

Exploring Exercise- and Context-Induced Peptide Changes in Mice by Quantitative Mass Spectrometry

Sarah E. Dowd^{†‡}, Martina L. Mustroph[‡], Elena V. Romanova[†], Bruce R. Southey[§], Heinrich Pinardo[¶], Justin S. Rhodes^{⊥¶}, Jonathan V. Sweedler^{†¶*}

[†]Department of Chemistry, [‡]Neuroscience Program, [¶]Beckman Institute, [§]Department of Animal Sciences, and [⊥]Department of Psychology, University of Illinois at Urbana–Champaign, Urbana, Illinois 61801, United States

[‡]Both authors contributed equally to this work.

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NOTE: The following are provided as separate Excel files:

Table S2. Peptides identified from the dentate gyrus extract using succinic anhydride labeling and not exhibiting a significant level change in response to exercise.

Table S3. Peptides identified from the amygdala extract using succinic anhydride labeling and not exhibiting a significant level change from exposure to a cocaine-associated context.

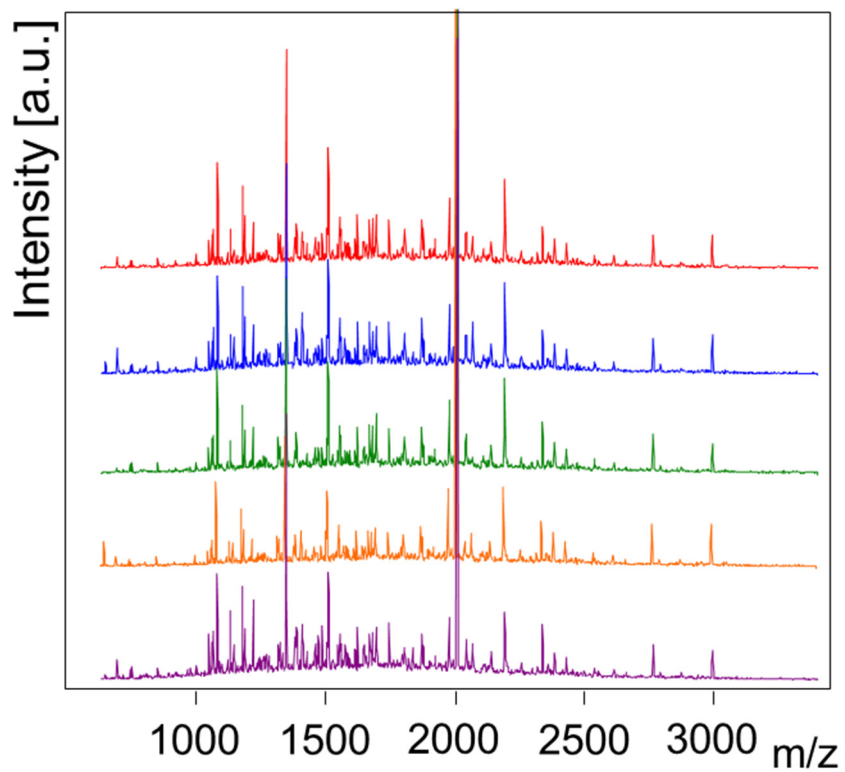


Figure S1: Representative MALDI MS spectra for the peptide extract collected from an individual animal. Each spectrum represents the technical replicates from 5 spots generated with the peptide extract spiked with the internal standard (MW 2960 Da) co-crystallized with α -cyano-4-hydroxycinnamic acid matrix.

Table S1. Identification details for peptides differentially detected in either the amygdala (Am) or dentate gyrus (DG) by stable isotopic labeling.

Protein Accession	Protein name	Peptide	-10lgP	Mass	ppm	Start	End	PTM	Brain localization
A8DUK4	A8DUK4_MOUSE	K.V(+100.07)VAGVAAALAHK(+100.07)YH	54.89	1605.923	-63	134	147	SA	Am
A8DUK4	A8DUK4_MOUSE	K.V(+104.09)VAGVAAALAHK(+104.09)YH	44.55	1613.963	-69.5	134	147	HAS	Am
F6ZIA4	F6ZIA4_MOUSE	A(+42.01)SQK(+100.02)RPSQRSK(+100.02).Y	19.48	1513.748	-3	1	11	SA	DG
F6ZIA4	F6ZIA4_MOUSE	M.D(+100.02)HARHGFLPRHRDTGILD.S	47	2212.089	-5.1	20	37	SA	DG
F6ZIA4	F6ZIA4_MOUSE	G.S(+104.04)LPQK(+104.04)SQHGRTQDENPVVH.F	50.01	2364.155	-4.5	67	85	SA	DG
F6ZIA4	F6ZIA4_MOUSE	G.S(+100.02)LPQK(+100.02)SQHGRTQDENPVVHF.F	45.84	2503.173	-2.6	67	86	SA	DG
P01942	HBA_MOUSE	T.L(+100.07)ASHHPADFTPAVH.A	90.48	1598.802	-31.9	110	123	SA	Am
P01942	HBA_MOUSE	T.L(+104.09)ASHHPADFTPAVH.A	87.33	1602.822	-28.4	110	123	HAS	Am
P01942	HBA_MOUSE	L.L(+100.07)VTLASHHPADFTPAVH.A	90.01	1912.002	-25	107	123	SA	Am
P01942	HBA_MOUSE	L.L(+104.09)VTLASHHPADFTPAVH.A	85.58	1916.022	-23.1	107	123	HAS	Am
P01942	HBA_MOUSE	L.L(+104.09)VTLASHHPADFTPAVHASLDK(+104.09).F	83.96	2534.387	-35.8	107	128	HAS	Am
P04370	MBP_MOUSE	R.H(+100.02)GFLPRHRDTG.I	17.29	1391.669	-5.1	158	168	SA	DG
P04370	MBP_MOUSE	M.A(+42.01)SQK(+100.02)RPSQRSK(+100.02).Y	19.48	1513.748	-3	135	145	SA	DG
P60710	ACTB_MOUSE	G.F(+100.07)AGDDAPRAVFPSPVGRPRHQG.V	79.67	2449.279	-38.5	21	42	SA	Am
P63260	ACTG_MOUSE	L.R(+100.02)VAPEEHPVL.L	40.82	1245.635	-4.2	95	104	SA	DG

(-10lgP) - indicates the statistical significance of the peptide-spectrum match; all included scores are above the threshold determined by FDR of 5%

Mass - theoretical monoisotopic mass of a peptide

ppm - parts per million

Start/End - indicates the numerical position of the first and last amino acid of the peptide on the corresponding protein sequence

SA - succinic anhydride

HSA - heavy succinic anhydride