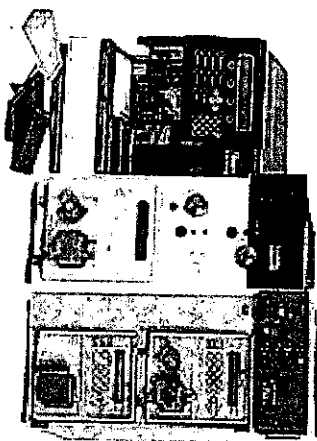
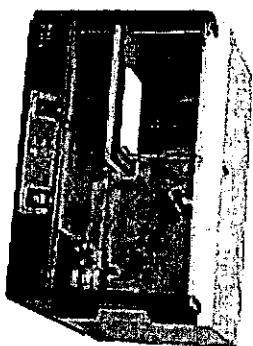


Fig. 6 LCからMALDI-TOF/TOF型マスへの展開

二次元ナノLC
Ultimate (LC Packings)



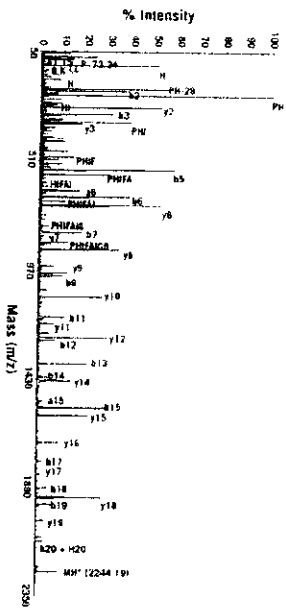
マイクロラクションコレクタ
Probot



オンライン

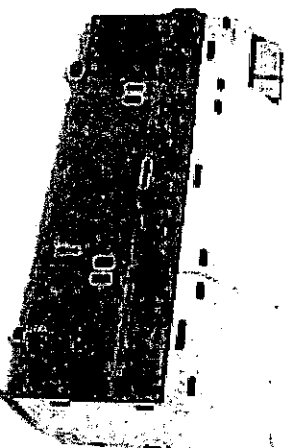
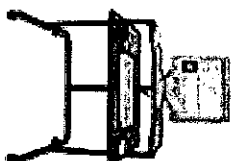
MALDIプレートへの
スポットティング

TWVPHFAQGDVYGGPMLAHK identifies
dihydroliposamide dihydrogenase ec 1.8.1
(sp | H03573 | hdnc2)



シーケンスタグによるタンパクの同定

AB 4700 MALDI-TOF/TOF Mass



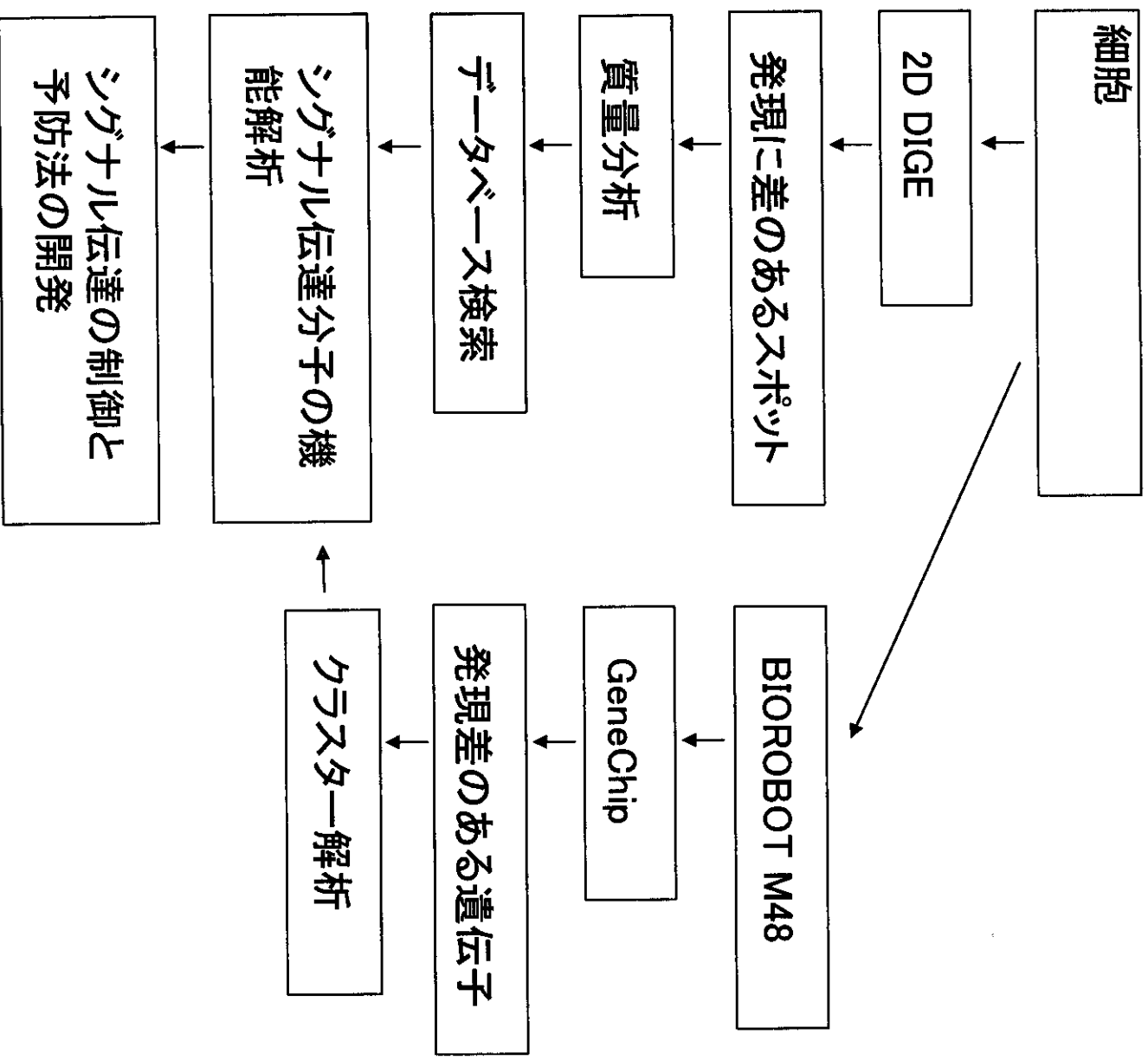


Fig. 7. シグナル伝達のプロファイリング方法

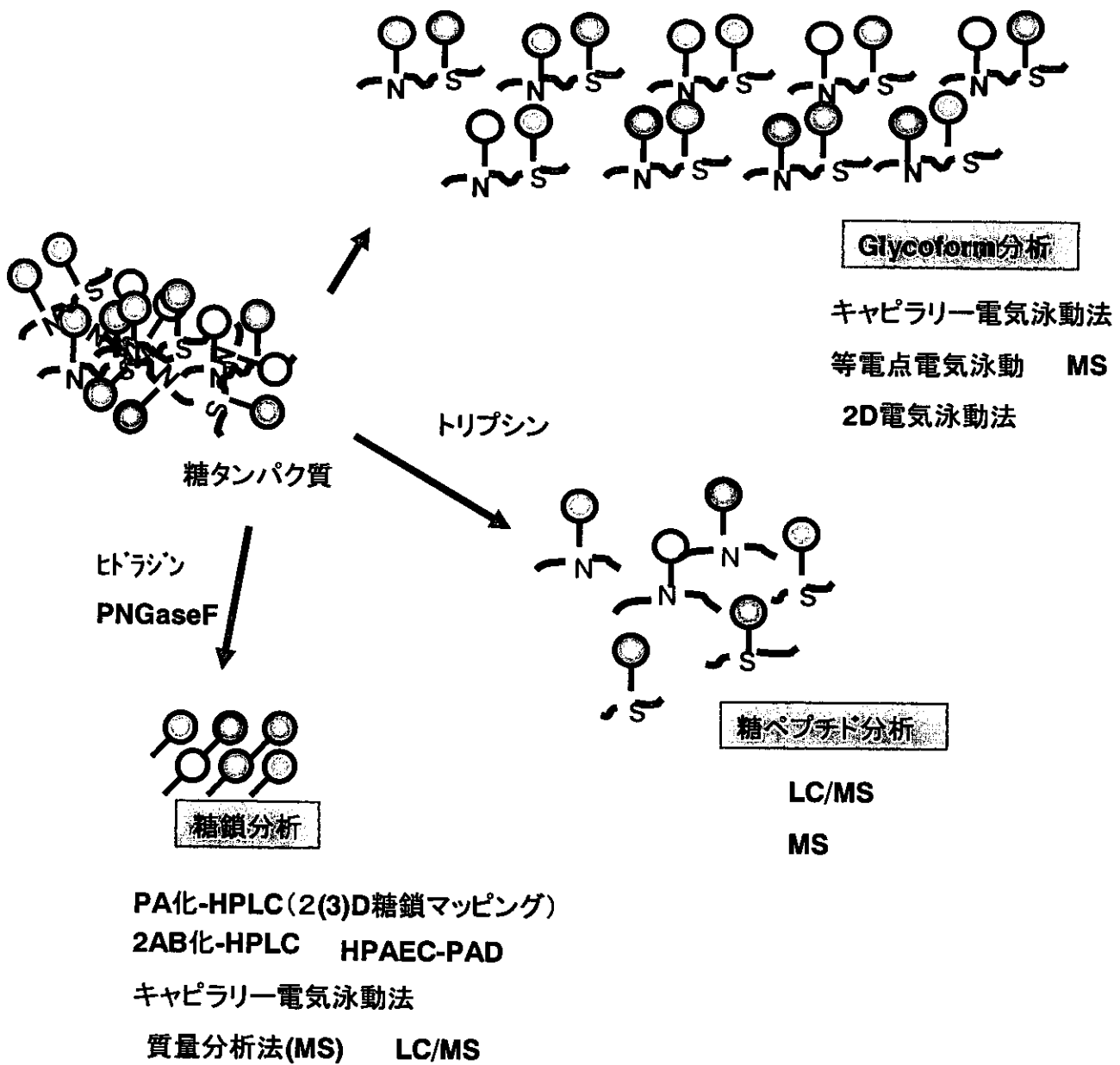


Fig. 8 Methods for the structural analysis of glycoproteins

mkwvesifli	fllnftesrt	lhrneygias	ildsyqetae	isladlatif
faqfvqeaty	kevskmvkda	ltaiekptgd	eqssgclenq	lpafleelch
ekeilekygh	sdccsqseeg	rhncflahkk	ptpasiplfq	vpepvtscea
yedretfmn	kfiyeiarrh	pflyaptill	waarydkiip	scckaenave
cfqtkaatvt	kelresslln	qhacavmknf	gtrtfqaitv	tklsqkftkv
<u>n</u>fteiqklvl	dvahvhehcc	rgdvldclqd	gekimsyics	qgdtsnkit
eccklttler	gqcihaend	ekpeglspl	nrflgdrdfn	qfssgekknif
lasfvheysr	rhpqlavsvi	lrvakgyqel	lekcfqtenp	lecqdkgeee
lqkyiqesqa	lakrscglfq	klgeyylqna	flvaytkkap	qltsselmai
trkmaataat	ccqlsedkll	acgegaadii	ighlclrhem	tpvnpvgvgqc
ctssyanrrp	cfsslvvdet	yvppafsddk	fifhkdlcqa	qgvalqtmkq
eflinlvkqk	pqiteeqlea	viadfsglle	kccqgqegev	cfaeegqkli
sktraalgv				

Fig. 9 Amino acid sequence and N-glycosylation sites of alpha-Fetoprotein
n: N-glycosylation site

(A) TIC for the full scan m/z 700-2000

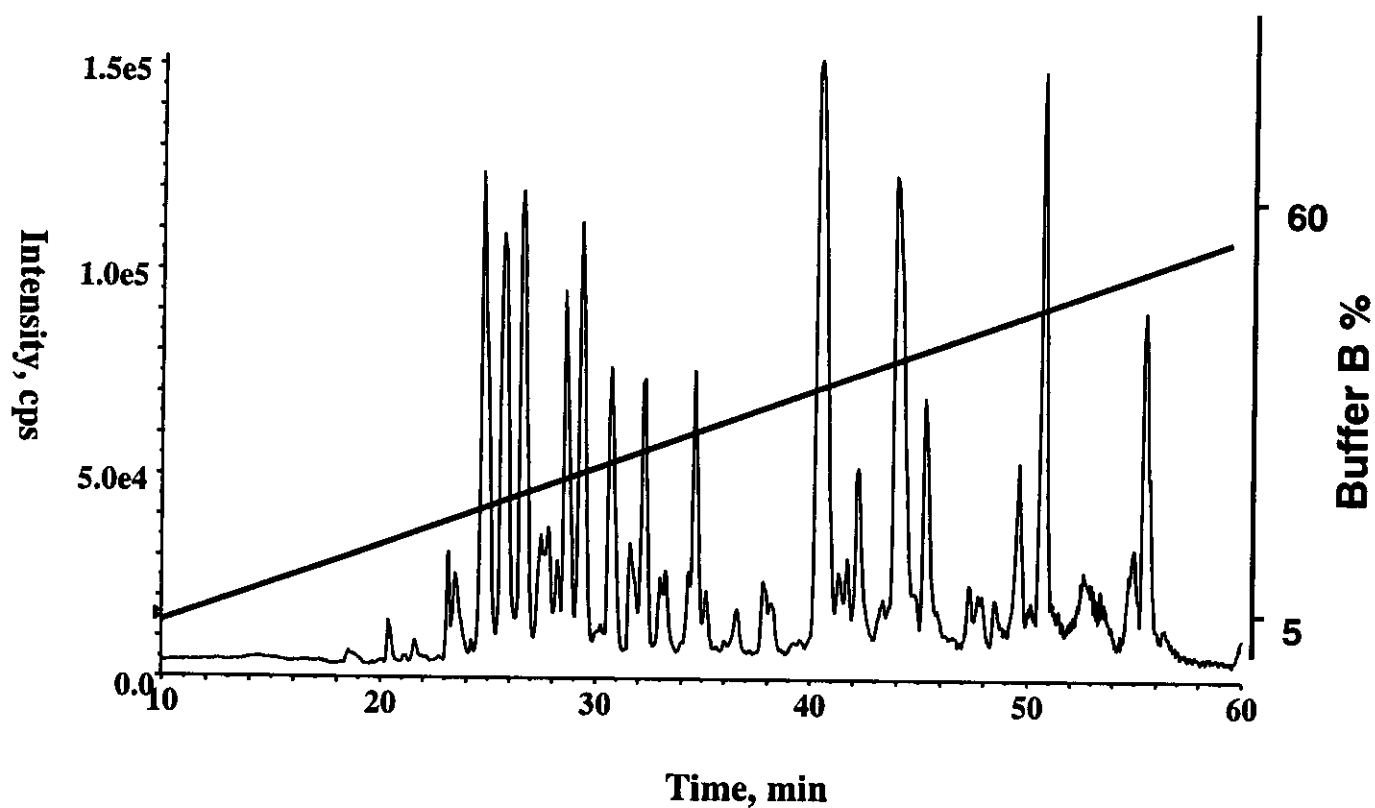


Fig. 10 LC-MS/MS of tryptic digest of α -fetoprotein

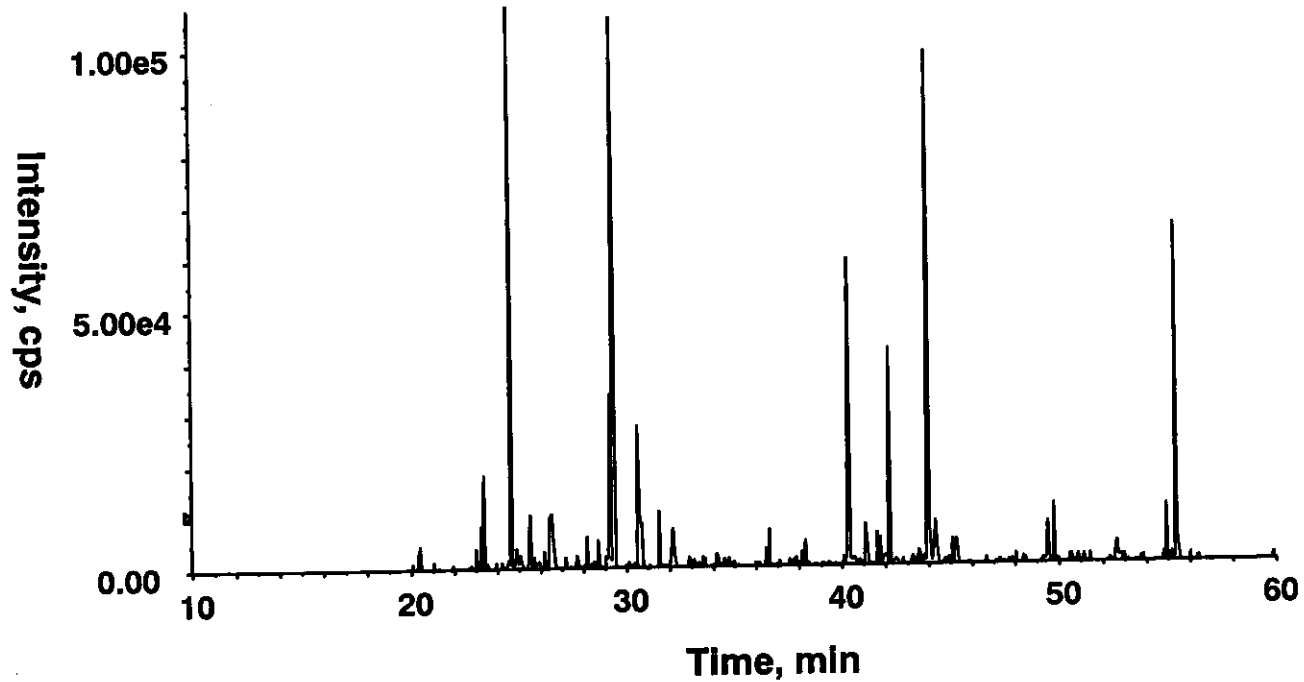
Column Magic C18

3 μ , 0.2*50 mm, 2 μ l/min

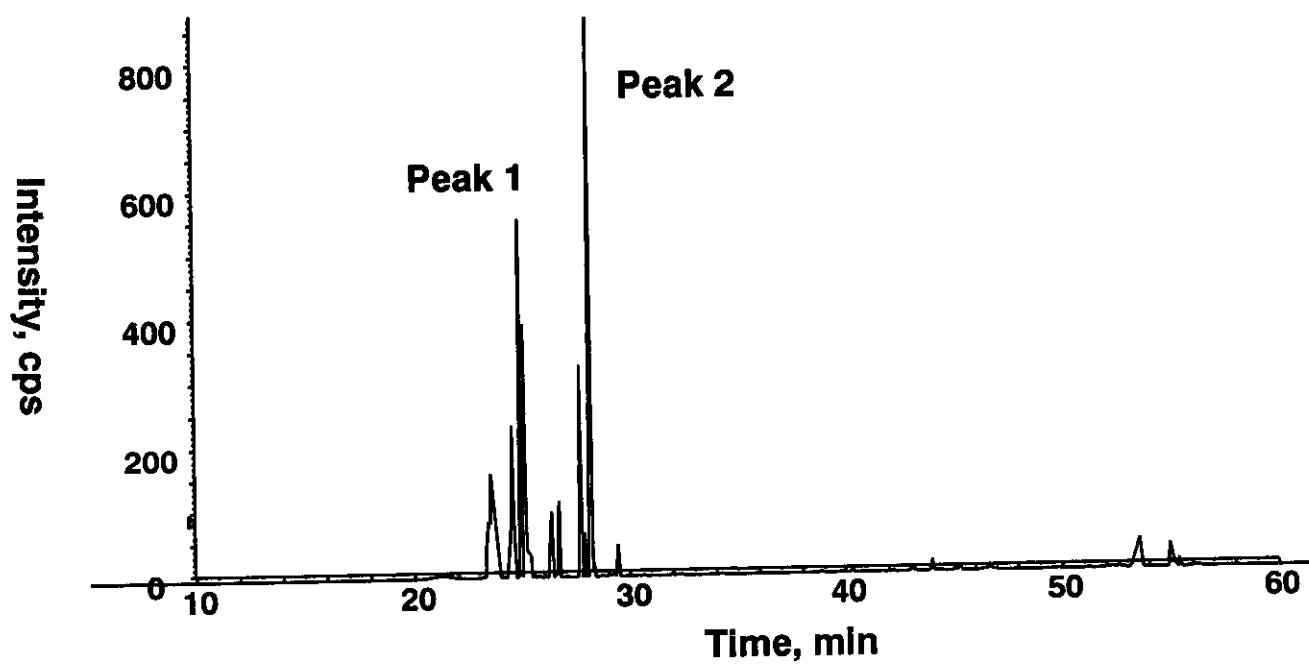
A: 2 % CH_3CN + 0.1 % formic acid

B: 90 % CH_3CN + 0.1 % formic acid

(B) TIC for the product ion scan at m/z 100 - 2000



(C) Product ion scan at m/z 204



Residue	Mass	b	b-NH3	y	y-NH3
V	99.07	100.08	83.05	978.53	961.50
N	114.04	214.12	197.09	879.46	862.43
F	147.07	361.19	344.16	765.41	748.39
T	101.05	462.23	445.21	618.35	601.32
E	129.04	591.28	574.25	517.30	500.27
I	113.08	704.36	687.33	388.26	371.23
Q	128.06	832.42	815.39	275.17	258.14
K	128.10	960.51	943.49	147.11	130.09

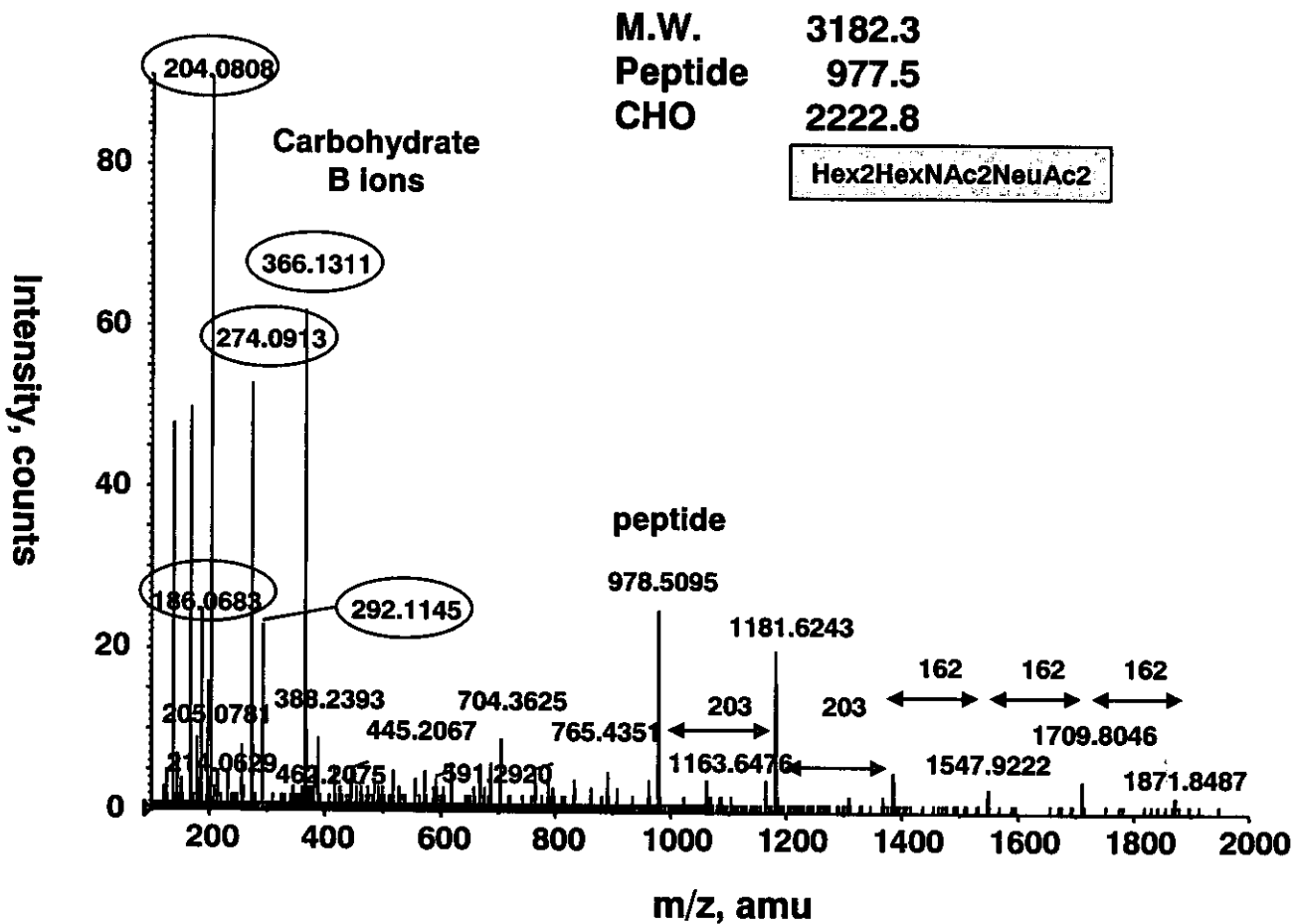


Fig. 11 Product ion spectrum of $M^+(m/z1061.8^{3+})$ at 25 min

mkililgfl	flestpawak	ekhyyigiie	ttwdyasdhg	ekklisvdte
hsniylqngp	drigrlykka	lylqytdetf	rttiekpowl	gflgpiikae
tgdkvyvhlk	nlasrpytfh	shgityykeh	egaiypd ¹ tt	dfqraddkvy
pgeqytymll	ateeqspgeg	dgnvcvtriyh	shidapkdia	sgligplii c
kkdsldkeke	khidrefvvm	fsvvde ¹ fs	yledniktyc	sepekvdkdn
edfqesnrmy	svngytfgs	pglsmcaedr	vkwyfmggn	evdvhaaffh
gqaltnknyr	idtinlfp at	lfdaymvaqn	pgewmlscqn	lnhlkaglqa
ffqvqec ¹ ks	sskdnirgkh	vrhyyiaaee	iiwnyapsgi	diftke ¹ lta
pgsdsavffe	qgtt ¹ riggsy	kklyreytd	asftnrkerg	peeehlgi
pviwaevgdt	irvtfhnkga	yplsiepigv	rfnknnegty	yspnynpqsr
svppsashva	ptetftyewt	vpkevgptna	dpvclakmyy	savdptkdif
tgligpmkic	kkgs ¹ lhangr	qkdvdkefyl	fptvfde ¹ es	lllednirmf
ttapdqvdke	dedfqesnkm	hsmngfmygn	qppltmckgd	svvwyf ¹ sag
neadvhgiyf	sgntylwrge	rrdtanlfpq	tslthmwpd	tegtfnvecl
ttdhytggmk	qkytvnqerr	qsedstfylg	ertyyiaave	vewdyspqr
wekelhlhqe	q ¹ vsnafldk	gefyigskyk	kvvyrqytds	tfrvpverka
eeehlgi	qlhadvgdkv	kiifknmatr	pysihahgvq	tesstvtptl
pgetltyvwk	ipersgagte	dsacipwayy	stvdqvkdl	sgligpliv c
rrpylkvfnp	rrklefallf	lvfde ¹ eswy	lddniktysd	hpekvnkdde
efiesnkmha	ingrmfgnlq	gltmhvgdev	nwymgmgne	idlhtvhfhg
hsfqykhrgv	yssdvfdifp	gtyqtlemfp	rtpgiwllhc	hvt ¹ dhihagm
ettytvlqne	dtks ¹ g			

Fig. 12 Amino acid sequence and N-glycosylation sites of ceruloplasmin (CP)

¹: Potential N-glycosylation sites

²: N-glycosylation sites

(A) TIC for the full scan m/z 1000-2000

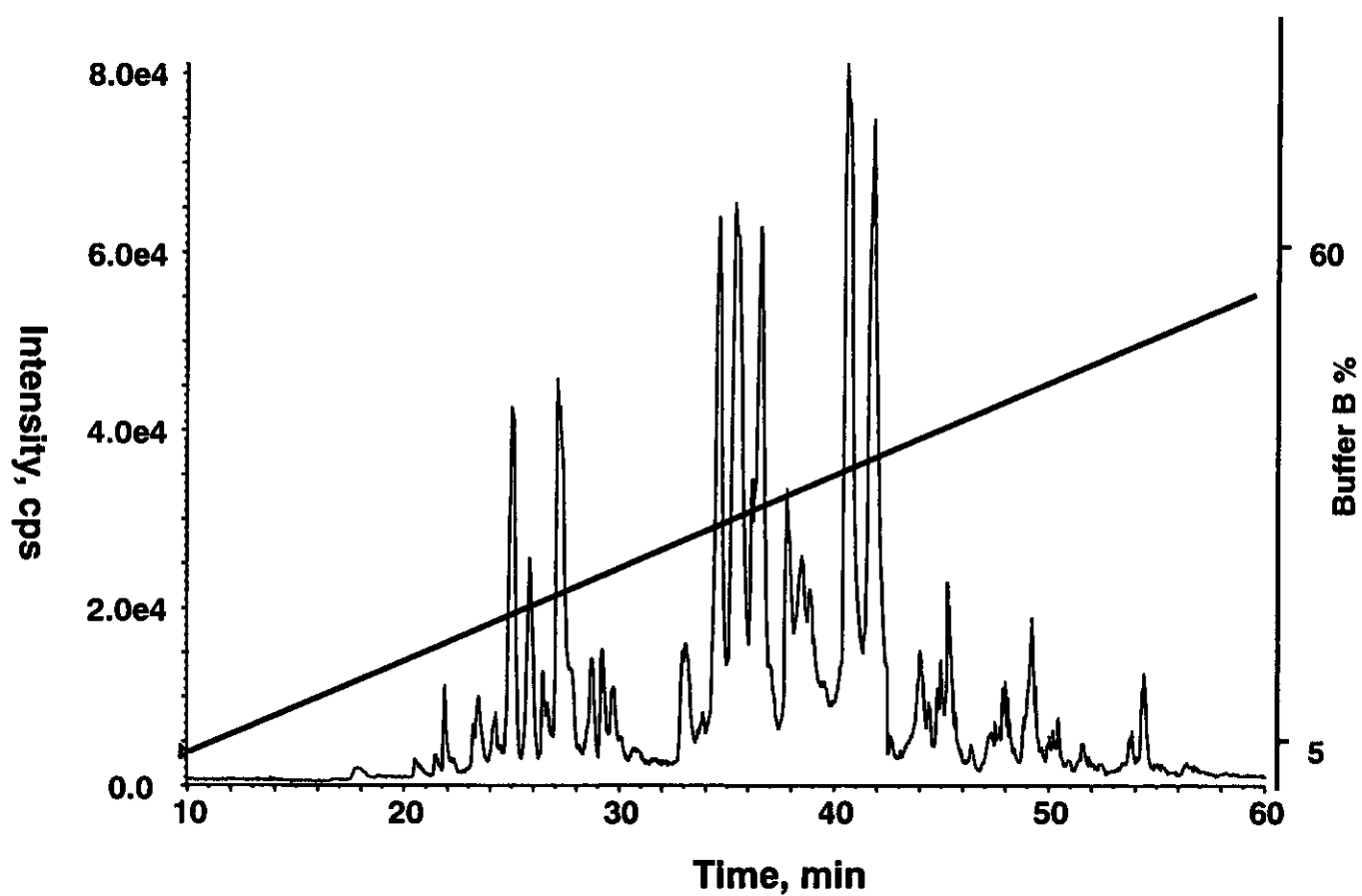


Fig. 13 LC-MS/MS of tryptic digest of ceruloplasmin

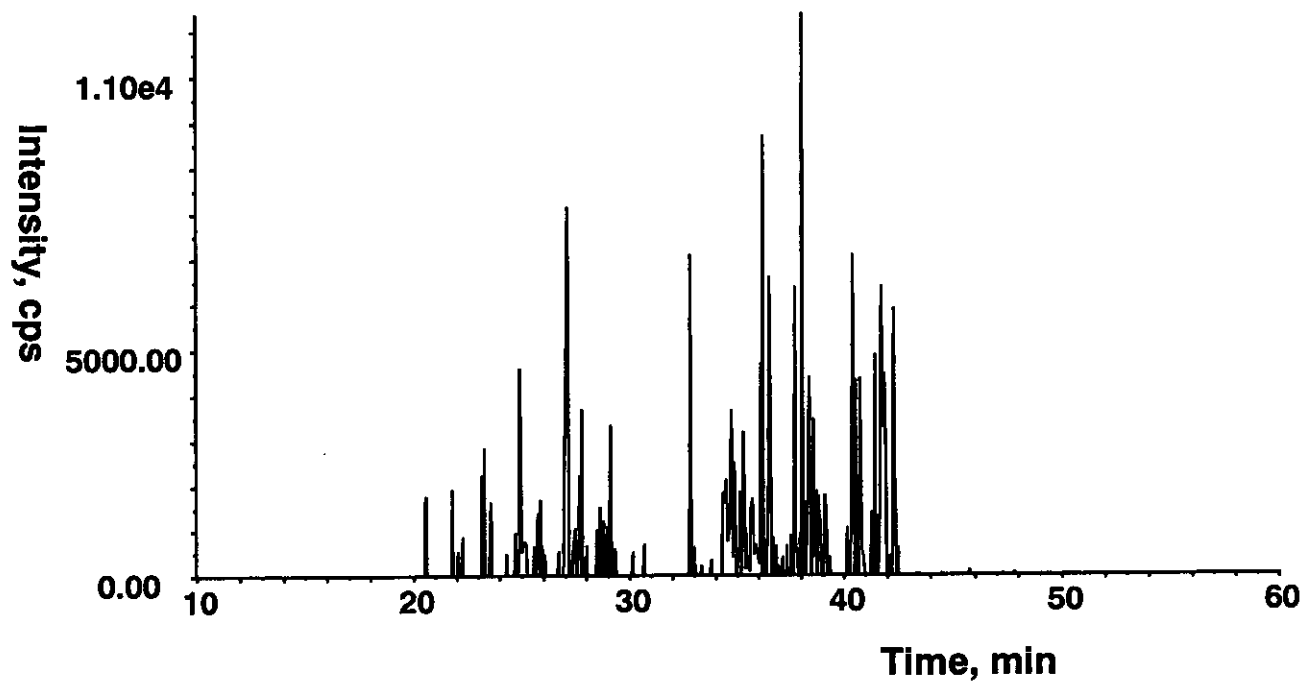
Column Magic C18

3 μ , 0.2*50 mm, 2 μ l/min

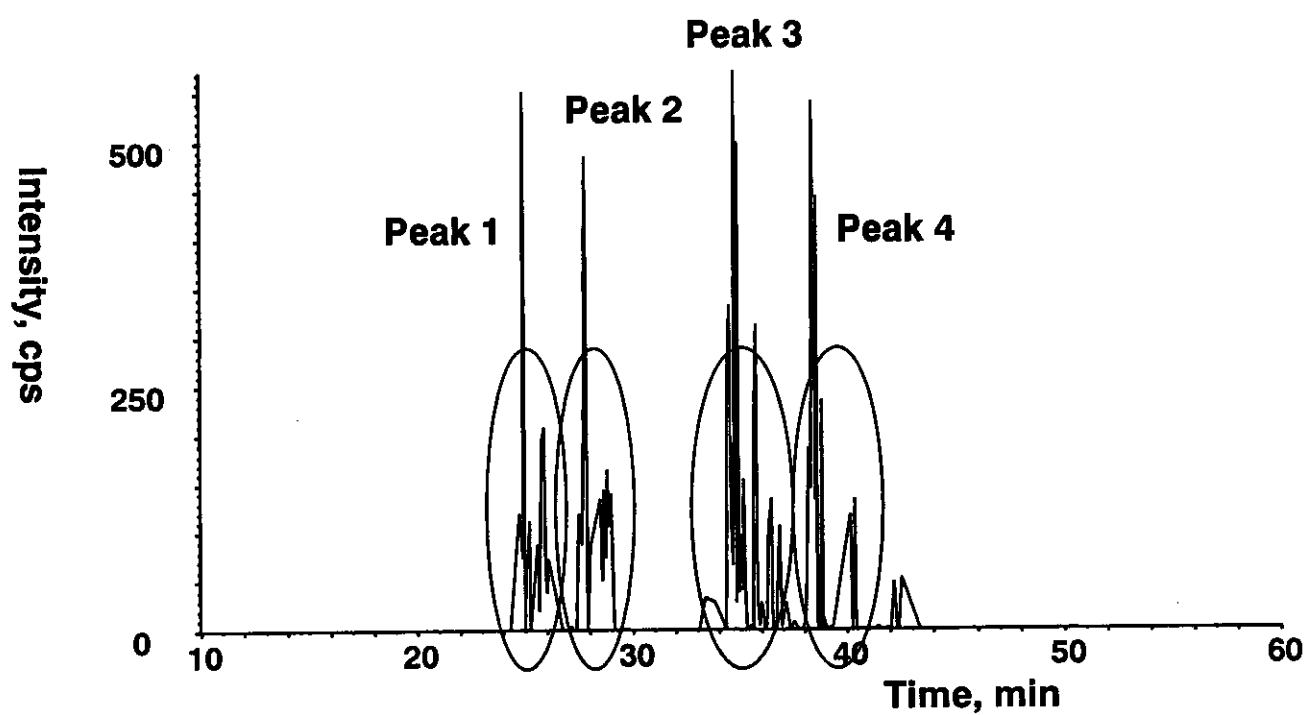
A: 2 % CH_3CN + 0.1 % formic acid

B: 90 % CH_3CN + 0.1 % formic acid

(B) TIC for the product ion scan at m/z 100 - 2000



(C) Product ion scan at m/z 204



M.W. 4096.6
 Peptide 1891.8
 CHO 2222.8

Hex₂HexNAc₂NeuAc₂

Residue	Mass	b	b-NH3	y	y-NH3
E	129.04	130.05	113.02	1892.84	1875.81
H	137.06	267.11	250.08	1763.80	1746.77
E	129.04	396.15	379.12	1626.74	1609.71
G	57.02	453.17	436.15	1497.70	1480.67
A	71.04	524.21	507.18	1440.68	1423.65
I	113.08	637.29	620.27	1369.64	1352.61
Y	163.06	800.36	783.33	1256.55	1239.53
P	97.05	897.41	880.38	1093.49	1076.46
D	115.03	1012.44	995.41	996.44	979.41
N	114.04	1126.48	1109.45	881.41	864.38
T	101.05	1227.53	1210.50	767.37	750.34
T	101.05	1328.58	1311.55	666.32	649.29
D	115.03	1443.60	1426.58	565.27	548.25
F	147.07	1590.67	1573.64	450.25	433.22
Q	128.06	1718.73	1701.70	303.18	286.15
R	156.10	1874.83	1857.80	175.12	158.09

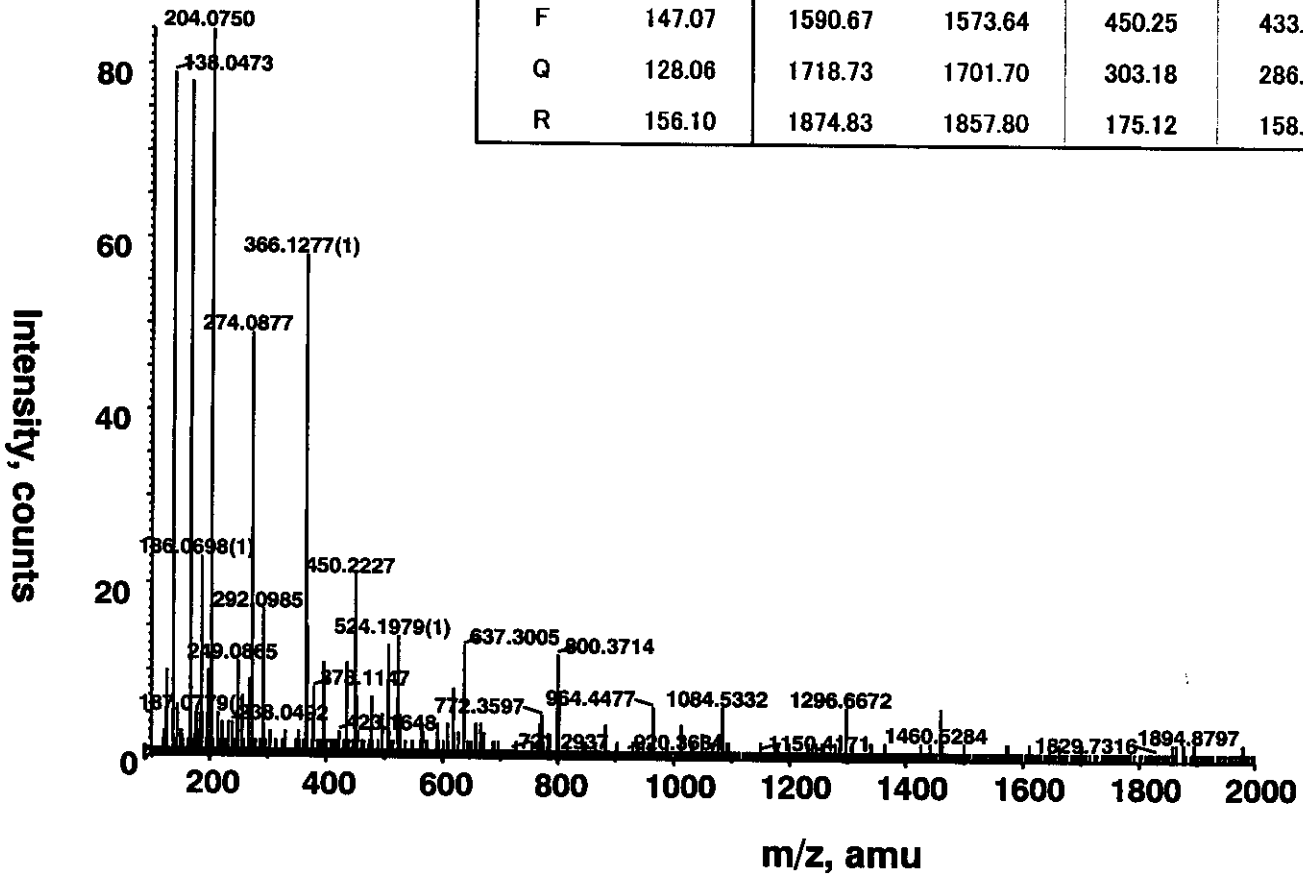


Fig. 14 Product ion spectrum of M⁺(m/z1366.6³⁺) at 25 min

(A) TIC for the full scan m/z 400-2000

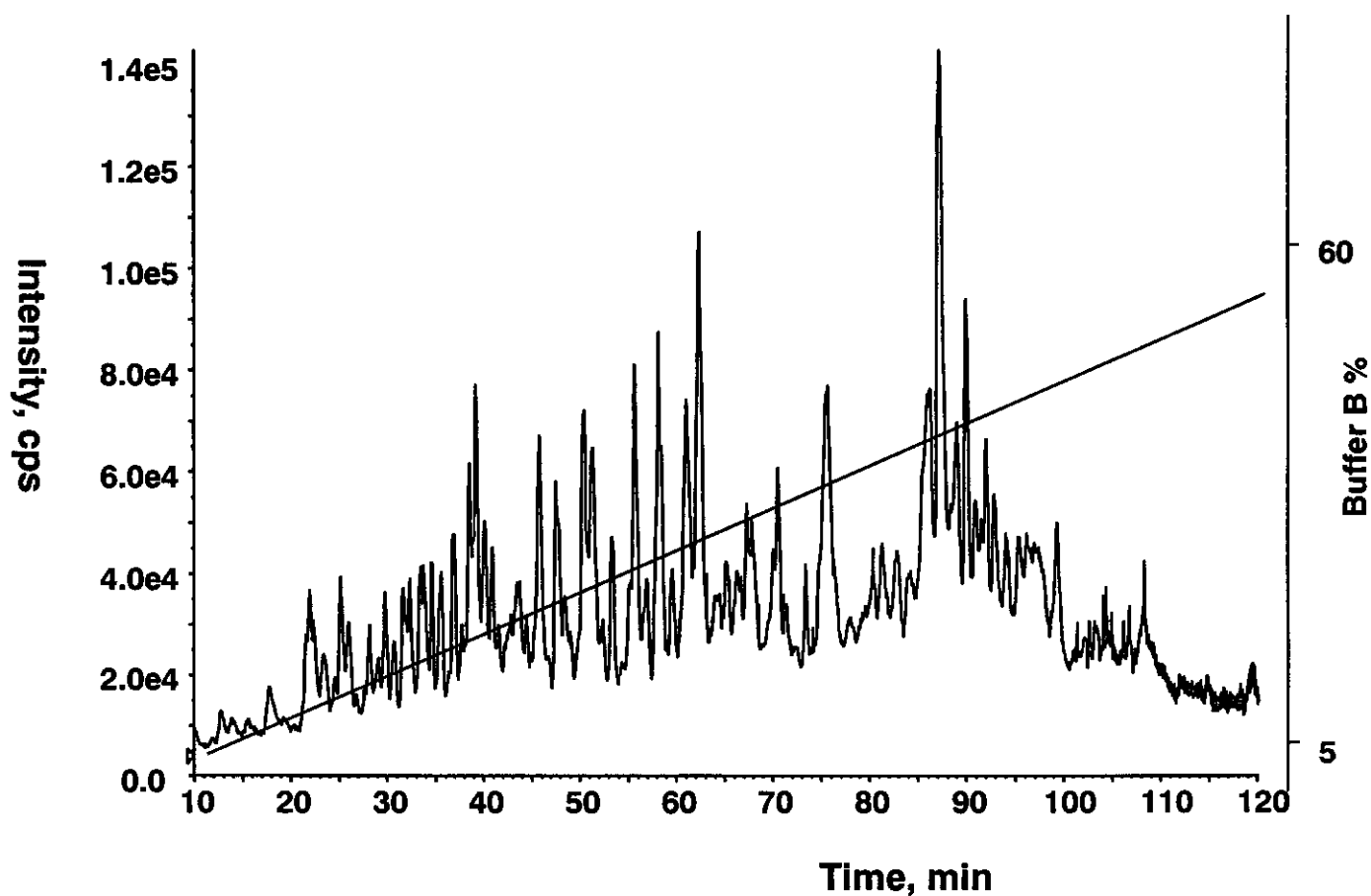


Fig. 15 LC-MS/MS of tryptic digest of human serum

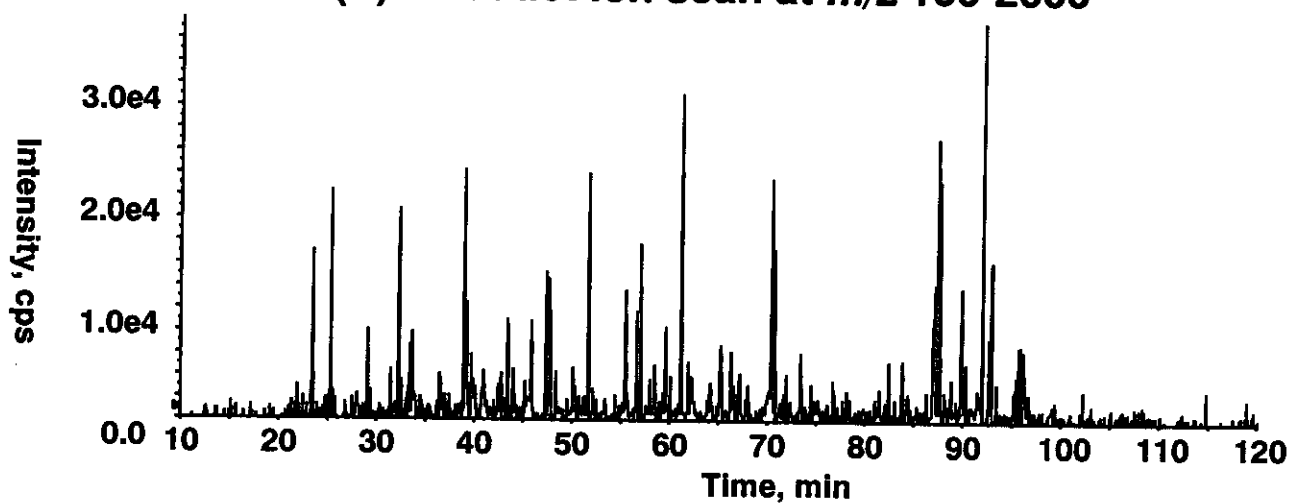
Column Magic C18

3 μ , 0.2*50 mm, 2 μ l/min

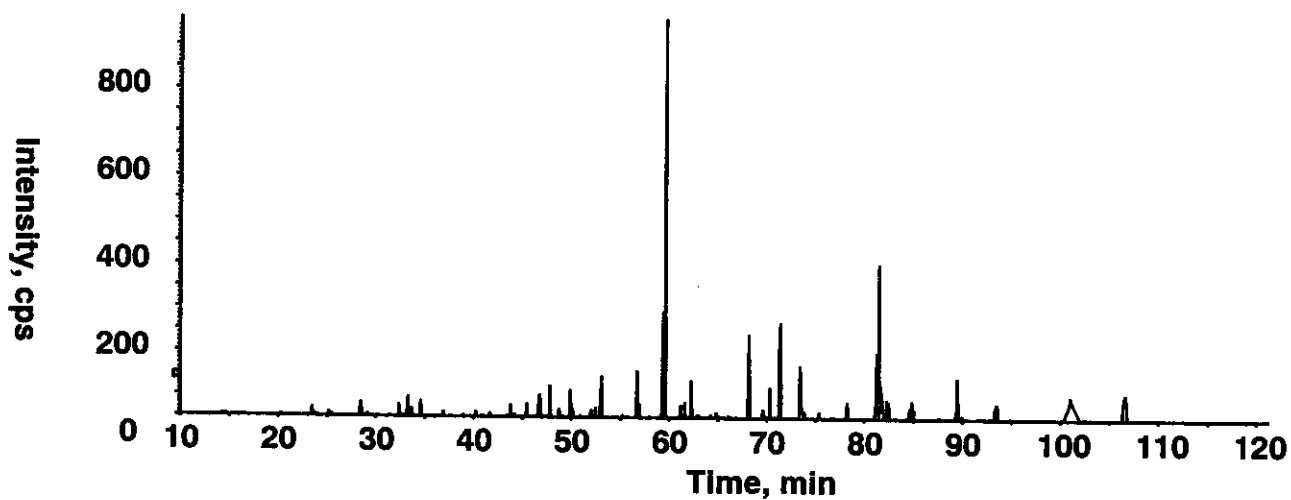
A: 2 % CH_3CN + 0.1 % formic acid

B: 90 % CH_3CN + 0.1 % formic acid

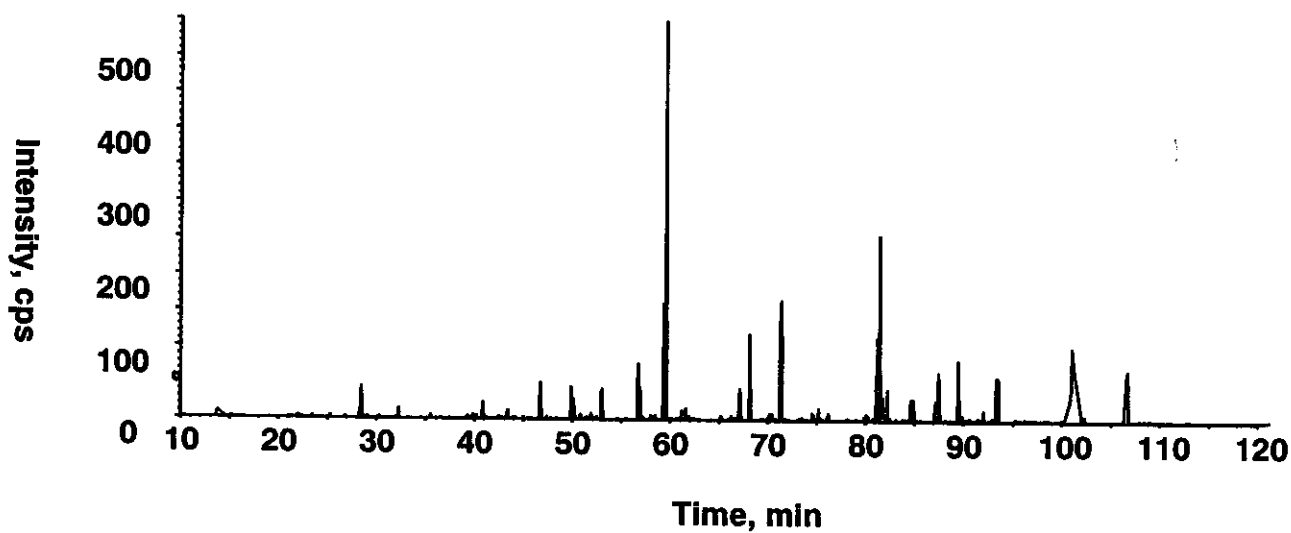
(B) Product ion scan at m/z 100-2000



(C) Product ion scan at m/z 204



(D) Product ion scan at m/z 366



M.W. 4882.8
Peptide 2678.4
CHO 2222.8

Residue	Mass	b	b-NH3	y	y-NH3
M	131.0	132.0	115.0	2679.4	2662.4
V	99.1	231.1	214.1	2548.4	2531.3
S	87.0	318.1	301.1	2449.3	2432.3
H	137.1	455.2	438.2	2362.3	2345.2
H	137.1	592.3	575.2	2225.2	2208.2
N	114.0	706.3	689.3	2088.1	2071.1
L	113.1	819.4	802.4	1974.1	1957.1
T	101.0	920.4	903.4	1861.0	1844.0
T	101.0	1021.5	1004.5	1760.0	1742.9
G	57.0	1078.5	1061.5	1658.9	1641.9
A	71.0	1149.5	1132.5	1601.9	1584.9
T	101.0	1250.6	1233.6	1530.9	1513.8
L	113.1	1363.7	1346.7	1429.8	1412.8
I	113.1	1476.8	1459.7	1316.7	1299.7
N	114.0	1590.8	1573.8	1203.6	1186.6
E	129.0	1719.8	1702.8	1089.6	1072.6
Q	128.1	1847.9	1830.9	960.6	943.5
W	186.1	2034.0	2017.0	832.5	815.5
L	113.1	2147.1	2130.0	646.4	629.4
L	113.1	2260.2	2243.1	533.3	516.3
T	101.0	2361.2	2344.2	420.2	403.2
T	101.0	2462.2	2445.2	319.2	302.2
A	71.0	2533.3	2516.3	218.1	201.1
K	128.1	2661.4	2644.4	147.1	130.1

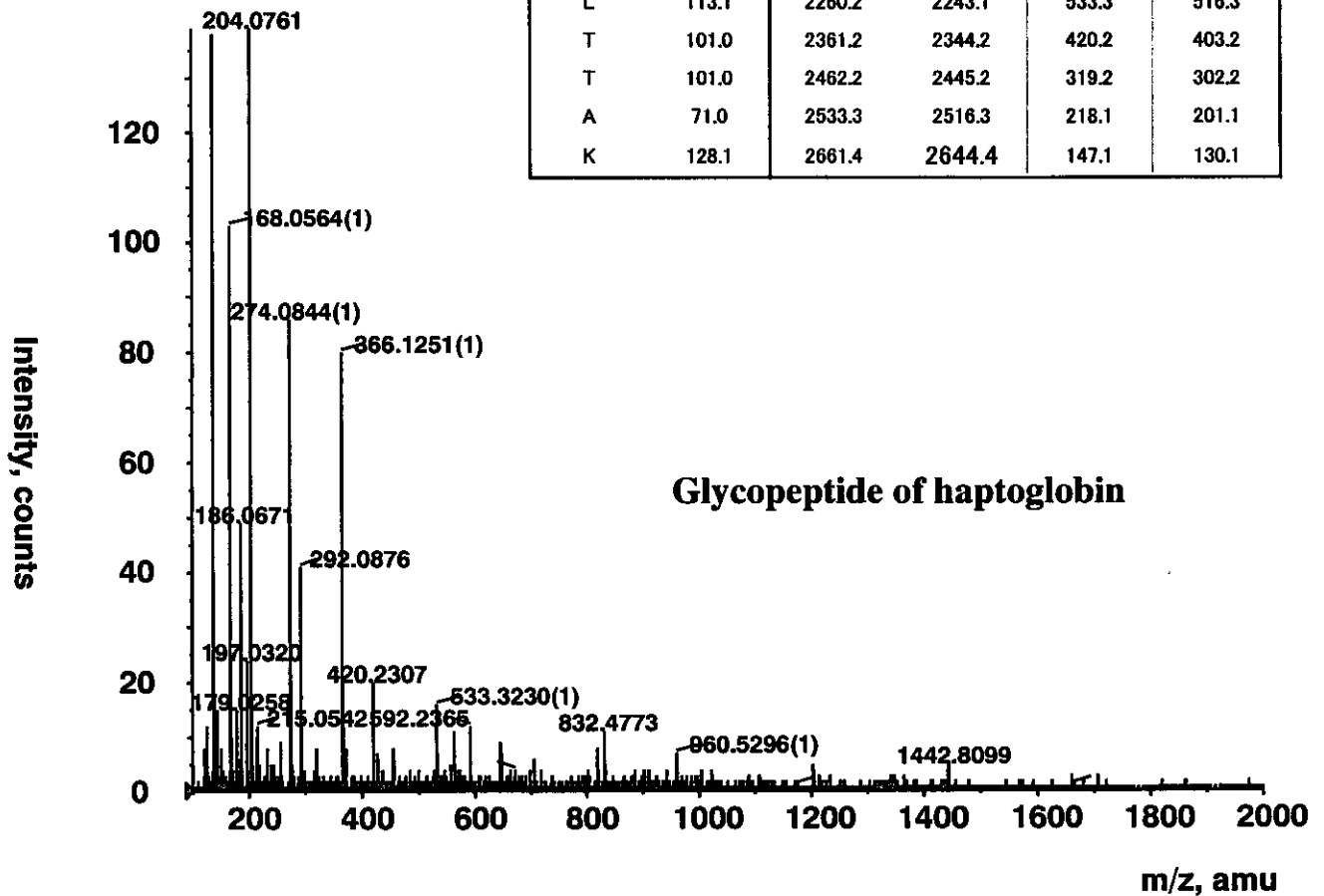


Fig. 16 Product ion spectrum of M⁺(m/z1221.7³⁺) at 26 min

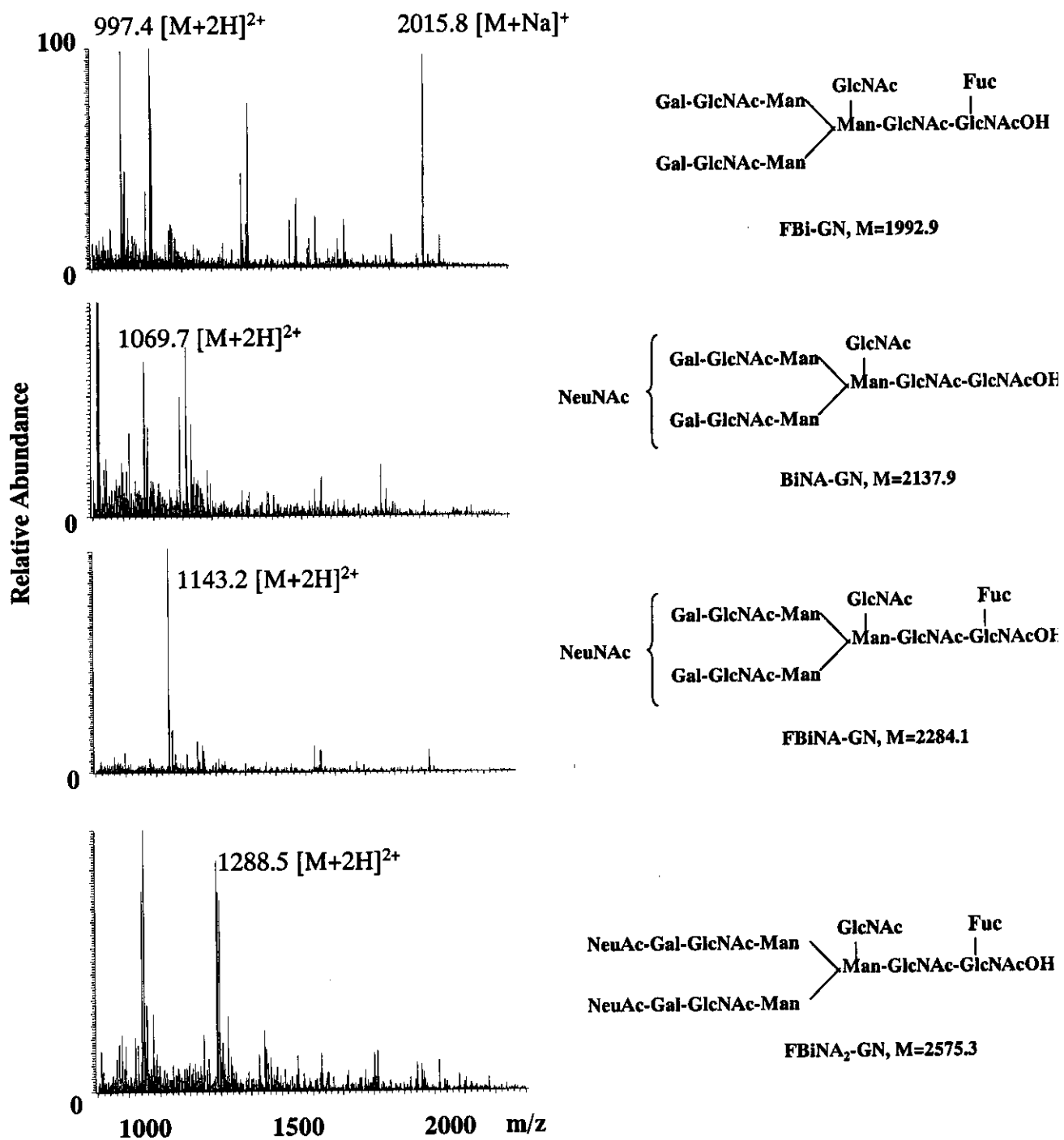


Fig. 18 Mass spectra of bisecting biantennaries from CHOIII membrane

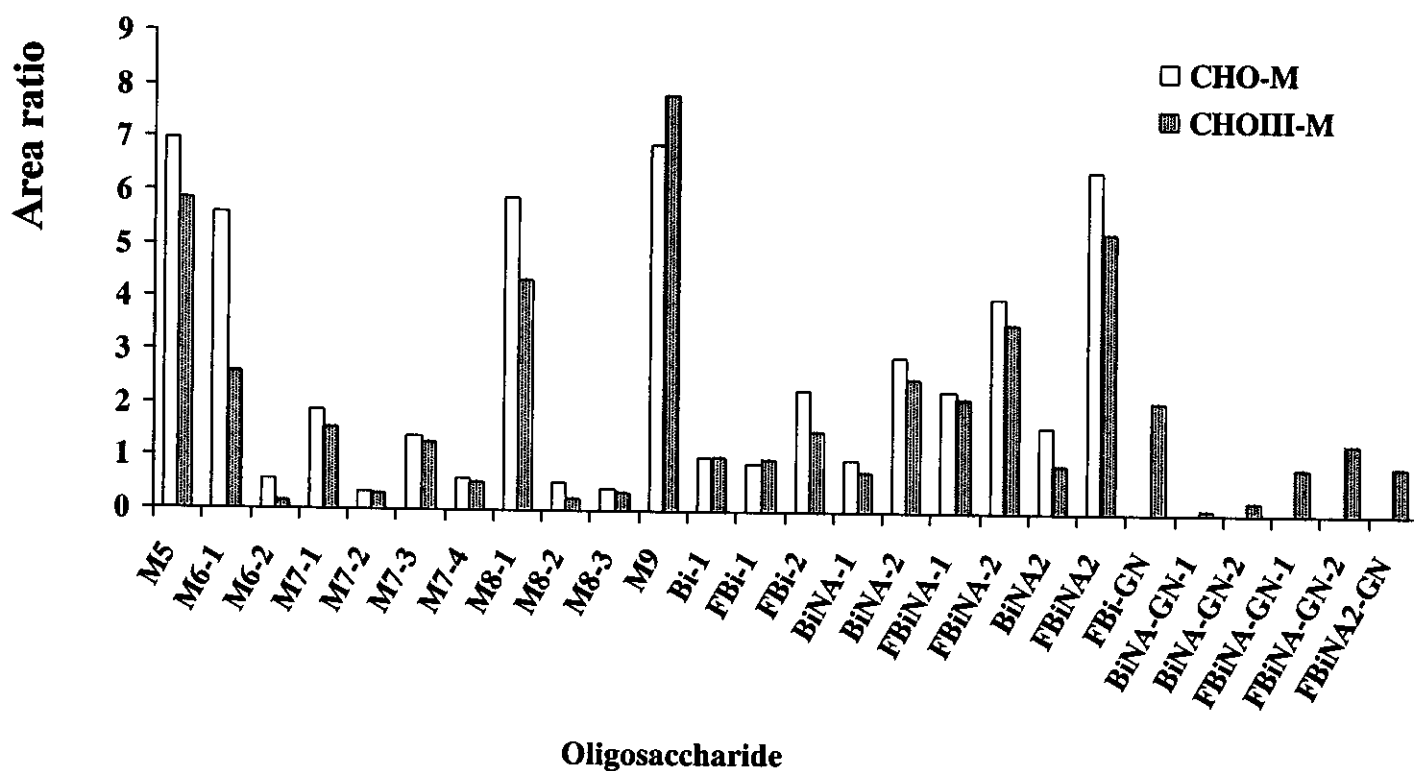
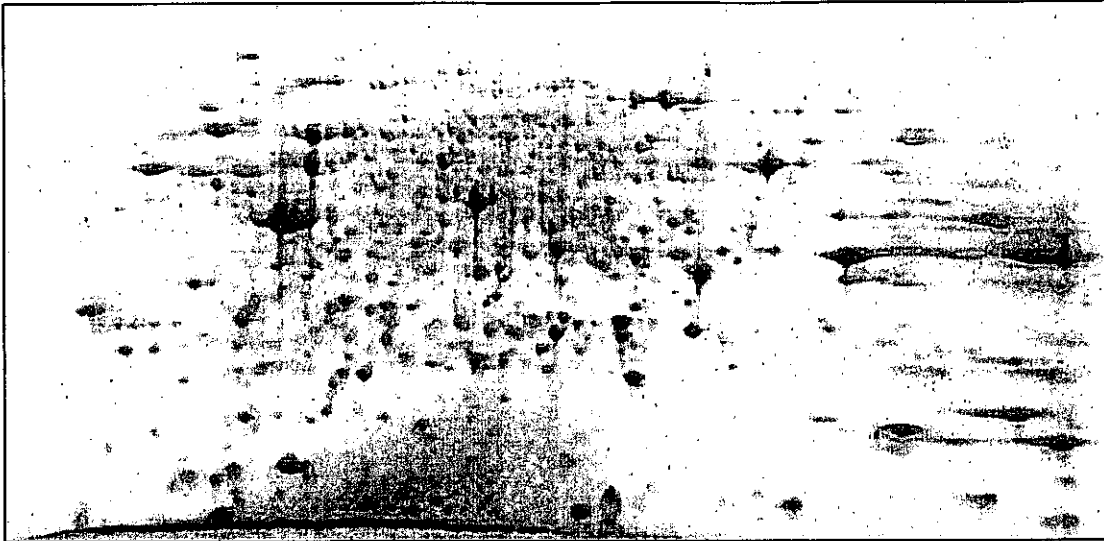


Fig. 19 Peak area ratio of oligosaccharides from CHO and CHOIII membrane

(A) 2D-PAGE



(B) Lectin blot

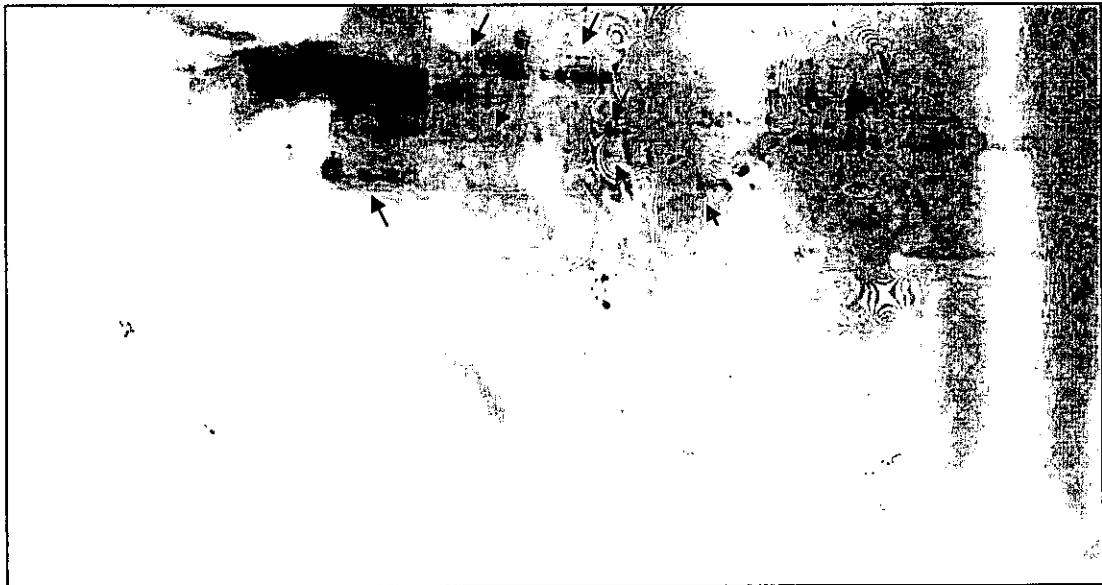
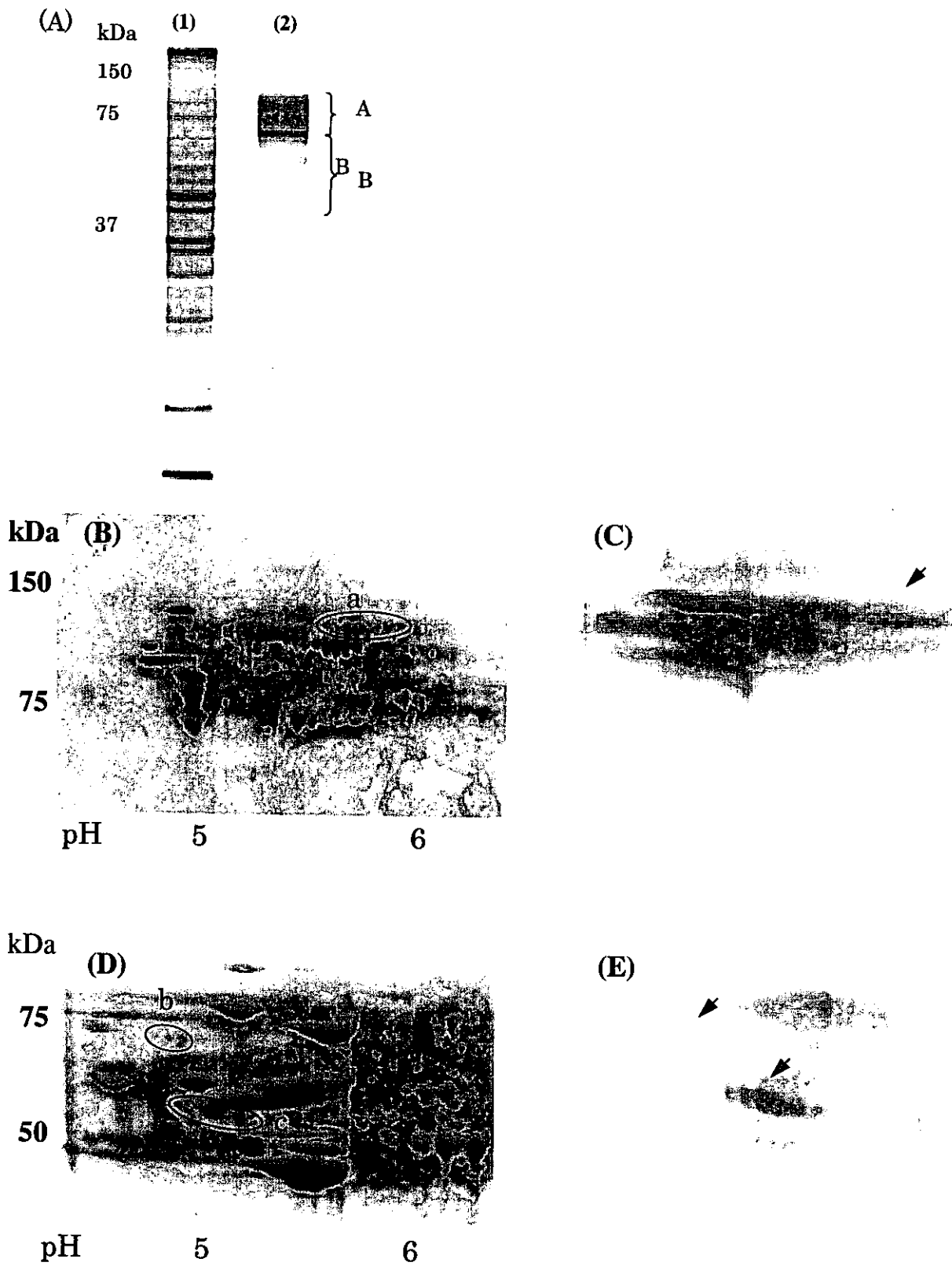


Fig. 20 2D-GE of CHO-III membrane proteins

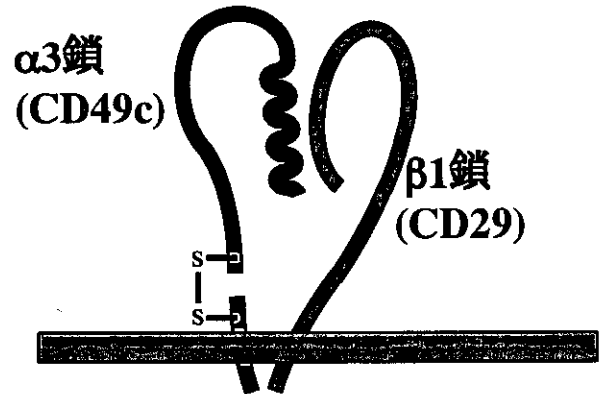
(A) Sypro Orange, (B) Lectin blot



**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



1	mgpgprcapg	dpgwnlgala	lnvaasgrfa	fafnldtrfl	vvkeavnpgs	lfgysvalhr	} Heavy chain (33~872)
61	qterqqryll	lagaprdlsv	adgytNrtga	vykpltalk	ddcermdise	ksdpdhhie	
121	dmwlgvtvas	qgpagrvlc	ahrytqvls	gmedqrrmv	kcyvrgndiq	ldpgddwqy	
181	hnemcnsntd	ylqtgmcqlg	tsggftqntv	yfgapgaynw	kgnsymiqrk	dwdlseysyk	
241	gsedqgnlyi	gytvqvsav	lhptyitvva	gaprhqhnga	vflsqesgg	dkrkvleg	
301	tqvgayfgsa	ialadlnndg	<u>wqdllvgapy</u>	yferkeevgg	avyvfmnqag	tsfpdqpsll	
361	lhgprsafg	isiasigdin	<u>qdgfgdiavg</u>	apfeglgkvy	iyhsssgll	rqpqqivhgd	
421	klglpglstf	gyslsgkmdv	<u>ddnsypdllv</u>	gslsdbivll	rarpvinilq	rtlvarpavl	
481	dpslciptsc	vqvelcfayN	qsagnpsyrr	Nitlaytlea	drdrpprlr	farsqsavfh	
541	gfllmpethe	qtieillmdn	vrdklrpivi	amNyslpirn	pdrkigmr	ldaypvlqqa	
601	qaleNhtevh	fqkecgpdnk	cdsnlqmraa	fvseqlqpls	rlqysrdtkk	lflsiNvnt	
661	psrerageda	heallilevp	palllssvrp	sgtcqaNeti	lcelgnpfr	nqrmelliaf	
721	evigvtlbr	dkaqllqst	sshqdnlqpm	tlilqvdytl	qaslslmthr	lqsffggtvm	
781	geagmktved	vgsplkyefq	vspvgdglaa	lgtlvglew	pyevngkwl	lypteiihs	
841	Neswpcqppg	nlvnpnlil	sdpgdkphsp	qrrrr			
				qldpg	gdqgsppvtl	aaakkakset	} Light chain (876~1066)
901	vltcasgrar	cwlecpipd	tsNvtNvtvk	arvwNstfie	dyrdfrvr	dgwatllfrrt	
961	siptinmeNk	ttwfsvdids	elveelpaei	elwlvvavs	agllllgll	illwkcgffk	
1021	ptryrimpk	yhavrireee	ryppgstlp	tkkhwtswq	irdryy		

Under line : Calcium binding region, N: Glycosylation site

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