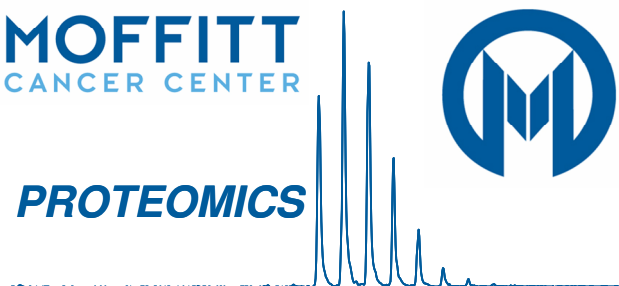


Peptide Synthesis Report

MOFFITT
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PROTEOMICS



Project Title: Internal standard for Nuclear factor NF-kappa-B p100 subunit (NFKB2_HUMAN)

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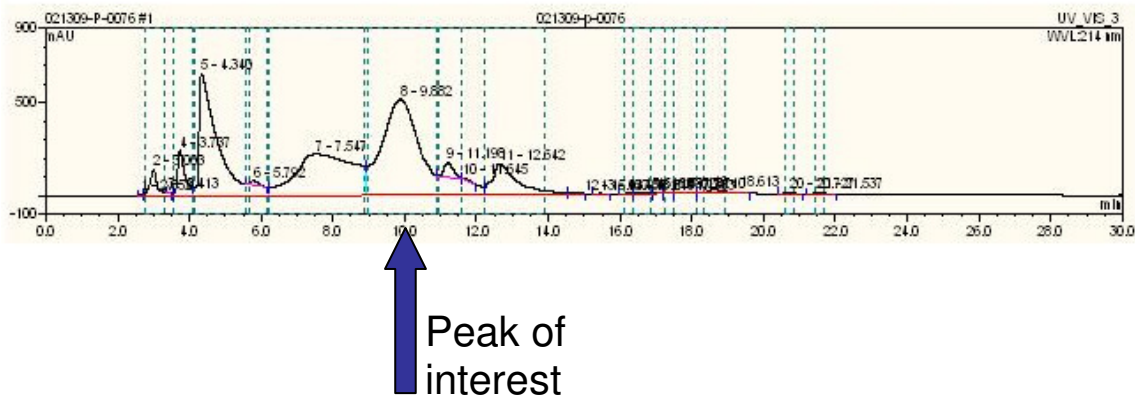
Design and Synthesis:

MPS#	Peptide Sequence	Residues	Modification	MWT Monoisotopic
p-0076	DSGEEAAEPSA P SR	415-428	Stable Isotope P U-13C5, 15N	1407.601

Solid state peptide synthesis (Symphony, Protein Technologies, Tucson, AZ) is used to make standards at the 25 micromole scale using standard Fmoc chemistry. Briefly, Wang resin (Novabiochem, Germany) serves as the support to initiate peptide formation. Activator solvents for the amino acid coupling consist of 150 mM N-Methylmorpholine in N-methylpyrrolidone (NMP) with 100 mM of O-benzotriazol-1-yl-N,N,N',N'-tetramethyluronium hexafluorophosphate (HBTU). Deprotection between couplings is achieved using 20% piperidine in NMP with 2% 1,8-diazabicyclo [5,4,0] undec-7-ene. Upon sequence completion, cleavage from the resin is performed using 95% TFA, 2.5% water, and 2.5% triisopropylsilane. Peptides are then precipitated in ice cold ethyl ether, washed twice, and resuspended in water prior to lyophilization.

Semi-preparative HPLC:

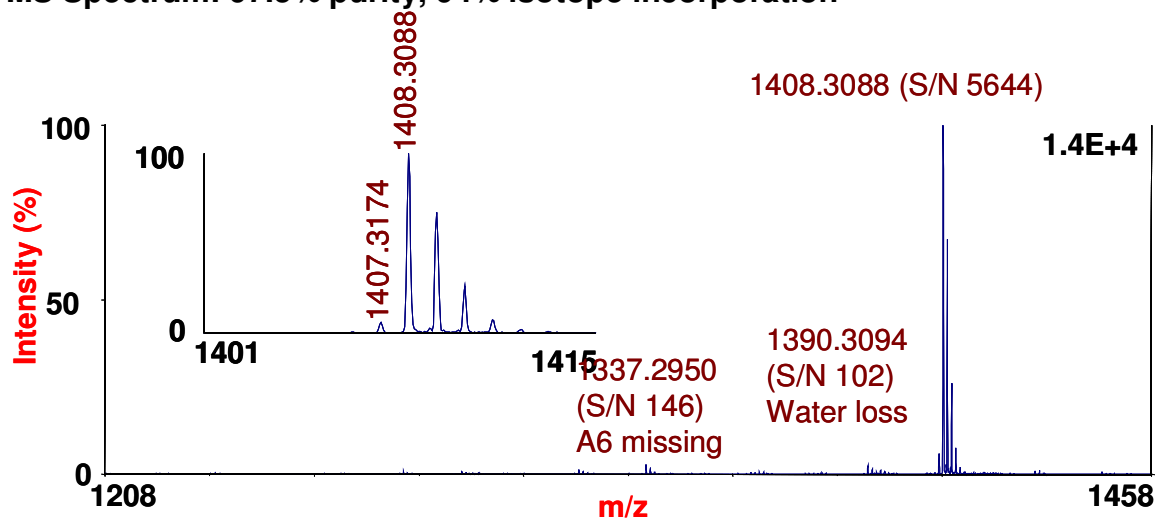
HPLC purification is performed on a semi-preparative system (U3000, Dionex, Sunnyvale, CA) using a C18 reverse phase column (TP 238, 250 x 10mm, 10-15 μ m particles, Grace Vydac, Deerfield, IL). Twenty minute gradients are run from 5% to 60% B solvent (A: 2% acetonitrile/0.1% formic acid; B: 100% acetonitrile/0.1% formic acid). Eluted peptides are measured at 214 nanometer wavelength and collected with automatic triggering (Foxy Jr, ISCO).



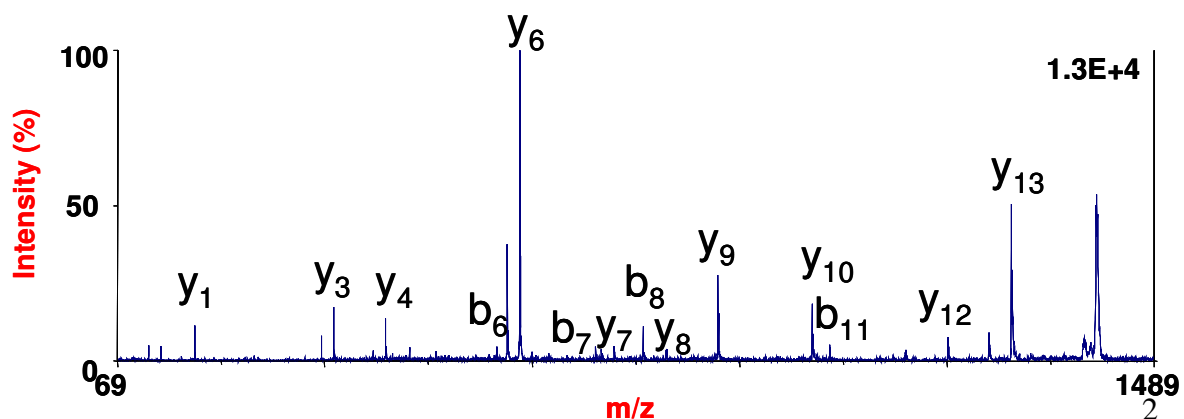
MALDI:

Purified peptides are analyzed with MALDI MS to verify purity and sequenced with MS/MS (4700, Applied Biosystems, Framingham, MA). Peptides in 2% ACN with 0.1% formic acid are mixed 1:1 with α -cyano-4-hydroxycinnamic acid (10 mg/ml) in 50% ACN and deposited in 1 microliter aliquots on the MALDI target.

MS Spectrum: 97.5% purity, 94% isotope incorporation



MS/MS spectrum:



Fragment Ion table with Identified peaks:

SEQ	#	B	Y	#
D	1	116.0348	1408.609	14
S	2	203.0668	1293.582	13
G	3	260.0883	1206.55	12
E	4	389.1309	1149.528	11
E	5	518.1735	1020.486	10
A	6	589.2106	891.4431	9
A	7	660.2477	820.406	8
E	8	789.2903	749.3688	7
P	9	886.3431	620.3262	6
S	10	973.3751	523.2735	5
A	11	1044.412	436.2415	4
P*				
Stable Isotope	12	1147.465	365.2043	3
S	13	1234.497	262.1516	2
R	14	1390.598	175.1196	1