

PROTEOMICS

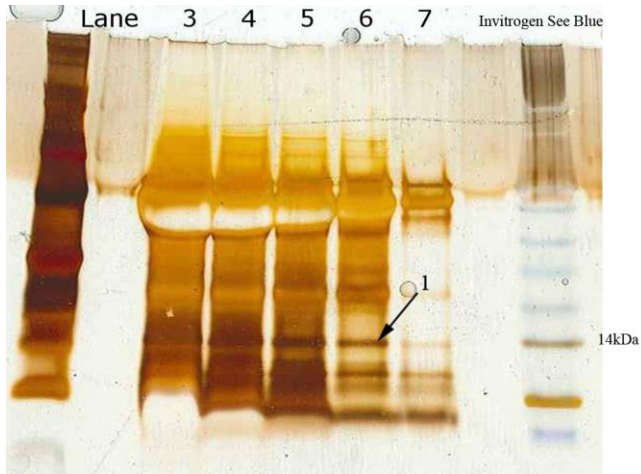
**Supporting Information
for Proteomics – Clinical Applications
DOI 10.1002/prca.201000110**

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**Discovery and initial validation of α 1-B glycoprotein fragmentation as a
differential urinary biomarker in pediatric steroid-resistant nephrotic syndrome**

Protein Identification of the 13.8kDa peak by tandem mass spectrometry.

Band of interest for protein identification



Mascot Search Parameters

Type of search : Sequence Query
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Deamidated (NQ), Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Fragment Mass Tolerance : ± 0.25 Da
Max Missed Cleavages : 2
Instrument type : MALDI-TOF-TOF

Protein hits at $p < 0.005$: [gi|69990](#) alpha-1-B-glycoprotein - human
[gi|219978](#) prealbumin [Homo sapiens]
[gi|28590](#) unnamed protein product [Homo sapiens]
[gi|4504893](#) kininogen-1 isoform 2 [Homo sapiens]

1. [gi|69990](#) Mass: 52479 Score: 273 Queries matched: 3
alpha-1-B-glycoprotein - human

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
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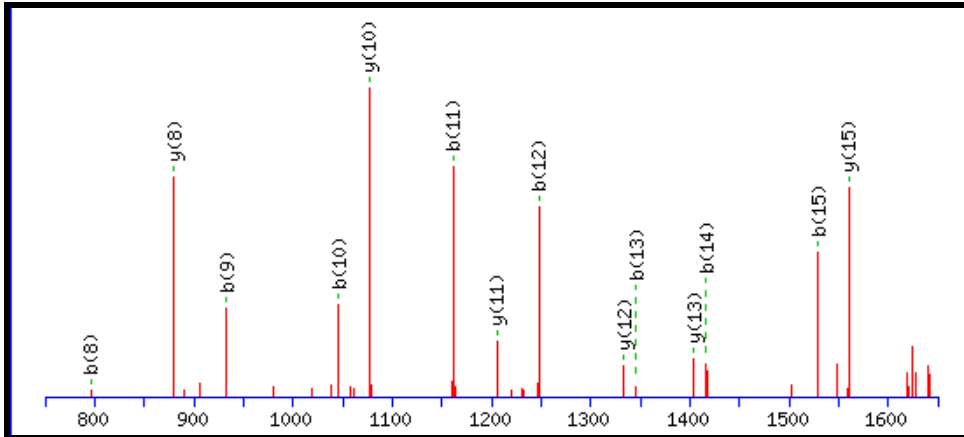
✓	29	1264.6481	1263.6408	1263.6459	-4.03	0	83	2.8e-06	1	R.SGLSTGWTQLSK.L
✓	39	1372.6962	1371.6889	1371.6895	-0.44	0	79	4e-06	1	K.HQFLLTGDTQGR.Y
✓	65	1675.8656	1674.8583	1674.8577	0.38	0	111	3.6e-09	1	K.NGVAQEPVHLDSPAIK.H + Deamidated (NQ)

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1 AIFYETQPSL WAESESLKLP LANVTLTQCA RLETPDFQLF KNGVAQEPVH
51 LDSPAIKHQF LLTGDTQGRY RCRSGLSTGW TQLSKLLELT GPKSLPAPWL
101 SMAPVSWITP GLKTTAVCRG VLRGVTFLLR REGDHEFLEV PEAQEDVEAT
151 FPVHQPGNYS CSYRTDGEGA LSEPSATVTI EELAAPPPPV LMHHGESSQV
201 LHPGNKVTLT CVAPLSGVDF QLRRGEKELL VPRSSTSPDR IFFHLNAVAL
251 GDGGHYTCRY RLHDNQNGWS GDSAPVELIL SDETLPAPEF SPEPESGRAL
301 RLRCLAPLEG ARFALVREDR GGRRVHRFQS PAGTEALFEL HNISVADSAN
351 YSCVYVDLKP PFGGSAPSER LELHVDGPPP RPQLRATWSG AVLAGRDAVL
401 RCEGPIPDVT FELLREGETK AVKTVRTPGA AANLELIFVG PQHAGNYRCR
451 YRSWVPHTFE SELSDPVELL VAES

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MS/MS Profile for 1675.9

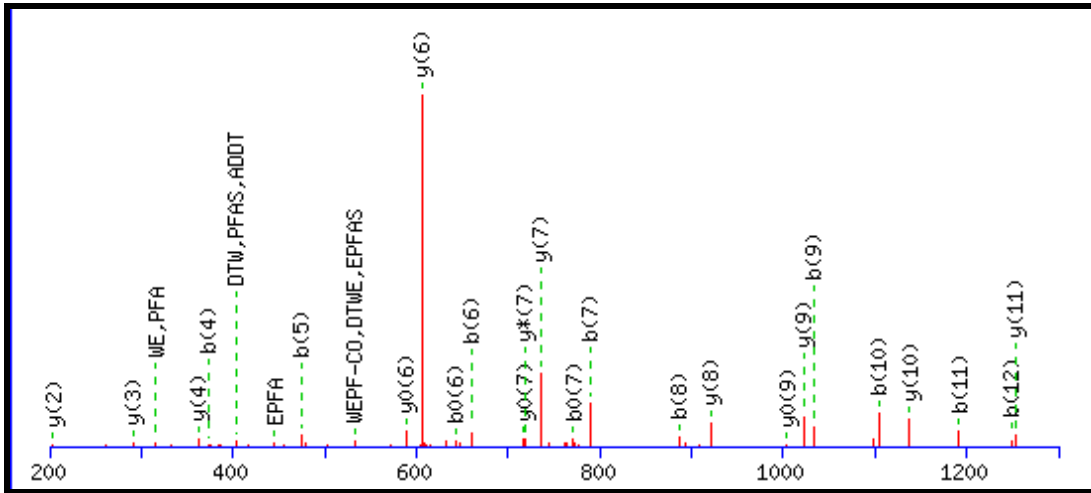


2. [gi|219978](#) Mass: 16023 Score: 175 Queries matched: 2
 prealbumin [Homo sapiens]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 41	1394.6208	1393.6135	1393.6150	-1.06	0	81	1.5e-06	1	K.AADDTWEPFASGK.T
<input checked="" type="checkbox"/> 50	1522.7173	1521.7100	1521.7100	0.04	1	94	1.2e-07	1	R.KAADDTWEPFASGK.T

1 MASHRLLLLC LAGLVFVSEA GPTGTGESKC PLMVKVLDAV RGSPAINVAM
 51 HVFR**KAADDT WEPFASGK**Ts ESGELHGLTT EEEFVEGIYK VEIDTKSYWK
 101 ALGISPFHEH AEVVFTANDS GPRRYTIAAL LSPYSYSTTA VVTNPKE

MS/MS Profile for 1394.6



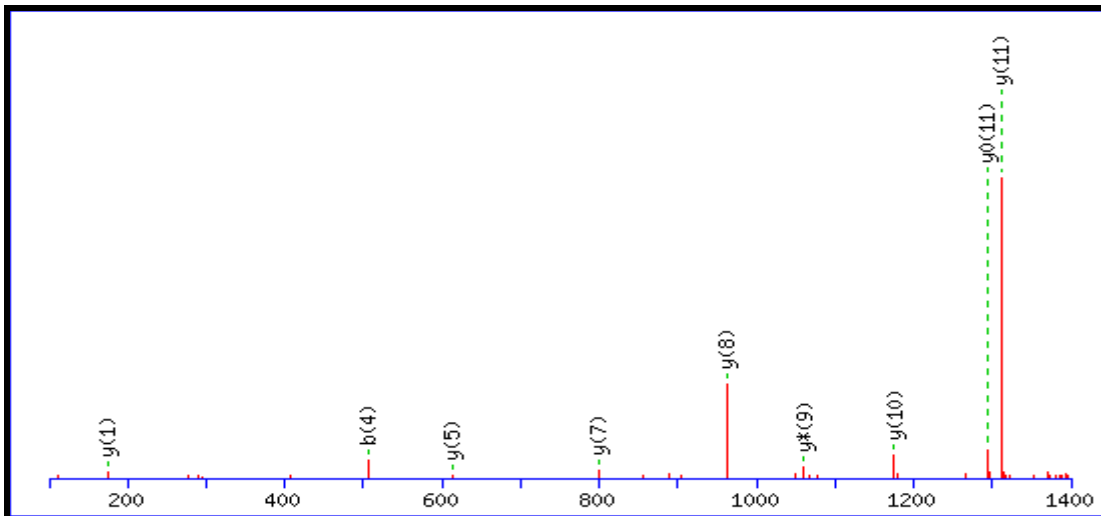
3. [gi|28592](#) Mass: 71316 Score: 109 Queries matched: 4
 serum albumin [Homo sapiens]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 1	927.4958	926.4885	926.4861	2.58	0	31	0.13	1	K.YLYE I AR.R
<input checked="" type="checkbox"/> 45	1467.8420	1466.8347	1466.8358	-0.71	1	38	0.023	1	R.RHPDYSV V LLLR.L
<input checked="" type="checkbox"/> 57	1623.7927	1622.7854	1622.7803	3.16	0	40	0.036	1	K.DVFLGMFLYE A AR.R
<input checked="" type="checkbox"/> 60	1639.7795	1638.7722	1638.7752	-1.82	0	(13)	17	1	K.DVFLGMFLYE A AR.R + Oxidation (M)

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1 MKWVTFISLL FLFSSAYSRG VFRRDAHKSE VAHRFKDLGE ENFKALVLIA
51 FAQYLQQCPF EDHVKLVNEV TEFAKTCVAD ESAENC DKSL HTLFGDKLCT
101 VATLRETYGE MADCCAQEP ERNECFLQHK DDNP NL PRLV RPEVDVMCTA
151 FHDNEETFLK KYLYEIARRH PYFYAPELLF FAKRYKAAFT ECCQAADKAA
201 CLLPKLDELR DEGKASSAQ RLKCASLQKF GERAFKAWAV ARLSQRFPKA
251 EFAEVSKLVT DLTKVHTECC HGDLLECADD RADLAKYICE NQDSISSKLK
301 ECCEKPLLEK SHCIAEVEND EMPADLPSLA ADFVESKDVC KNYAEAKDVF
351 LGMFLYEAAR RHPDYSVVLL LRLAKTYETT LEKCCAAADP HECYAKVFDE
401 FKPLVEEPQN LIKQNCELFK QLGEYKFQNA LLVRYTKKVP QVSTPTLVEV
451 SRNLGKVGSK CCKHPEAKRM PCAEDYLSVV LNQLCVLHEK TPVSDRVTKC
501 CTESLVNRRP CFSALEVDET YVPKEFNAET FTFHADICTL SEKERQIKKQ
551 TALVELVKHK PKATKEQLKA VMDDFAAFVE KCCKADDKET CFAEEGKKLV
601 AASQAALGL
  
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MS/MS Profile for 1467.8



4. [gi|4504893](#) Mass: 48936 Score: 102 Queries matched: 2
 kininogen-1 isoform 2 [Homo sapiens]

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 48	1514.6633	1513.6560	1513.6507	3.50	1	37	0.028	1	K.TWQDCEYKDAAK.A
<input checked="" type="checkbox"/> 70	1875.8988	1874.8915	1874.8547	19.6	0	65	0.00012	1	K.YNSQNSNNQFVLYR.I + Deamidated (NQ)

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1 MKLITILFLC SRLLLSLTQE SQSEEIDCND KDLFKAVDAA LKKYNSQNS
51 NNQFVLYRIT EATKTVGSDT FYSFKYEIKE GDCPVQSGKT WQDCEYKDA
101 KAATGECTAT VGKRSSTKFS VATQTCQITP AEGPVVTAQY DCLGCVHPIS
151 TQSPDLEPIL RHGIQYFNNN TQHSSLFMLN EVKRAQRQVV AGLNFRITYS
201 IVQTNCSEKEN FLFLTPDCKS LWNGDTGECT DNAYIDIQLR IASFSQNCDI
251 YPGKDFVQPP TKICVGCPRD IPTNSPELEE TLTHTITKLN AENNATFYFK
301 IDNVKKARVQ VVAGKKYFID FVARETTCSK ESNEELTESC ETKKLQSLD
351 CNAEVYVVPW EKKIYPTVNC QPLGMISLMK RPPGFSPFRS SRIGEIKEET
401 TSHLRSCCEYK GRPPKAGAEP ASEREVS
  
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MS/MS profile for 1875.9

