## Affinity purification of ubiquitinated proteins and peptides from rat brain extracts



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## INTRODUCTION

Post-translational modifications allow dynamic regulation of proteins in the nerve terminal that can respond quickly to physiological and non-physiological stimuli.

Protein ubiquitination plays an important role in many aspects of neuronal function including regulation of endocytosis, signaling, gene expression and protein degradation by the proteasome.

Ubiquitin binding domains (UBD's) are found in many proteins and have differing specificity for mono- and poly ubiquitin

After trypsin digestion, ubiquitinated peptides retain the two C-terminal glycine residues attached by a peptide bond. A peptide mass increase of 114 Da was used to assign specific-sites of protein

✤ Ubiquitin Branch Motif (K-ε-GG) antibody can be used to selectively enrich for ubiquitinated peptides after trypsin digestion (Kim, W., et al, 2011 and Lee, K.A., et al, 2011)

We are interested in purifying ubiquitinated proteins from brain tissue with the aim to purify ubiquitinated proteins after exposure to drugs of abuse

## **METHODS**

Rats were sacrificed either by rapid decapitation or by Focused Microwave Irradiation (FMI) according to Yale University IACUC approved methods. Biochemical subcellular fractionation of rat brain tissue was performed as previously described (Hallett *et al* 2008). Primary cortical cultures were prepared from cortices at E18 and cultured using standard methods for DIV14-21.

Enrichment of ubiquitinated proteins from protein extracts. Protein extracts were incubated with Ubiquitin Binding Domains (UBD's) to purify ubiquitinated proteins. GST-S5a, GST-Ataxin-3-UIM, Dsk2-UBA (Biomol),Tubes 1 and Tubes 2 (LifeSciences) were used in the study. The bound proteins were washed and eluted using SDS buffer and analyzed by SDS-PAGE. Proteins were transferred to nitrocellulose membrane for western blotting, incubated with primary antibodies and scanned using the LICOR system. The remainder of the eluted protein was analyzed by SDS-PAGE, proteins detected using Coomassie blue protein gel stain and gel bands cut out and subjected to trypsin digestion and LC-MSMS.

**Enrichment of ubiquitinated peptides from protein extracts.** Protein Extracts were digested with Lys-C (3h, RT), diluted and then digested with trypsin (16h, 37° C). Peptides were purified using a Sep-Pak cartridge and freeze-dried overnight. The Ubiquitin Branch Motif (K-ε-GG) Immunoaffinity Beads (Cell Signaling Technology cs#1990) was used to immunoprecipitate ubiquitinated peptides from the peptide mixture. Beads were washed and bound peptides eluted using 0.15% TFA.

Mass spectrometry. Tryptic peptides were separated by the nanoACQUITY Ultra Performance LC and analyzed on the Thermo linear lon trap (LTQ)- Orbitrap XL mass spectrometer (Thermo-Electron Corp) at the Keck laboratories. The MS data was processed and files searched against the SWISSPROT (rat) database using the MASCOT server. The search was performed using the search parameters choosing trypsin with 3 miss-cleavages with variable modifications Propionamide (C), Oxidation (M), Deamidated (NQ) and GlyGly (K). Ubiquitinated petides were identified by mass spextrometry by 114 Da mass increase (GlyGly (K) left over after trypsin digestion.



PEP_SCORE	PEP_EXPECT	Modified lysine(s)	PEPTIDE_SEQUENCE	PROTEIN_ID	PROTEIN_NAME
26.21	2 305-07	¥61	K DSY//GDEAOS KR G + Gh/Gh/ (K)	ACTR PAT	Artin outcolarmic
24.22	0.1	¥390	R UDGESSEAL WAEK R + GLIGL/MI	SALDIA PAT	AASD TA
89.45	1.205-08	K50	R NI I SVAVENUVGAR R + GUGU (K)	14337 RAT	14.3.3 motein zeta/delta
01.26	3 406.09	VE40	K WANTEGOESCACTANDUM VEDESD ( + CLUSH, IV)	MANG DAT	Muslin accordated abconcotele
94.10	1.405-02	X60	K TRECEDOSENTEESETCACKINDER & Chick (K)	TOALA BAT	Tubulo aloba 14
Victores and	Phoenbotorer	NOU	K. Hoddobarni Fractond Kriterik + diyan (k)	10ACD4_AD41	rubum alpha-19
24.04	0.18	1/21	K ELDOWIEDINECKOLSESOWKS & GIUGH IN	PP7AA PAT	PP2A catabatic subunit alaba
87.90	6.806.09	¥21	K ELDOWNEDI NECKOLNEND/R T & CHCH (K)	PP2AB BAT	0034 catalytic subunit bats
61.65	0.0000046	×146		KCC3A BAT	CALIFY and unit alloha
63.99	0.0003	K140		KCC2A DAT	CANNEL SUDDING alpha
94.52	1 105-07	N220	K DEDETITIVE ETUMP S + ELICITIVE	CALM PAT	Calmodulia
76.28	0.0000011	122 - 121	K EARSIED KOGOGTITT KEIGTIGAR S. + 3 (E.C. IV)	CALM RAT	Calmodulin
70.20	0.000	K214	R THE COTON ADDITING A CHICK IN	KADCA RAT	CAND dependent protein kinaro catal dis subunit alaba
33.4	0.021	8,2.14	R. IWIECOIPETDPEILSKOTAKA + Olyoly (k)	MAPLA MAI	cover-dependent protein kinase catalytic subunit alpha
synaptic pro	ceins -		A 11 (A 11))))))))))	INCLO DAT	
45.24	0.10	8224	K LLUTHUTKEGENIKL + GIJUTY (K)	IRKIU RAI	A IP-sensitive inward rectifier potassium channel
21.59	0.19	N23		STUB RAT	Beta-synuclein
52.04	0.00014	1.38	K.AEGAGTEEEGTQ KESEPQAAADATEVK.E * GIYGIY (K)	BASP1 RAT	Brain acid soluble protein 1
69.01	0.0000024	K235	K.IIDGGAAQKDGKL * GYGIY (K)	DLG2_RAT	Disks large homolog 2
68.17	0.0000034	K258	R.SOPYHATTGPLSPSKOCGSPK.Y + GlyGly (K)	CKA1_RAT	Gap junction alpha-1
00.85	0.000012	K303	IN THE CASE OF WARTS ALCONE, M + GROUP (K)	CARL RAT	Cap Junction alpha-1
37.71	0.0041	N340	K KYAAOHEEUPOAYDQAFSSKA * Giyary (k)	CAAL RAT	Cap Junction alpha-1
22.23	0.14	N330	K. FETGILEHOK. V + GIYGIY (K)	COAL HOAT	Gap Junction alpha-1
94.16	9.60E-09	K13	K.VTFNSALAQKEAK.K + GlyGly (K)	ITM28_RAT	Integral membrane protein 28
43.51	0.0019	K30	K.GEAAAERPGEAAVASSPSKANGQENGHVK.V + 2 Deamidated (NQ); GlyGly (K)	MARCS_RAT	Myristoylated alanine-rich C-kinase substrate
23.31	0.19	K11	K. TAAKGEAAAERYGEAAVASSYSK.A + GIYGIY (K)	MARLS RAT	Myristoylated alanine-rich C-kinase substrate
40.12	0.002	K375	K.RPDEVPDAGPMKTNSTNNHK.D + 2 Deamidated (NQ); GlyGly (K)	NPTN_RAT	Neuroplastin
47,08	0.00021	K1700	K.APAAPKTPSK.A + GlyGly (K)	NRX2A_RAT	Neurexin-2-alpha
60,4	0.00001	K148	K.KLTPITYPQGLAMAKEIGAVK.Y + GlyGly (K)	RAC1_RAT	Ras-related C3 botulinum toxin substrate
54.29	0.00023	K595	R.LQVMIQPSEDIVRPENGPEQPQAGSSASKEAYL- + GlyGly (K)	SCGA1_RAT	Sodium- and chloride-dependent GABA transporter
47.9	0.00026	1605	R.AAVPDAVGKCR.S + GlyGly (K)	AT1A1_RAT	Sodium/potassium-transporting ATPase subunit alpha-1
37.08	0.0036	K661	R.DAKACVVHGSDLK.D + GlyGly (K)	AT1A1_RAT	Sodium/potassium-transporting ATPase subunit alpha-1
29.51	0.014	K9	R.D.KYEPAAVSEHGOK.K + GlyGly (K)	AT1A1 RAT	Sodium/potassium-transporting ATPase subunit alpha-1
45.67	0.00095	K40	R.MLQLVEESKDAGIR.T + GIVGIV (K)	SNP25 RAT	Synaptosomal-associated protein 25
25.31	0.036	1096	K.LKSSDAYK.K + GlyGly (K)	SNP25_RAT	Synaptosomal-associated protein 25
63.95	0.000013	K70	K.HSAILASPNPDEKTK.E + GIVGIV (K)	STX1A_RAT	Syntaxin-1A
42.16	0.0016	K104	K.NAINMKDVK.D + GlyGly (K)	SYT1_RAT	Synaptotagmin-1
27.36	0.029	K111	K.DLGKTMK.D + GlyGly (K)	SYT1_RAT	Synaptotagmin-1
21.05	0.14	K267	R.DLQSAEKEEQEK.L + GlyGly (K)	SYT1_RAT	Synaptotapmin 1
51.36	0.00018	K369	K.IGKNDAIGK.V + GlyGly (K)	SYT1_RAT	Synaptotagmin-1
103.23	2.20E-09	K47	R. DOKLSELDORADALQAGASQFETSAAK.L + GIVGIV (K)	VAMP3 RAT	Vesicle-associated membrane protein 3
74.43	0.0000018	K70	K LSELDDRADALQAGASQFETSAAKLK R + GIVGIV (K)	VAMP3 RAT	Vesicle-associated membrane protein 3
41.82	0.0024	K70	R ADALDAGASOFETSAAKLK R + GIVGIV (K)	VAMP3 RAT	Vesicle-associated membrane protein 3

\* Ongoing studies examining activity-dependent changes

in protein ubiquitination after exposure to drugs of abuse

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