Peptide Synthesis Report

MOFFITT CANCER CENTER

PROTEOMICS

Project Title: Internal standard for Axis inhibition protein 1 (AXN1_HUMAN)

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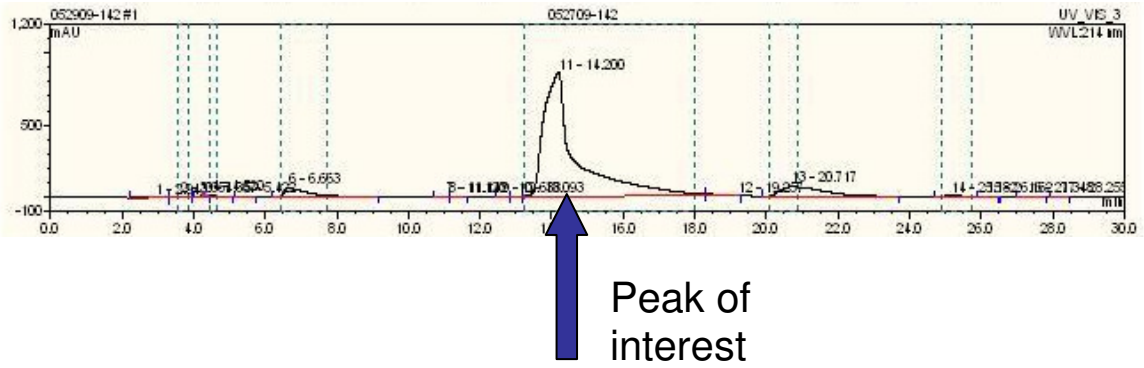
Design and Synthesis:

MPS#	Peptide Sequence	Residues	Modification	MWT Monoisotopic
p-0142	LLLETAAPR	271-279	Stable Isotope P U-13C5, 15N	988.5812

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:

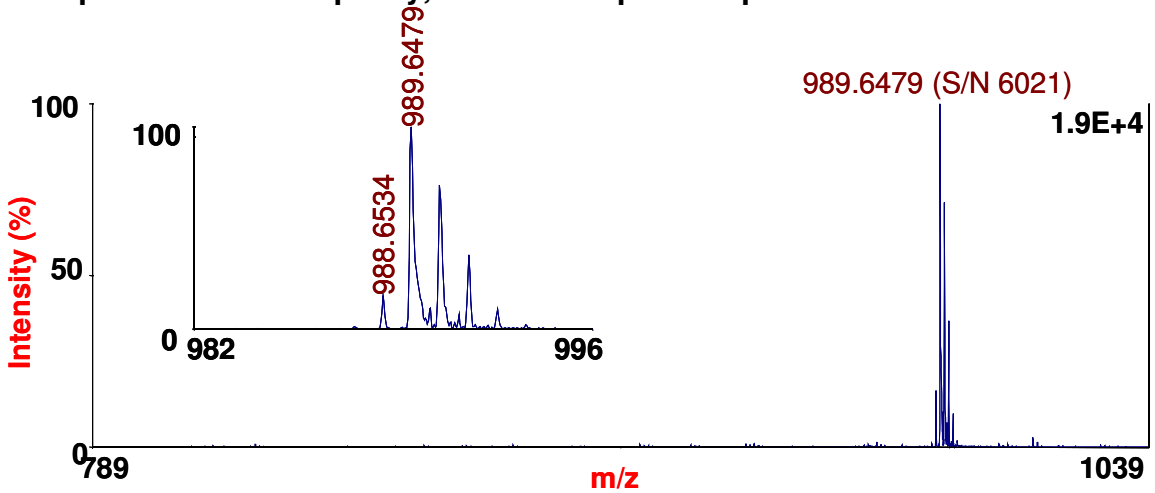
HPLC purification is performed on a semi-preparative system (U3000, Dionex, Sunnyvale, CA) using a C18 reverse phase column (TP 238, 250 x 10mm, 10-15 μm particles, Grace Vydac, Deerfield, IL). Twenty minute gradients are run from 5% to 60% B solvent (A: 2% acetonitrile/0.1% formic acid; B: 100% acetonitrile/0.1%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



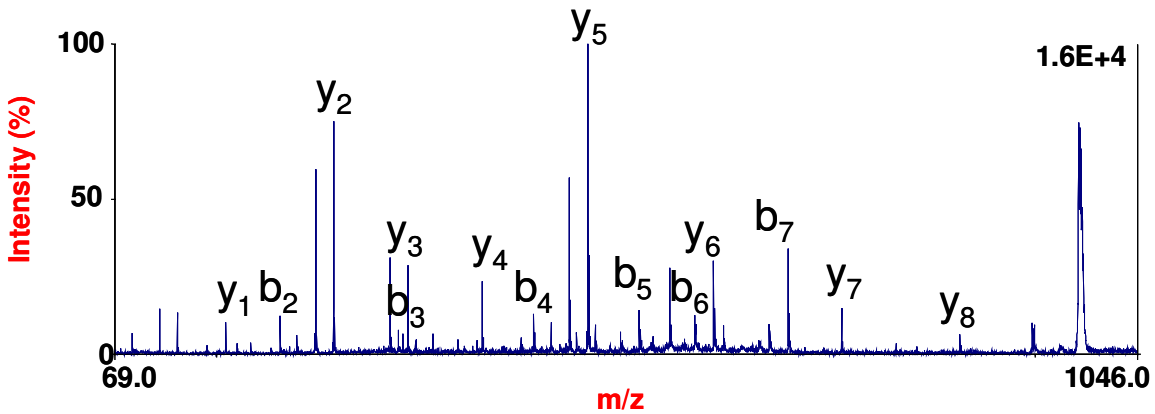
MALDI:

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 a-cyano-4-hydroxycinnamic acid (10 mg/ml) in 50% ACN and deposited in 1 microliter aliquots on the MALDI target.

MS Spectrum: ~100% purity, 86.9% isotope incorporation



MS/MS spectrum:



Fragment Ion table with Identified peaks:

SEQ	#	B	Y	#
L	1	114.0919	989.589	9
L	2	227.176	876.5049	8
L	3	340.2601	763.4209	7
E	4	469.3027	650.3368	6
T	5	570.3503	521.2942	5
A	6	641.3875	420.2465	4
A	7	712.4246	349.2094	3
P* Stable Isotope	8	815.4773	278.1723	2
R	9	971.5784	175.1196	1