24	+3	4347.7	ENLTAPGSDSAVFFEQGTTR	2126.0	[HexNAc]4[Hex]5[Neu5Ac]2+NH3	2239.7
34	1083.68	+4	4330.7	ENLTAPGSDSAVFFEQGTTR	2126.0	[HexNAc]4[Hex]5[Neu5Ac]2	2222.7
34	1444.56	+3	4330.7	ENLTAPGSDSAVFFEQGTTR	2126.0	[HexNAc]4[Hex]5[Neu5Ac]2	2222.7
34	1493.28	+3	4476.8	ENLTAPGSDSAVFFEQGTTR	2126.0	[HexNAc]4[Hex]5[Neu5Ac]2[Fuc]1	2368.8
34	1089.17	+4	4352.7	ENLTAPGSDSAVFFEQGTTR	2126.0	[HexNAc]4[Hex]5[Neu5Ac]2+Na	2244.7
35	1668.97	+3	5003.9	ENLTAPGSDSAVFFEQGTTR	2126.0	[HexNAc]5[Hex]6[Neu5Ac]3+NH3	2895.9
35	1663.29	+3	4986.9	ENLTAPGSDSAVFFEQGTTR	2126.0	[HexNAc]5[Hex]6[Neu5Ac]3	2878.9
35	1247.72	+4	4986.9	ENLTAPGSDSAVFFEQGTTR	2126.0	[HexNAc]5[Hex]6[Neu5Ac]3	2878.9
37	1282.48	+3	3844.4	AGLOAFFQVQECNK	1639.7	[HexNAc]4[Hex]5[Neu5Ac]2	2222.7
37	1923.24	+2	3844.5	AGLOAFFQVQECNK	1639.7	[HexNAc]4[Hex]5[Neu5Ac]2[Fuc]1	2368.8
38	1331.17	+3	3990.5	AGLOAFFQVQECNK	1639.7	[HexNAc]4[Hex]5[Neu5Ac]2+Na	2244.7
38	1289.81	+3	3866.4	AGLOAFFQVQECNK	1639.7	[HexNAc]4[Hex]5[Neu5Ac]2	2222.7

**Table 6 Ad vectors used in this study**

Ad vector	Foreign gene					
	E1 deletion region		E3 deletion region		Region between E4 and 3'ITR	
	Promoter	GOI	Promoter	GOI	Promoter	GOI
AdOn-L4	TRE/CMV	Luciferase	CMV	rtTA	—	—
AdBI-rtTA-L	TRE/CMV	Luciferase+rtTA	—	—	—	—
Ad-rtTA-IRES-tTS-L	TRE/CMV	Luciferase	CMV	rtTA+tTS	—	—
Ad-tTS-BI-rtTA-L	TRE/CMV	Luciferase+rtTA	—	—	EF-1 $\alpha$	tTS
Ad-rtTA-tTS-L	TRE/CMV	Luciferase	CMV	rtTA	EF-1 $\alpha$	tTS
Ad-L2	CMV	Luciferase	—	—	—	—
AdOn-SEAP4	TRE/CMV	SEAP	CMV	rtTA	—	—
Ad-M2-SEAP4	TRE/CMV	SEAP	CMV	rtTA2 <sup>S</sup> -M2	—	—
Ad-S2-SEAP4	TRE/CMV	SEAP	CMV	rtTA2 <sup>S</sup> -S2	—	—
Ad-rtTA-tTS-SEAP	TRE/CMV	SEAP	CMV	rtTA	EF-1 $\alpha$	tTS
Ad-M2-tTS-SEAP	TRE/CMV	SEAP	CMV	rtTA2 <sup>S</sup> -M2	EF-1 $\alpha$	tTS
Ad-S2-tTS-SEAP	TRE/CMV	SEAP	CMV	rtTA2 <sup>S</sup> -S2	EF-1 $\alpha$	tTS
Ad-SEAP2	CMV	SEAP	—	—	—	—

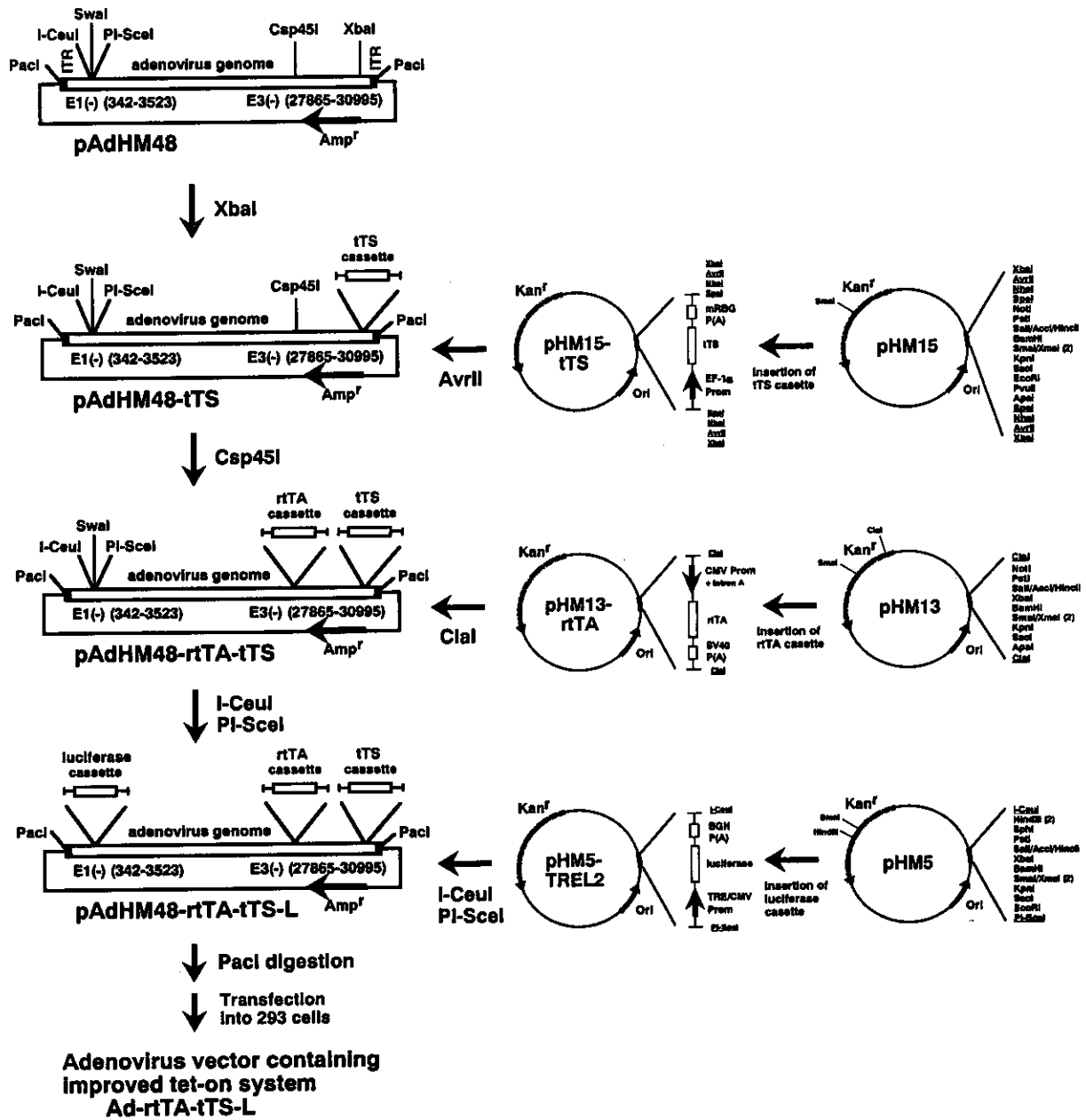
CMV = CMV intermediate-early promoter / enhancer

TRE/CMV = tet-responsive promoter containing minimal CMV promoter

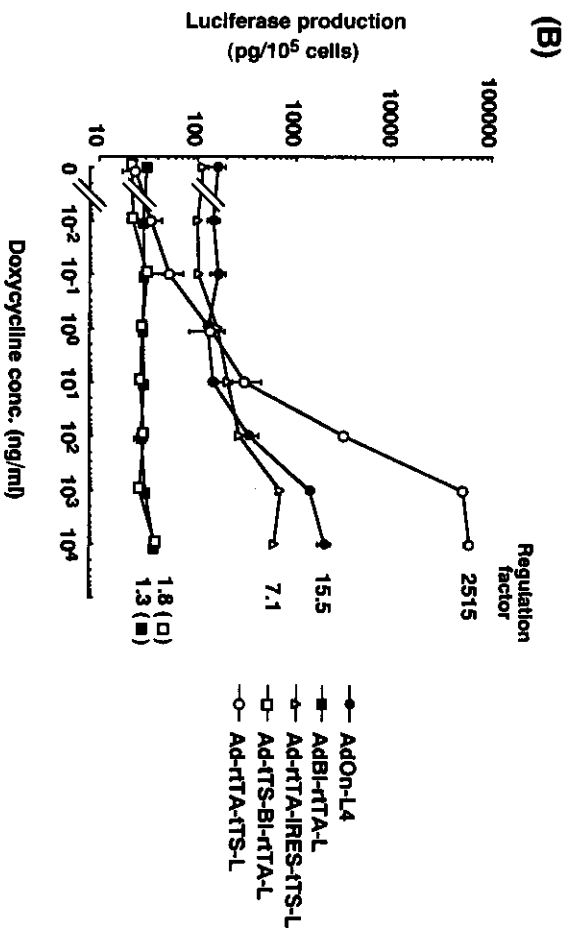
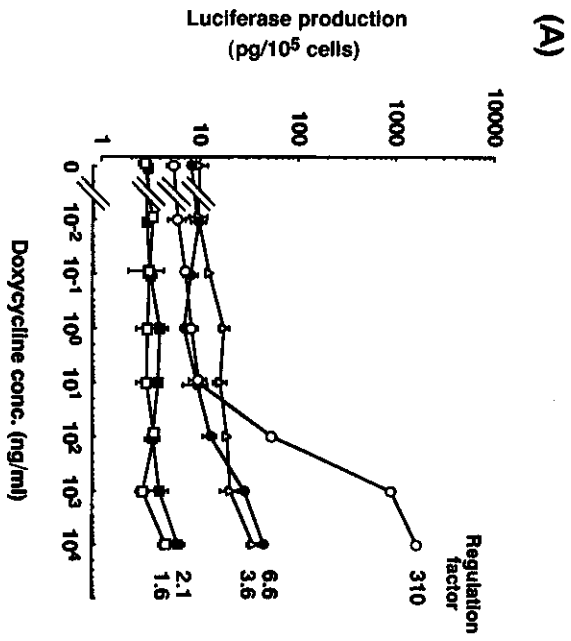
EF-1 $\alpha$  = human elongation factor-1 $\alpha$  promoter

Ad-rtTA-IRES-tTS-L contains CMV promoter / Intron A / rtTA / IRES / tTS / P(A) cassette in the E3 deletion region.

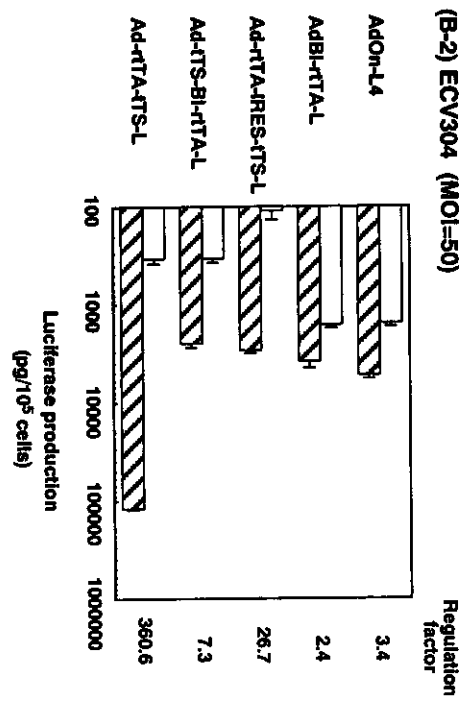
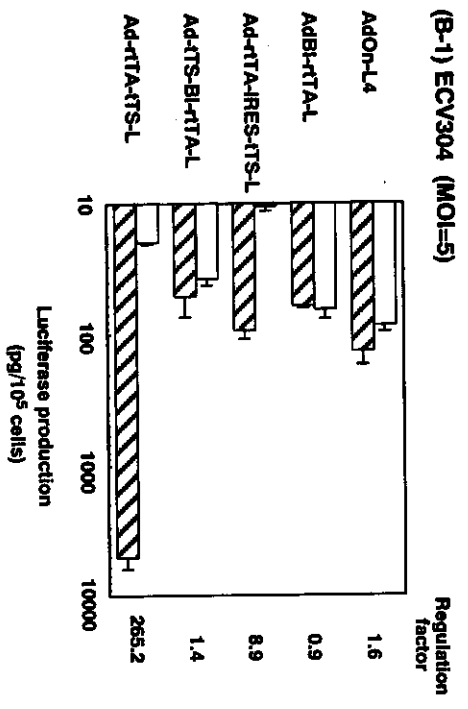
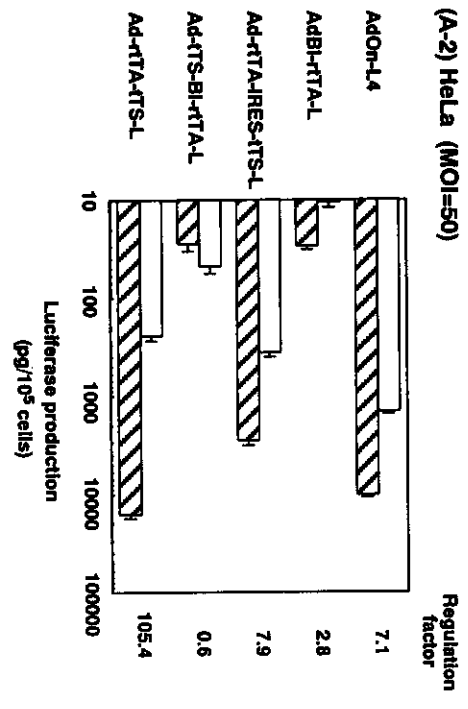
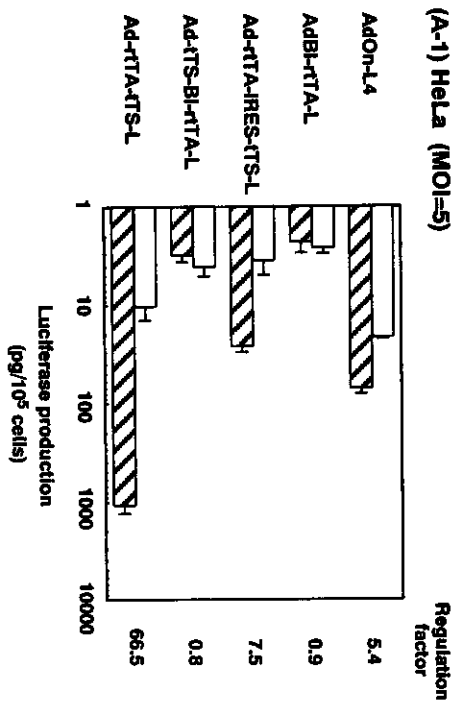
AdBI-rtTA-L and Ad-tTS-BI-rtTA-L express luciferase and rtTA from one bidirectional tet-responsive promoter cloned in the E1 deletion region.



**Fig.27 The construction strategy of Ad vectors containing the triple gene expression system.**

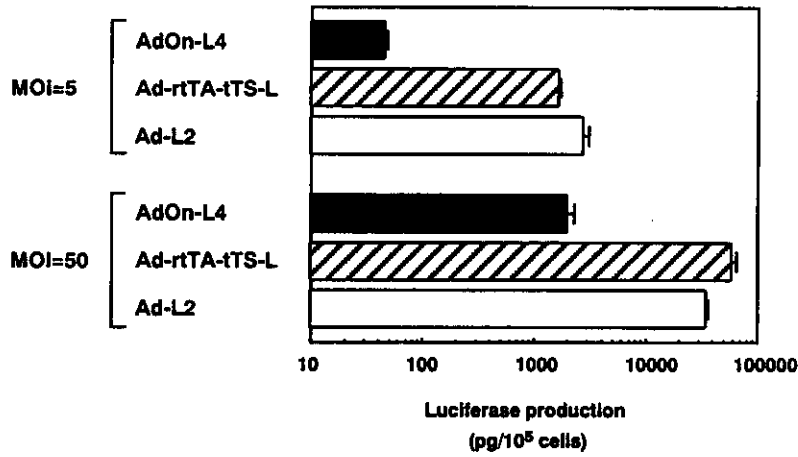


**Fig.28 Regulated luciferase expression in SK HEP-1 cells transduced with various Ad-mediated tet-on systems.**

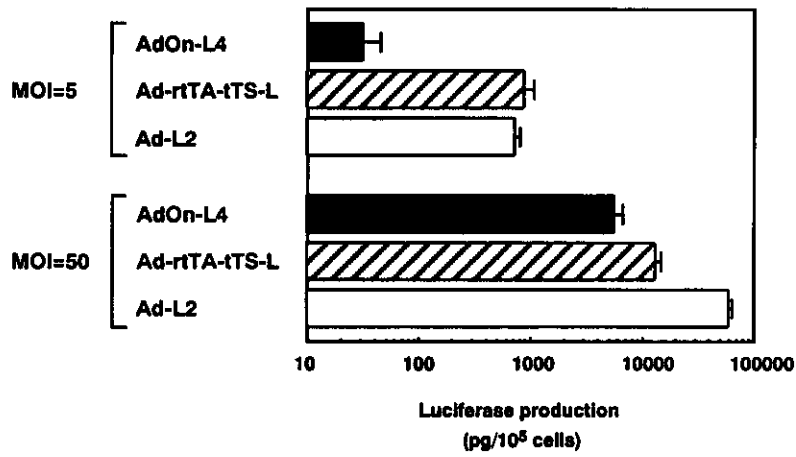


**Fig.29 Regulated luciferase expression in HeLa and ECV304 cells transduced with various Ad-mediated tet-on systems.**

(A) SK HEP-1



(B) HeLa



(C) ECV304

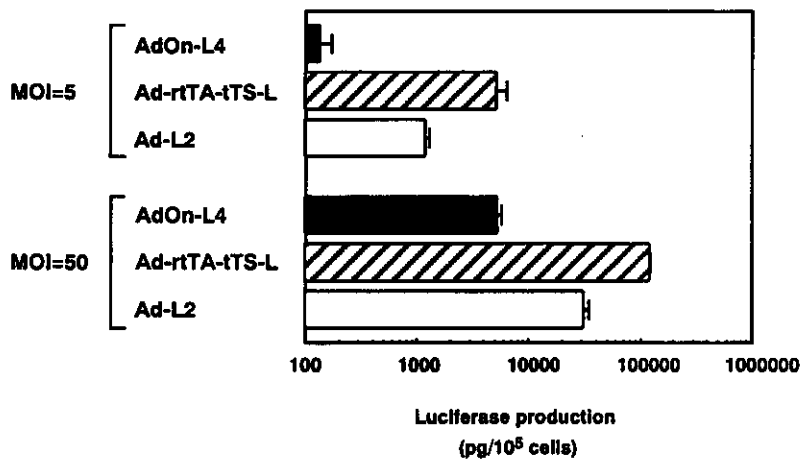
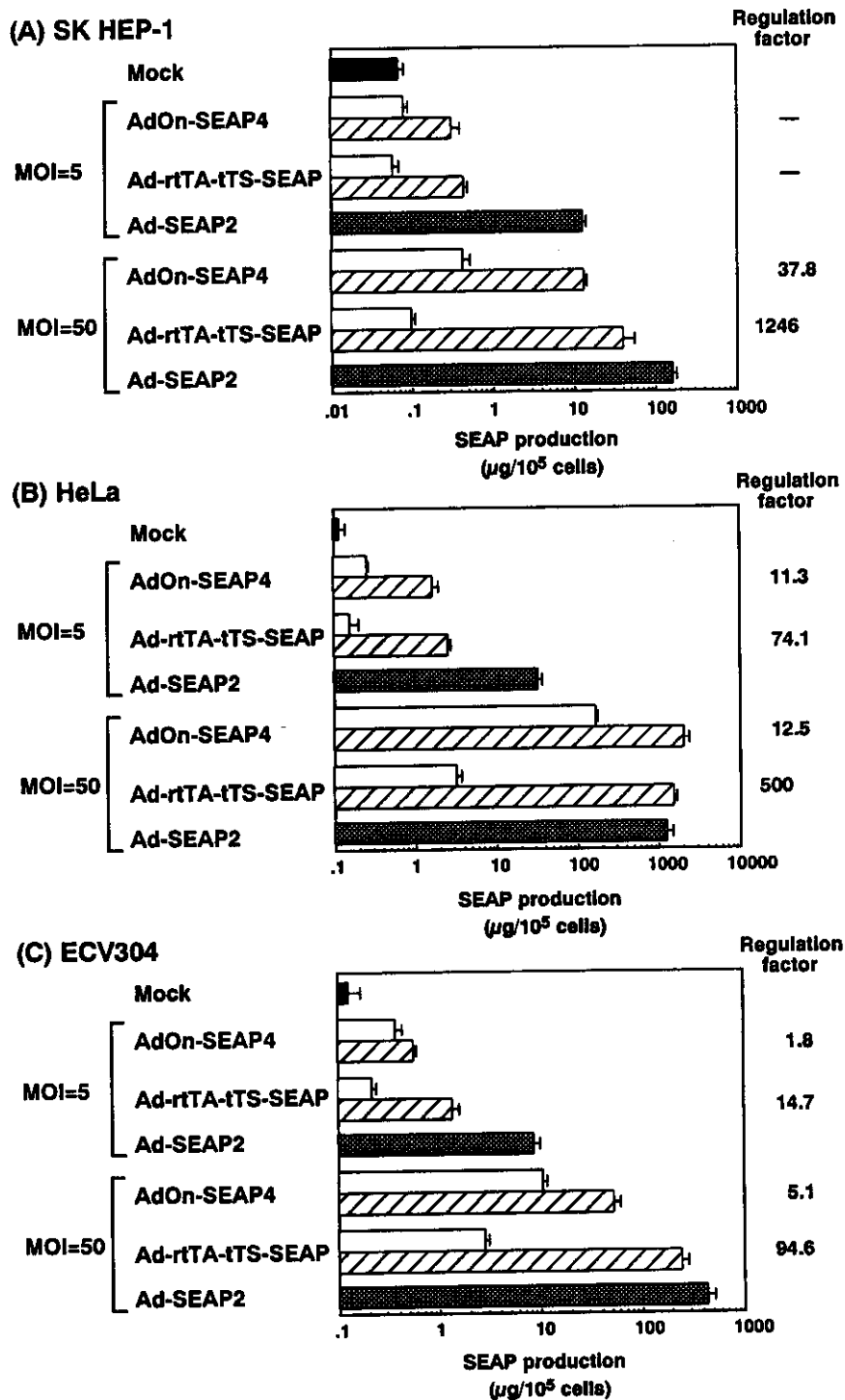
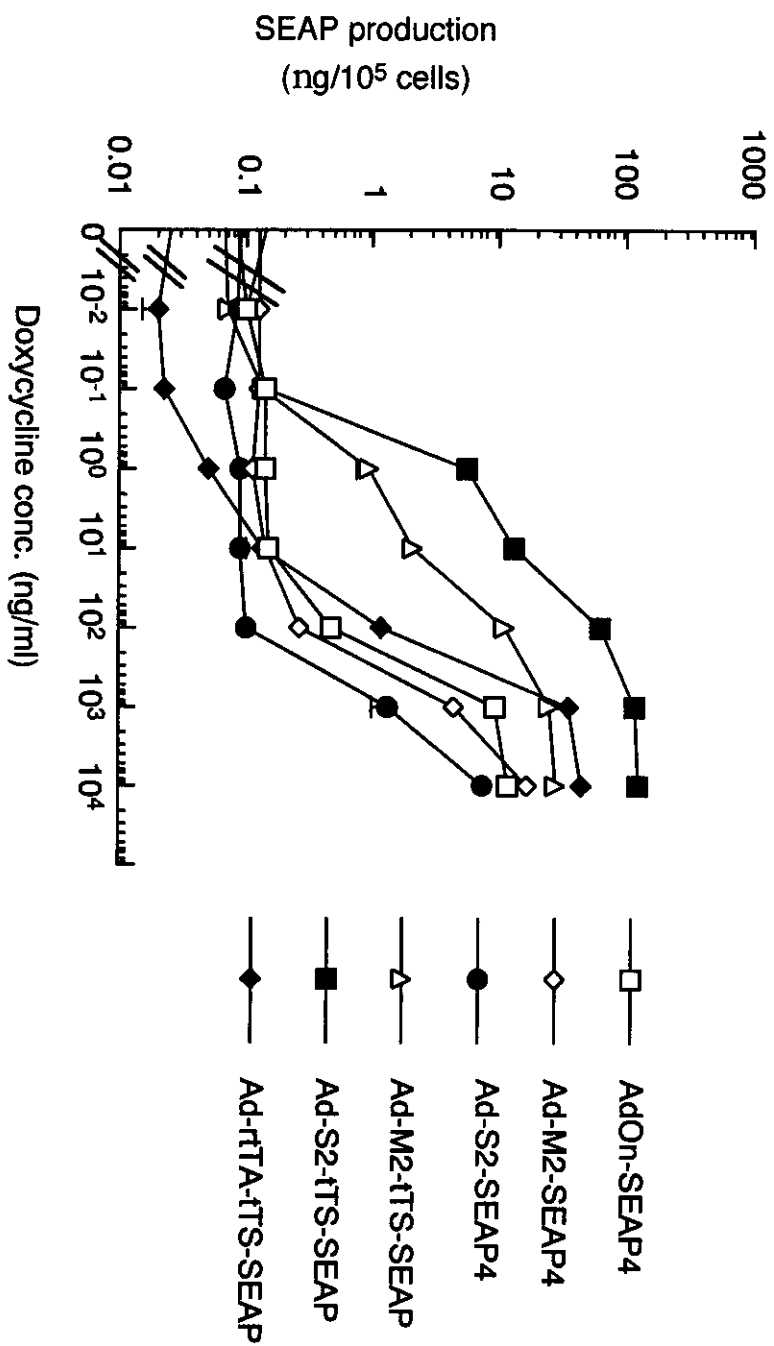


Fig.30 Comparison of induced (maximum) luciferase production in cells transduced with AdOn-L4, Ad-rtTA-tTS-L, or Ad-L2.

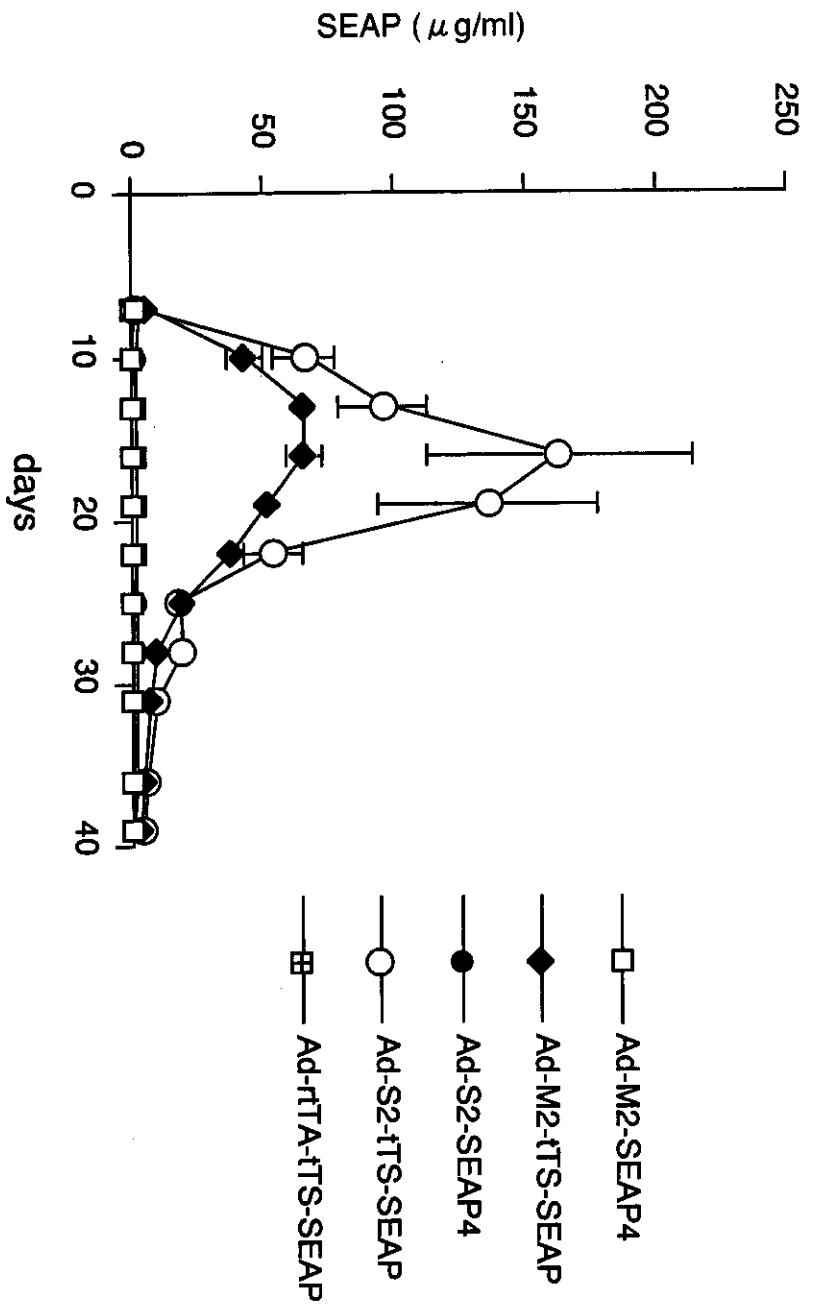


**Fig.31 Regulated SEAP expression in SK HEP-1, HeLa, and ECV304 cells transduced with AdOn-SEAP4 or Ad-rTA-tTS-SEAP.**

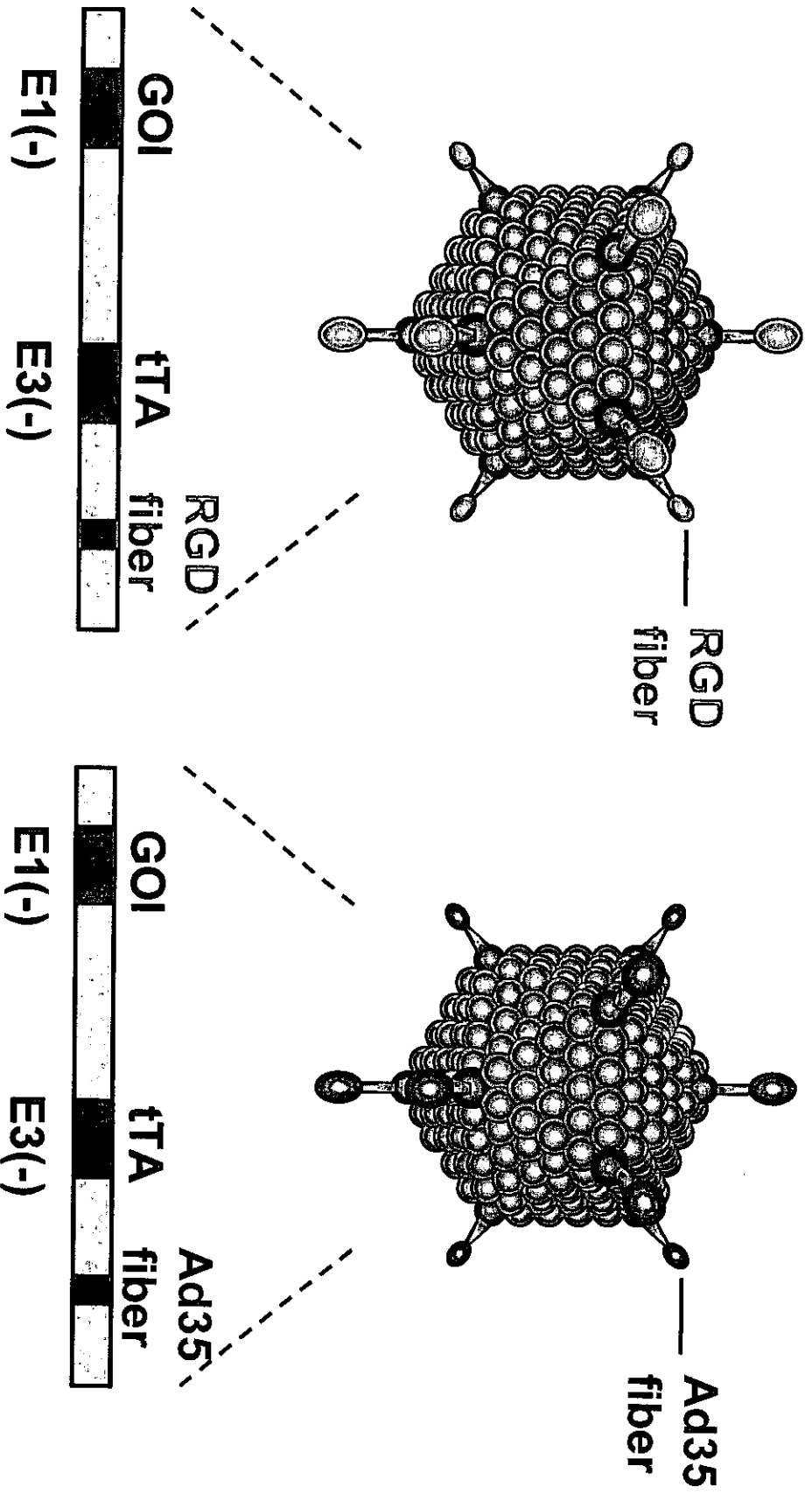




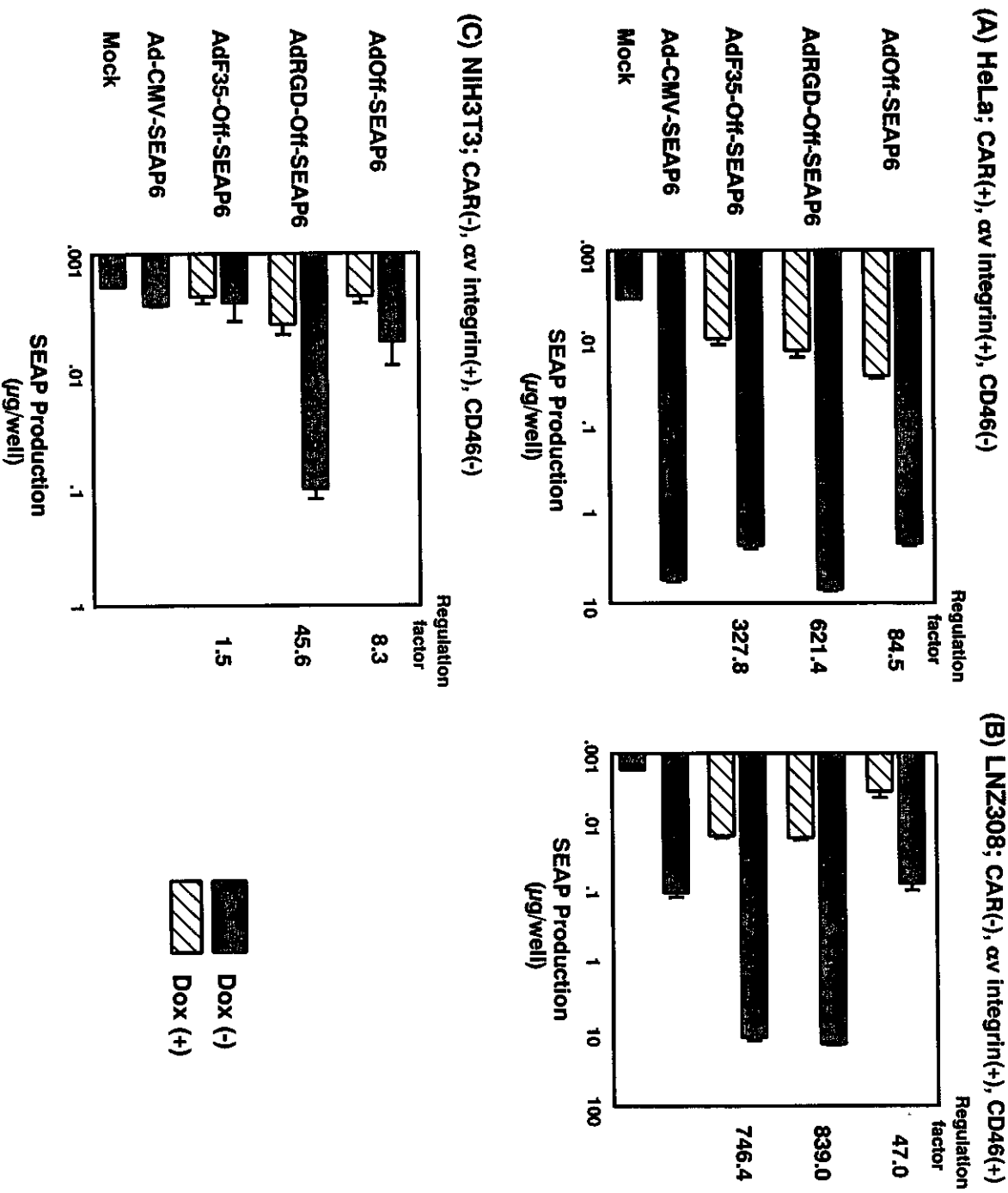
**Fig.32 Regulated SEAP expression in SK HEP-1 cells transduced with various Ad-mediated tet-on systems.**



**Fig. 33 Regulated SEAP expression in Balb/c nude mice.**



**Fig.34 Capsid-modified single adenovirus vectors containing tet-off system**



**Fig. 35 Capsid-modified single adenovirus vectors containing tet-off system**