BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Klykov, Oleg

eRA COMMONS USER NAME (credential, e.g., agency login): OLEGVK

POSITION TITLE: Scientist

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Lomonosov Moscow State University, Moscow, Russia	MS (Diploma)	06/2012	Organic Chemistry
Utrecht University, Utrecht, The Netherlands	Ph.D.	10/2019	Pharmaceutical Sciences
Columbia University, New York, USA	-	01/2022	Molecular Biochemistry and Biophysics
New York Structural Biology Center	-	-	*In-situ* cryo-ET

A. Personal Statement

My long-term research goals and career interest lie in the field of neurobiology. I aim to delve into the mechanisms of how our brain is functioning by several multidisciplinary approaches. The main target is the synaptic receptor proteins involved in communication between neurons. Before focusing on the brain proteins, I have gained extensive academic training and diverse research experience that have provided me with an excellent background in analytical, organic, and biochemistry. After I graduated from university with distinction, I have spent three years at BAM Federal Institute (Berlin, Germany) studying small molecules and protein purification by means of analytical chemistry. For my predoctoral studies, I joined the group of Dr. Albert J.R. Heck at Utrecht Institute of Pharmaceutical Sciences within Utrecht University (Utrecht, The Netherlands). My research was focused on the development and application of MS-based structural characterization of various biological samples and potential drug targets. I took a part in developing a novel protocol for structural MS analysis of complex biological samples and gained expertise in computational structural biology. While being the first author of several methodological papers, I was also able to follow my main research interest and took a part in a project devoted to transport neuronal proteins. During my predoctoral studies, I have received three travel awards (American MS Society, European Molecular Biology Organization, and the Dutch MS Society). For my postdoctoral studies, I joined the lab of Dr. Alexander Sobolevsky at Columbia University. After studying purified synaptic receptor complexes from a structural and electrophysiological perspective, I moved to the NCITU (National Center for in-situ Tomographic Ultramicroscopy) division at SEMC-NYSBC, first as an embedded postdoc and then as a scientist. At NCITU, we mostly work on cryoelectron tomography (cryo-ET) method development and support users with their biological challenging projects. My focus at NCITU is cryo-ET investigations of membrane proteins through high-resolution subtomogram averaging pipeline. I have successfully learned and optimized high-pressure freezing vitrification of thick biological samples followed by cryo-FLM screening, FIB-SEM sample thinning, and high-resolution ET data acquisition toward membrane protein receptor complexes. With the expertise I learned throughout my career, I am now ready to conduct research investigations as an independent group leader.

1. Klykov O., Kopylov M., Carragher B., Heck A.J.R., Noble A.J., Scheltema R.A.S. Label-free visual proteomics: Coupling MS- and EM-based approaches in structural biology. Molecular Cell, 82 (2), 2022, 285-303

2. Kelley K.†, Raczkowski A.M.*, Klykov O.*, Jaroenlak P.*, Bobe D.*, Kopylov M., Eng E.T., Bhabha G., Potter C.S., Carragher B., Noble A.J. Waffle Method: A general and flexible approach for FIB-milling small and anisotropically oriented samples. Nature Communications, 13, 2022, 1857

3. Klykov O.*, Gangwar S.P.*, Yelshanskaya M.V.*, Yen L., Sobolevsky A.I. Structure and desensitization of AMPA receptor complexes with type II TARP gamma-5 and GSG1L. Molecular Cell, 81 (23), 2021, 4771-4783

B. Positions and Honors

Positions and Employment

2007 – 2012	Pre-diploma Research Fellow, Lomonosov Moscow State University
2012 – 2015	Research Scientist, BAM Federal Institute For Materials Research and Testing, Berlin, Germany
2015 – 2019	Predoctoral Research Fellow, Utrecht University, Utrecht, The Netherlands
2020 – 2022	Postdoctoral Research Fellow, Columbia University
2022 –	Scientist, New York Structural Biology Center

Other Experience and Professional Memberships

2012 – 2015	DGMS, German Society for Mass Spectrometry
2015 –	NVMS, Dutch Society for Mass Spectrometry
2020 –	AHA partner, American Heart Association

Honors

2008	Undergraduate Annual Thesis Competition on Analytical Chemistry at the Lomonosov University, Winner
2018	American Society for Mass Spectrometry (ASMS), Sanibel Conference Travel Grant
2019	Netherlands Society for Mass Spectrometry (NVMS) Conference, Fund Award
2019	European Molecular Biology Organization Practical Course: Integrative and cellular structural Biology, Travel Award
2022	Biophysical Society 66th Annual Meeting, Travel Award

C. Contributions to Science

1. **Early Career:** My early career contributions were focused on method developments and application of analytical techniques for analysis of biological samples. I worked at the physical chemistry lab at the university of North Dakota where I was operating the Graphite Atomic Absorption Furnace Spectrometer and performed the analysis of the acquired data. For my diploma degree project, I was analyzing a part of mass spectrometric outputs within a laboratory of Organic Analysis at the Lomonosov Moscow State University. I was also a part of the Protein Analysis group within a BAM Federal Institute in Germany where I was mostly maintaining the chromatography equipment and eventually me and my supervisor developed a quantitative chromatography-based technique to detect one of the products of decomposition of commonly used biochemical reagent.
   a. Raeva A.A., Klykov O.V., Kozliak E.I., Pierce D.T., Seames W.S. (2011) In Situ Evaluation of Inorganic Matrix Effects on the Partitioning of Three Trace Elements (As, Sb, Se) at the Outset of Coal Combustion. Energy & Fuels 25: 4290-4298
   b. Samgina T.Y., Gorshkov V.A., Artemenko K.A., Vorontsov E.A., Klykov O.V., Ogourtsov S.V., Zubarev, R.A., Lebedev A.T. (2012) LC–MS/MS with 2D mass mapping of skin secretions' peptides

as a reliable tool for interspecies identification inside Rana esculenta complex. Peptides 34: 296-302.PMID: 22401909

   c. Klykov O., Weller M.G. (2015) Quantification of N-hydroxysuccinimide and N-hydroxysulfosuccinimide by hydrophilic interaction chromatography (HILIC) Anal. Methods 7:6443-6448.

2. **Graduate Career:** My graduate research contributions focused on the application of structural mass spectrometry to protein targets and whole cell lysates. As a result of my work, crosslinking MS approach has become widely accepted and applicable to whole-cell and extremely complex biological samples as in comparison to the protein complexes of limited complexity. I have developed and optimized the whole pipeline including sample preparation, data acquisition protocol, and data analysis platform. I have applied this protocol to get an insight into the structures of the gene-editing protein complex and the mechanism of neuronal dense-core vesicle transport. I also applied it to study the protein-based fibrin blood clot biopolymer. For the first time it was possible to show the arrangement of the assembled fibrin clot on a molecular level and describe the mechanism of interference of high albumin concentration in blood with coagulation process. Results of these investigations were published in peer-reviewed scientific journals.
   a. Fagerlund R.D., Wilkinson M.E., Klykov O, Barendregt A., Pearce G.F., Kieper S.N., Maxwell H.W.R., Capolupo A., Heck A.J.R., Krause K.L., Bostina M., Scheltema R.A., Staals R.H.J., Fineran P.C. (2017) Spacer capture and integration by a type IF Cas1–Cas2-3 CRISPR adaptation complex. PNAS 114:E5122-E5128. PMCID: PMC5495228
   b. Klykov O., Steigenberger B., Pektas S., Fasci D., Heck A.J.R., Scheltema R.A. (2018) Efficient and robust proteome-wide approaches for proteome-wide crosslinking mass spectrometry. Nat. Protoc. 13: 2694-2990.PMID: 30446747
   c. Stucchi R., Plucinska G., Hummel J.J.A., Zahavi E.E., San Juan I.G., Klykov O., Scheltema R.A., Altelaar A.F.M., Hoogenraad C.C. (2018) Regulation of KIF1A-driven dense core vesicle transport: Ca2+/CaM controls DCV binding and Liprin-a/TANC2 recruits DCVs to postsynaptic sites. Cell Rep. 24: 685-700 PMCID: PMC6077247
   d. Klykov O, van der Zwaan C., Heck A.J.R., Meijer A.B., Scheltema R.A. (2020) Missing regions within the molecular architecture of human fibrin clots structurally resolved by XL-MS and integrative structural modeling. PNAS 117(4):1976-1987; PMCID: PMC6995014

3. **Postdoctoral Career:** After graduation, I am working on cryo-EM/ET studies of membrane protein complexes and cryo-ET method development. In addition to numerous collaborative users projects in progress, my main achievements are automation of the waffle method with novel FIB-SEM setups as well as obtaining the structure of the AMPARs complexes with previously undescribed type II auxiliary subunits.

   a. Kelley K.†, Raczkowski A.M.*, Klykov O.*, Jaroenlak P.*, Bobe D.*, Kopylov M., Eng E.T., Bhabha G., Potter C.S., Carragher B., Noble A.J. Waffle Method: A general and flexible approach for FIB-milling small and anisotropically oriented samples. Nature Communications, 13, 2022, 1857

   b. Klykov O.*, Gangwar S.P.*, Yelshanskaya M.V.*, Yen L., Sobolevsky A.I. Structure and desensitization of AMPA receptor complexes with type II TARP gamma-5 and GSG1L. Molecular Cell, 81 (23), 2021, 4771-4783

Complete List of Published Work in My Bibliography:
https://www.ncbi.nlm.nih.gov/myncbi/1ZEenY0ebbnAq/bibliography/public/

D. Additional Information: Research Support and/or Scholastic Performance

Scholastic Performance

I have attended most of the courses in Russia and Europe and therefore I do not indicate them here. While being a part of Utrecht Institute for Pharmaceutical Sciences (UIPS) within Graduate School of Life Sciences (GS-LS), I have attended several external and internal courses with no grades but passed mark.

YEAR	COURSE TITLE	GRADE
2015	Biomolecular Mass Spectrometry and Proteomics	PASSED
2015	UIPS Introductory Course	PASSED
2016	MaxQuant Summer School (Oxford, UK)	PASSED
2016	Giving Effective Oral Presentation	PASSED
2016	Safe Research Data Management	PASSED
2017	Introduction to Python for Life Sciences	PASSED
2017	Introduction to R & Data	PASSED
2017	Advanced R for Life Sciences	PASSED
2017	Writing Successful Grant Proposals	PASSED
2017	GS-LS PhD Day 2017: Getting Published from A to Z	PASSED
2018	EMBO Practical Course: Integrative modelling of biomolecular interactions (Barcelona, Spain)	PASSED

YEAR	COURSE TITLE	GRADE
2018	Scientific Presentation Skills	PASSED
2018	GS-LS PhD Day 2018: Talkin' Science: Getting Your Message Across	PASSED
2019	Introductory Biostatistics for Researches	PASSED
2019	Preparation Course for Pitch Competition: Breaking Science	PASSED
2019	EMBO Practical Course: Integrative and cellular structural biology (Paris, France)	PASSED