Yale/NIDA Neuroproteomics Center Newsletter

(Established 8/23/2004/Supported by NIH/NIDA Grant DA018343) Sept., 2020

Welcome to our Center's first newsletter since our successful competing grant application. Highlights of this issue include a reminder about the approaching 10/1/2020 deadline for submitting pilot project grant applications and announcement of Grant Year 15 Pilot Project Grant Awardees, spotlight on a new technology available from the Biophysics Section of the Discovery Proteomics Core, announcement of three new Center Investigators, the final table of contents from the Proteomes Special Issue on Neuroproteomics, recent Center publications and much more! Finally, we would like to add a farewell and thank you to Rashaun Wilson who left the Targeted Proteomics Core to take an exciting position in industry. We certainly wish her well in her new position.

Pilot Projects Grants Opportunity

The Center is delighted to announce that four Pilot Project grants were awarded in Grant Year 15 (**Table 1** below) and that applications are now being accepted for Pilot Projects for Grant Year 16. The goals of this program are to encourage young investigators in our Center's laboratories to embark on careers in substance abuse research, disseminate the Center's core technologies to researchers investigating the neurobiology of addiction who are not yet using neuroproteomics technologies, and to expand the technical abilities of the Center. Pilot Grants provide short term funding to obtain preliminary data so applicants can apply for longer term grant support. These awards provide $7,500 D.C. to help pay for the cost of preparing samples for analysis in the Center's Cores and free access to all of the Center's Cores. Applications are accepted from investigators and their Graduate Students, Postdoctoral Fellows and higher level research staff who are: 1) members of the Yale/NIDA Neuroproteomics Center, 2) non-members of the Center who are expert in substance abuse with interests in initiating research in neuroproteomics, and 3) non-members of the Center with expertise in cellular and molecular aspects of neuronal signaling with interests in initiating neuroproteomics research. Awards are from one - two years for research that is directly related to the Center's theme of the "Proteomics of Altered Signaling in Addiction" and that propose to apply existing technologies from the Cores or to develop new technologies. Awards to non-Center investigators will be accompanied by Center membership for the term of the award. Priority will be given to new projects that are related to our Center's theme, to collaborative projects involving multiple investigators, and to Technology Development projects. The receipt deadline for Grant Year 16 applications is Thursday, October 1, 2020. Please contact the Director of the Pilot Projects Core, Dr. Marina Picciotto (marina.picciotto@yale.edu), to ensure that new projects and potential pilot project proposals qualify for Center support. Additional information is here: https://medicine.yale.edu/keck/nida/pilot_projects/

Spotlight on a New Technology

Probing Interactions of GPCRs in Lipid Environments Using Surface Plasmon Resonance

The Biophysics Section of the Discovery Proteomics Core has implemented a new experimental platform that allows label-free affinity quantitation of interactions between ligands and transmembrane proteins maintained in a lipid environment. The approach combines nanodisc (ND) purification of transmembrane proteins with surface plasmon resonance (SPR). The transmembrane protein purified in NDs is captured on a Ni^{2+}-NTA (NTA: nitrilotriacetic acid) sensor chip by His-tags bound to the membrane scaffold protein (MSP) that stabilizes the ND via an NTA-chelated nickel atom. The approach was evaluated in a collaborative study with Dr. Elsa Yan (Yale U.) by analyzing interactions between parathyroid hormone 1 receptor (PTH1R) family B GPCR with a truncated native ligand, parathyroid hormone (PTH; 1-34). PTH1R was first purified in NDs in the Yan Lab and then analyzed using Size Exclusion Chromatography/Laser Light Scattering (SEC/MALS) by the Biophysics Section. The purified assembly was determined to be an oligomer of ~220 kDa, consisting of ~130 kDa of polypeptide that is associated with ~90 kDa of lipids. The molar mass of the polypeptide is consistent with the molar mass expected for a single PTH1R associated with two MSP proteins that form the ND. SPR was carried out on NDs with the incorporated receptor (PTH1R-ND) that was captured via a His_6-tag linked to MSP on an NTA chip versus an empty ND. As illustrated in **Figure 1** (see below), PTH binds specifically to PTH1R-ND with a Kd of 6.3±0.8 μM while no interaction was observed between PTH and the empty ND. This assay requires only microgram amounts of sample and it allows introduction of mutations, changing binding partners, etc. The ND purification is effective for a wide range of transmembrane proteins and allows access to both the intracellular and extracellular domains of membrane proteins. The label-free SPR approach

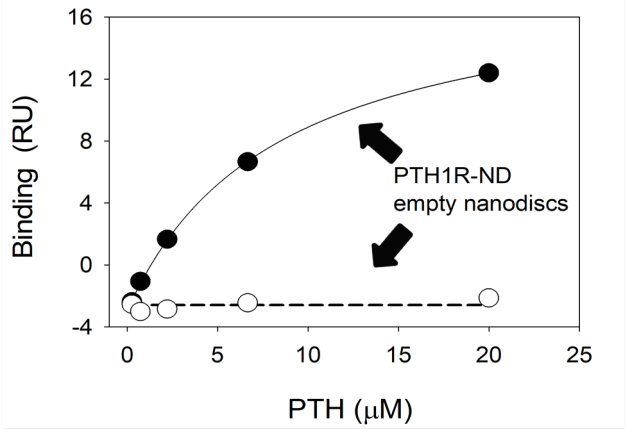

Figure 1. Binding isotherms for interaction of PTH with PTH1R (solid circles and solid line) and empty NDs (empty circles). PTH was injected from a three-fold dilution series in concentrations from 0.27 to 20 μM. Data were doubly-referenced against the signal collected on the reference cell and responses generated on the active cells during buffer injections.

can yield kinetic and thermodynamic information. For additional information on this approach and the broad range of other technologies available from the Biophysics Section please see here and email the Director of the Biophysics Section, Dr. Ewa Folta-Stogniew.

New Yale/NIDA Neuroproteomics Center Investigators

After a short leave, the Center welcomes back Dr. Yasmin Hurd (Mount Sinai School of Medicine) and new investigators Drs. Christie Fowler (U. California, Irvine) and Stephanie Groman (Yale U., U. Minnesota,1/2021). Descriptions of these investigators' research projects are below. The Center now has 25 investigators from 10 institutions.

Christie Fowler

Nicotine-Mediated Proteomic Changes in Habenular Neurons

The Fowler laboratory seeks to define the actions of nicotine and THC on extracellular vesicle signaling in the brain and periphery. They have previously found that nicotine and THC induce the release of extracellular vesicles from cellular subpopulations in the brain. When isolated from the cerebrospinal fluid (CSF), these vesicles have been found to contain various RNA transcripts, including miRNAs. Since miRNAs have been shown to participate in cell-to-cell signaling as extracellular vesicle cargo, they have been working to identify which miRNAs are transferred between cells in the brain, and what subsequent impact this signaling has on extracellular communication. For this project, which is supported by a NIDA Avenir Award (DA039658), they are now seeking to determine which proteomic changes occur in the medial habenula during nicotine consumption. They have found that the choroid plexus releases miRNAs into the CSF during intravenous nicotine self-administration, a model of drug reinforcement/dependence. They have further shown that extracellular vesicles in the CSF integrate into habenular neurons, and choroid plexus-derived miRNAs are enriched in the habenula. Given that the habenula has been shown to mediate an aversion signal that controls drug intake, changes in the function of habenular neurons via altered protein modulation may underlie drug intake and/or serve as a novel target for therapeutic development. Therefore, they hypothesize that nicotine induces the release of extracellular vesicles, leading to the uptake and integration of miRNAs in habenular neurons, which then induces altered expression of proteins in the habenula. This proposed proteomics study thus will be a final piece of evidence to demonstrate the functional significance of nicotine-mediated effects on extracellular vesicle signaling in vivo. To this end, they have collected brain tissue at two time points following the nicotine self-administration session to determine which proteins in the medial habenula become dysregulated. In addition to assessing proteins targeted by identified miRNAs, they are also interested in analyzing for the presence of extracellular vesicle specific proteins, which would provide further support for this type of nicotine-mediated signaling. These findings will thereby link the changes in protein expression to the miRNAs and proteins in extracellular vesicles infiltrating into the habenular neurons from the CSF. In sum, this project has high relevance to the Center's theme, "Proteomics of Altered Signaling in Addiction", as it seeks to analyze neuronal signal transduction mechanisms and the adaptive changes in these processes that occur in response to nicotine.

Stephanie Groman

Protein Mechanisms of Drug Use Susceptibility

Although many people will use a drug of abuse at least once in their lifetime, only a subset of these individuals will develop an addiction. This suggests that some individuals may be more susceptible to developing an addiction compared to others and, importantly, if the Groman laboratory can identify the neurobiological mechanisms that mediate this susceptibility, they may be able to prevent addiction. The Groman laboratory is focused on identifying the protein mechanisms that mediate susceptibility to drug use in rodent models. Their ongoing work – in collaboration with the Yale/NIDA Neuroproteomics Center – uses a reinforcement-learning platform to isolate protein targets that are disrupted by chronic exposure to drugs of abuse from those that influence

early-stage drug use. Their goal is to generate mechanistic bridges between proteins and complex behavioral phenotypes. Through a funded NIDA K01 award (DA051598; Mentor: Angus Nairn) they are 1) using novel viral approaches to investigate the role of three proteins (ATXN2L, SNX1, and RYR2) they hypothesize to mediate drug use susceptibility, 2) determining how these proteins and others are altered in a genetic rat model of addiction susceptibility, and 3) identifying the protein mechanisms that are altered in an environmental rat model of addiction susceptibility. This work, collectively, will identify novel biomarkers of addiction susceptibility that can be used to identify at risk humans. A second interest of the Groman laboratory is understanding the neurodevelopmental mechanisms that influence addiction susceptibility. Through pilot funding provided by the Yale/NIDA Neuroproteomics Center they have recently completed a study investigating the protein mechanisms underlying age-related changes in decision-making. Their preliminary data suggests that decision-making improves during adolescence in the rat and that this improvement is associated with changes in the expression of perineuronal net proteins. They hypothesize, therefore, that alterations in the expression of perineuronal net proteins during adolescence could impact susceptibility to drug use in adulthood by altering the formation of neural circuits, and their ongoing work is testing these hypotheses. They plan to integrate their collaborative work with the Yale/NIDA Neuroproteomics Center with magnetic resonance measurements at the University of Minnesota Magnetic Resonance Research Center (MRRC) in order to identify a non-invasive neuroimaging measure that could be used to assess addiction susceptibility in humans.

Yasmin Hurd

Proteomic Analysis of Neural Epigenetic Mechanisms and Immune System Underlying Long-Lasting Effects of Developmental Cannabis Exposure

While developmental marijuana exposure has been shown to result in life-long vulnerability to reward, motivation and cognitive impairments in the offspring, the cellular and molecular mechanisms that mediate impairments of neuronal development and synaptogenesis remain largely elusive. Recently, epigenetic regulatory mechanisms of gene expression emerged as prime biological candidates to establish and maintain persistent aberrant neuronal processing as a result of developmental drug exposure. Since these mechanisms are highly dynamic and readily influenced by environmental agents including drugs of abuse, the developing brain might be particularly sensitive to epigenetic influences, given the dynamic neuroplasticity characteristic of this period. The Hurd laboratory have observed that in utero or adolescent exposure to THC leads to epigenetic and transcriptional changes of genes linked to dopamine and glutamate receptor disturbances in the nucleus accumbens that appear to have relevance to specific striatal pathways. Moreover, these patterns persist into adulthood. In this project (DA030359), they will study THC-related changes in epigenetic regulatory mechanisms at affected genes that might underlie the persistent alterations in gene expression. Their preliminary results indicate that post-translational modifications of histone H3 (i.e. H3K4me3) and specific histone modifying enzymes (Kmt2a) are affected by developmental THC exposure. However, histone modifications are known to influence each other and to act in combination. Moreover, several different enzyme complexes might be involved in establishing disease-specific anomalies of these marks. Using a proteomic approach, their goal is to explore the combinatorial histone modification landscape at specific loci, as well as the associated protein complexes that mediate these modifications.

A second important use of a proteomic approach in their research program relates to studying placental specimens from women who used cannabis while pregnant since they have observed significant alterations of the transcriptome (assessed with RNA-sequencing) in which there was a marked alteration of the immune gene expression signature. It is important to determine whether these gene expression changes relate to functional proteins. As such they will use proteomic approaches to determine the protein profile within the human cannabis-exposed placenta as well as placenta from a rat prenatal THC model. This project is a focus of their competitive renewal grant application (DA030359).

Special Issue of the Journal *Proteomes* on Neuroproteomics

With 16 published articles this Special Issue on Neuroproteomics that was Co-Edited by Co-Directors Angus Nairn and Ken Williams is now complete and is available in a printed edition. As described in more detail here and as summarized in **Table 2** below, this issue contains an Editorial Overview and articles by Investigators Thomas Biederer, Lakshmi Devi, Elizabeth Eipper, Drew Kiraly, Angus Nairn, Marina Picciotto, Jane Taylor, and Mary Torregrossa; and Pilot Project Awardees Becky Carlyle and Deborah Schechtman. Included among the other contributors are Steven Arnold, Anthony Baucum, Seth Grant, Fernanda Laezza, Joongkyu Park, Junmin Peng, Jeffrey Savas, and John Yates.

Table 1: Grant Year 15 Pilot Projects

PI	Title	Institution	Center Investigator	Non-Center Investigator Mentor	Project Title
Kristen Brennand	Associate Professor	Mt. Sinai School of Medicine	N.A.	N.A.	Impact of NRXN1α Alternative Splicing Changes on Synaptic Composition.
Yifei Cai	Postdoctoral Associate	Yale U.	N.A.	Jaime Grutzendler	Proteomic Screening of Neuronal and Glial Subcellular Compartments Isolated by Proximity Labeling and FACS in Fixed and Fresh Brain Samples
Mohammad Shahid Mansuri	Postdoctoral Associate	Yale U.	Angus Nairn	N.A.	Ultra-deep Brain Tyrosine Phosphoproteomic Profiling by SH2-Superbinder
James Quinn	Postdoctoral Fellow	Mass. General Hospital	N.A.	Steven Arnold	Analyzing the Role of Neuropeptides in the Neurobiology and Physiology of Addiction

Table 2: Publications in the Special Issue of the Journal *Proteomes* on Neuroproteomics

#	Authors	Title, Reference and Link to Publication	Institution
1	Bertholomey, M.L., Stone, K.L., Lam, T.T., Bang, S., Wu, W., Nairn, A.C., Taylor, J.R., Torregrossa, M.M.	Phosphoproteomic Analysis of the Amygdala Response to Adolescent Glucocorticoid Exposure Reveals G-protein Coupled Receptor Kinase 2 as a Target for Reducing Motivation for Alcohol, *Proteomes* (2018) 6(4):41 (PMCID: PMC6313880)	University of Pittsburgh
2	Carlyle, B., Trombetta, B., Arnold, S.	Proteomic Approaches for the Discovery of Biofluid Biomarkers of Neurodegenerative Dementias, *Proteomes* (2018) 6(3): 32 (PMCID: PMC6161166)	Massachusetts General Hospital
3	Cijsouw, T., Ramsey, A., Lam, T., Carbone, B., Blanpied, T., Biederer, T.	Mapping the Proteome of the Synaptic Cleft Through Proximity Labeling Reveals New Cleft Proteins, *Proteomes* (2018) 6(4): 48 (PMCID: PMC6313906)	Tufts University
4	Lutz, B., Peng, J.	Deep Profiling of the Aggregated Proteome in Alzheimer's Disease: From Pathology to Disease Mechanisms, *Proteomes* (2018) 6(4): 46 (PMCID: PMC6313861)	St. Judes Childrens Research Hospital
5	Luxmi, R., Blaby-Haas, C., Kumar, D., Rauniyar, N., King, S., Mains, R., Eipper, B.	Proteases Shape the *Chlamydomonas* Secretome: Comparison to Classical Neuropeptide Processing Machinery, *Proteomes* (2018) 6(4): 36 (PMCID: PMC6313938)	U. Connecticut Health Center
6	Mervosh, N., Wilson, R., Rauniyar, N., Hofford, R., Kutlu, M., Calipari, E., Lam, T. T., Kiraly, D.	Granulocyte-colony Stimulating Factor Alters the Proteomic Landscape of the Ventral Tegmental Area, *Proteomes* (2018) 6(4): 35 (PMCID: PMC6313867)	Mount Sinai School of Medicine
7	Miller, M., Wilson, R., Lam, T., Nairn, A., Picciotto, M.	Evaluation of the Phosphoproteome of Mouse Alpha 4/Beta 2-Containing Nicotinic Acetylcholine Receptors In Vitro and In Vivo, *Proteomes,* (2018) 6(4): 42 (PMCID: PMC6313896)	Yale University
8	Natividad, L., Buczynski, M., McClatch, D., Yates, J.	From Synapse to Function: A Perspective on the Role of Neuroproteomics in Elucidating Mechanisms of Drug Addiction, *Proteomes* (2018) 6(4): 50 (PMCID: PMC6315754)	Scripps Research Institute
9	Park, J.	Phosphorylation of the AMPAR-TARP Complex in Synaptic Plasticity, *Proteomes* (2018) 6(4): 40 (PMCID: PMC6313930)	Wayne State U.
10	Pena, D., Duarte, M., Pramio, D., Devi, L., Schechtman, D.	Exploring Morphine-Triggered PKC-targets and Their Interaction with Signaling Pathways Leading to Pain via TrkA, *Proteomes* (2018) 6(4): 39 (PMCID: PMC6313901)	Mount Sinai School of Medicine
11	Roy, M., Sorokina, O., McLean, C., Tapia-González, S., DeFelipe, J., Armstrong, J., Grant, S.	Regional Diversity in the Postsynaptic Proteome of the Mouse Brain, *Proteomes* (2018) 6(3): 31 (PMCID: PMC6161190).	Edinburgh University

Table 2: Publications in the Special Issue of the Journal *Proteomes* on Neuroproteomics

#	Authors	Title, Reference and Link to Publication	Institution
12	Sowers, M., Re, J., Wadsworth, P., Shavkunov, A., Lichti, C., Zhang, K., Laezza, F.	Sex-specific Proteomic Changes Induced by Genetic Deletion of Fibroblast Growth Factor 14 (FGF14), a Regulator of Neuronal Ion Channels, *Proteomes* (2019) 7(1): 5 (PMCID: PMC6473632)	University of Texas Medical Branch
13	Wang, Y., Savas, J.	Uncovering Discrete Synaptic Proteomes to Understand Neurological Disorders, *Proteomes* (2018) 6(3): 30 (PMCID: PMC6161107).	Northwestern University
14	Watkins, D., True, J., Mosley, A., Baucum, A.	Proteomic Analysis of the Spinophilin Interactome in Rodent Striatum Following Psychostimulant Sensitization, *Proteomes* (2018) 6(4): 53 (PMCID: PMC6313900)	Indiana University
15	Wilson, R., Nairn, A.	Cell-type-specific Proteomics: A Neuroscience Perspective, *Proteomes* (2018) 6(4): 51 (PMCID: PMC6313874).	Yale University
16	Wilson, R., Rauniyar, N., Sakaue, F., Lam, T., Williams, K., Nairn, A.,	Development of Targeted Mass Spectrometry-Based Approaches for Quantitation of Proteins Enriched in the Postsynaptic Density (PSD), *Proteomes* (2019) 7(2): 12 (PMCID: PMC6630806)	Yale University
17	Williams, K., Nairn, A.	Editorial for Special Issue: Neuroproteomics, *Proteomes* (2019), 7(2) 24 (PMCID: PMC6630506)	Yale University

Table 3: Yale/NIDA Neuroproteomics Center Cores

Core	Name	Role	Email
Administrative	Angus Nairn	Co-Director/PI	angus.nairn@yale.edu
	Kenneth Williams	Co-Director/PI	kenneth.williams@yale.edu
Discovery Proteomics	TuKiet Lam	Core Director and Protein Identification and Profiling	tukiet.lam@yale.edu
	Pietro DeCamilli	Analysis of Phosphoinositides, Their Interactions, Metabolism, and Transport; Recombinant Protein Expression and Purification	pietro.decamilli@yale.edu
	Ewa Folta-Stogniew	Biophysics	ewa.folta-stogniew@yale.edu
	Angus Nairn	Recombinant Protein Expression and Purification	angus.nairn@yale.edu
Targeted Proteomics	Kenneth Williams	Core Director	kenneth.williams@yale.edu
Bioinformatics and Biostatistics Core (BBC)	Angus Nairn	Core Director	angus.nairn@yale.edu
	Robert Bjornson	High Performance Computing	robert.bjornson@yale.edu
	Mark Gerstein	Bioinformatics	mark.gerstein@yale.edu
	Hongyu Zhao	Biostatistics	hongyu.zhao@yale.edu
Pilot Research Projects	Marina Picciotto	Core Director	marina.picciotto@yale.edu

2019- Present Publications from the Yale/NIDA Neuroproteomics Center

Please inform Angus Nairn and Ken Williams of all newly submitted manuscripts and publications and acknowledge the Center's grant, DA018343, in all publications that were supported by the Center's Cores and/or Pilot Project Grants.

2019

1. Bian, X., De Camilli, P. (2019) In vitro assays to measure the membrane tethering and lipid transport activities of the Extended Synaptotagmins. Methods Mol Biol. 1949:201-212 (PMCID: PMC6481592, PMID:30790258).
2. Bian, X., Zhang. Z., De Camilli, P., Lin, C. (2019) A programmable DNA-origami platform for studying protein-mediated lipid transfer between bilayers. Nature Chem. Biol. 15(8) 830-837 (PMCID:PMC6650167, PMID: 31320758).
3. Chen Y, Youn J, Martinez A, Yang Y, Wu Y, De Camilli P, Fernandez-Busnadiego R, and Wu M. (2019). Dynamic instability of clathrin assembly provides proofreadying control for endocytosis. J. Cell Biol. 218: 3200-3211 (PMCID: PMC6781453, PMID: 31451612).
4. Guillén-Samander, A., Bian, X. and De Camilli, P. (2019) PDZD8 mediates a Rab7 dependent interaction of the ER with late endosomes and lysosomes. Proc. Natl. Acad. Sci. USA. 116: 22619-22623 (PMCID: PMC6842579, PMID:31636202).
5. Gunther, E.,Smith, L., Kostylev, M.,Cox, T., Kaufman, A., Lee, S., Folta-Stogniew, E., Maynard, G., Um, J., Stagi, M., Heiss, J., Stoner, A., Noble, J., Takahashi, H., Haas,L., Schneekloth, J., Merkel, J., Teran, C., Naderi, Z., Supattapone, S., Strittmatter, S.M. (2019) Rescue of transgenic Alzheimer's pathophysiology by polymeric cellular Prion Protein antagonists. Cell Reports 26(1) 145-158 (PMCID: PMC6358723, PMID:30605671).
6. Jin, J., Bhatti, D.L., Lee, K.W, Medrihan, L., Cheng, J., Wei, J., Zhong, P., Yan, Z., Kooiker, C., Song, C., Ahn, J.H., Obermair, G.J., Lee, A., Gresack, J., Greengard, P., Kim, Y.. (2019) Ahnak scaffolds p11/Anxa2 complex and L-type voltage-gated calcium channel and modulates depressive behavior. Mol Psychiatry. 25(5) 1035-1049 (PMCID: PMC6692256, PMID:30760886).
7. Koopmans, F., van Nierop, P., Andres-Alonso, M., Byrnesm A., Cijsouw, T., Cobam M.P., Cornelissem L.N., Farrellm R.J., Goldschmidtm H.L., Howriganm D.P., Hussain, N.K., Imig, C., de Jong, A.P.H., Jung, H., Kohansalnodehi, M., Kramarz, B., Lipstein, N., Lovering, R.C., MacGillavry, H., Mariano, V., Mi, H., Nivo, M., Osumi-Sutherland, D., Pielot, R., Smalla, K.H., Tang, H., Tashman, K., Toonen, R.F.G., Verpelli, C., Reig-Viader, R., Watanabe, K., van Weering, J., Achsel, T., Ashrafi, G., Asi, N., Brown, T.C., De Camilli, P., Feuermann, M., Foulger, R.E., Gaudet, P., Joglekar, A., Kanellopoulos, A., Lalenka, R., Nicoll, R.A., Pulido, C., de Juan-Sanz, J., Sheng, M., Sudhof, T.C., Tilgner, H.U., Bagni, C., Baysés, A., Biederer, T., Brose, N., Chua, J.J.E., Dieterich, D.C., Gundelfinger, E.D., Hoogenraad, C,. Huganir, R.L., Jahn, R., Kaeser, P.S., Kim, E., Kreutz, M.R., McPherson, P.S., Neale, B.M., O'Connor, V., Posthuma, D., Ryan, T.A., Sala, C., Feng, G., Hyman, S.E., Thomas, P.D., Smit, A.B., and Verhage, M.. 2019. SynGO: and evidence-based, expert-curated knowledgebase for the synapse. Neuron. 103: 217-234 (PMCID: PMC6764089, PMID:31171447).
8. Luscher, A., Fröhlich, F., Barisch, C., Littlewood, C., Metcalfe, J., Leuba, F., Palma, A., Pirruccello, M., Cesareni, G., Stagi, M., Walther, T.C., Soldati, T., De Camilli, P. and Swan, L.E. (2019) Lowe syndrome-linked endocytic adaptors direct membrane cycling kinetics with OCRL in Dictyostelium discoideum. Mol Biol Cell. 30: 2268-2282 (PMCID: PMC6743453, PMID:31216233).
9. Rao, V., Zavala, G., Roy, A., Mains, R., Eipper, B. (2019) A pH-sensitive luminal His-cluster promotes interaction of PAM with V-ATPase along the secretory and endocytic pathways of peptidergic cells. J. Cellular Physiology (PMCID:PMC6395498, PMID: 30317586).
10. Sun, E.W., Guillén-Samander, A., Bian, X., Wu, Y., Cai, Y., Messa, M., De Camilli, P. (2019) The lipid transporter TMEM24/C2CD2L is a Ca2+-regulated component of ER-plasma membrane contacts in mammalian neurons. Proc. Nat. Acad. Sci. 116(12):5775-5784 (PMCID:PMC6431226, PMID:30819882).
11. Taguchi, Y.V., Nagy, M., Thrasher, D, Gorenberg, E., Fenton, W., Volpicelli-Daley, L. Horwich, A.L., Chandra, S.S. (2019). Hsp110 disaggregase influences α-synuclein pathology in vivo. Proc. Natl. Acad. Sci. 116(48): 24310-24316 (PMCID:PMC6883785, PMID:31685606).
12. Torregrossa, M., MacDonald, M., Stone, K.L., Lam, T.T., Nairn, A.C., Taylor, J.R. (2019) Phosphoproteomic analysis of cocaine memory extinction and reconsolidation in the nucleus accumbens, Psychopharmacology 236(1) 531-543 (PMCID:PMC6374162, PMID: 30411139).

13. Williams, K., Nairn, A. (2019) Editorial for Special Issue: Neuroproteomics, Proteomes Special Issue on Neuroproteomics, Proteomes Special Issue on Neuroproteomics, 7(2) (PMCID:PMC6630506, PMID: 31159207).
14. Wilson, R. Rauniyar, N., Sakaue, F., Lam, T., Williams, K., Nairn, A. (2019) Development of targeted mass spectrometry-based approaches for quantitation of proteins enriched in the postsynaptic density (PSD), Proteomes Special Issue on Neuroproteomics, 7(2) (PMCID:PMC6630806, PMID:30986977).

2020

15. Cao, M , Park D, Wu Y and De Camilli P, (2020) Absence of Sac2/INPP5F enhances the phenotype of a Parkinson's disease mutation of synaptojanin 1. Proc. Natl. Acad. Sci. U.S.A. 117(22) 12428-1434 (PMCID: PMC7275725, PMID: 32424101)
16. Girault, J. A. and Nairn, A.C. (2020) DARPP-32 40 years later. Advances in Pharmacology, in press.
17. Christensen, K.R., and Nairn, A.C. (2020) cAMP-Regulated phosphoproteins DARPP-32, ARPP16/19, and RCS modulate striatal signal transduction through protein kinases and phosphatases. Advances in Pharmacology, in press.
18. Li, X., Terunuma, M., Deeb, T.G., Wiseman, S., Pangalos, M.N., Nairn, A.C., Moss, S.J., Slesinger, P.A. (2020) Direct interaction of PP2A phosphatase with GABAB receptors alters functional signaling. J. Neurosci. 40(14) 2808-2816 (PMID: 32111696, PMCID: PMC7117905, available on 2020-10-01).
19. Moin, A.M.A., Keip, A.J., Taylor, J.R., Lee, D., Groman, S.M. (2020) Adolescent-related changes in reinforcement learning and decision making in the rat. J. Neuroscience in press.
20. Nakamura, Y., Morrow, D.H., Nathanson, A.J., Henley, J.M., Wilkinson, K.A., Moss, S.J. (2020) Phosphorylation on Ser-359 of the a2 subunit in GABA type A receptors down-regulates their density at inhibitory synapses. J. Biol. Chem. 295(35) 12330-12342 (JBC Editor's Pick Publication, PMCID: PMC7458806, PMID: 32620552
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