### **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: Sobolevsky, Alexander

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

POSITION TITLE: Associate Professor

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	END DATE	FIELD OF STUDY
	(if applicable)	MM/YYYY	
Moscow Inst. of Physics and Technology, Moscow	MS	06/1996	Bioengineering
Moscow Inst. of Physics and Technology, Moscow	PHD	11/1999	Biophysics

# A. Personal Statement

My lab studies structure and function of ion channels, including ionotropic glutamate receptors (iGluRs) and transient receptor potential (TRP) channels, using a combination of biochemical and biophysical methods and cryo-electron microscopy (cryo-EM) in particular. I have an expertise in solving structures of integral membrane proteins by both X-ray crystallography and cryo-EM and an extensive experience in using methods of characterizing ion channels function, including patch-clamp, double-electrode voltage-clamp recordings and Fura-2-based ratiometric fluorescent measurements of intracellular calcium. I also have an expertise in analyzing different types of ion channel inhibition using a combination of electrophysiology, protein engineering and kinetic modeling. With such expertise and experiences. I studied the mechanisms of ionotropic glutamate receptor (iGluR) inhibition by ion channel blockers, including the only FDA-approved NMDA receptor channel blocker Memantine, currently used for treatment of Alzheimer's disease. I solved the first full length crystal structure of ionotropic glutamate receptor. My lab solved numerous structures of full-length iGluRs, including the first agonistbound, open and desensitized state structures and proposed the first complete structural model of iGluR gating. Using X-ray crystallography, my lab determined the structural mechanism of iGluR inhibition by noncompetitive inhibitors, including Perampanel that is currently used for treatment of epilepsy. My lab also solved the first TRP channel crystal structure. Using cryo-EM, my lab determined structures of human TRPV6 in different conformations and proposed the mechanism of TRPV6 activation. Similarly, my lab solved the first structures of TRPV3 in different conformations and proposed the mechanism of ligand-induced TRPV3 activation. As a result of my previous experiences. I am aware of the importance of frequent communication among project members and of constructing a realistic research plan, timeline, and budget. My current research plans build logically on my prior work.

- McGoldrick LL, Singh AK, Saotome K, Yelshanskaya MV, Twomey EC, Grassucci RA, Sobolevsky AI. Opening of the human epithelial calcium channel TRPV6. Nature. 2018 Jan 11;553(7687):233-237. PubMed PMID: 29258289; PubMed Central PMCID: PMC5854407.
- Twomey EC, Yelshanskaya MV, Grassucci RA, Frank J, Sobolevsky AI. Channel opening and gating mechanism in AMPA-subtype glutamate receptors. Nature. 2017 Sep 7;549(7670):60-65. PubMed PMID: <u>28737760</u>; PubMed Central PMCID: <u>PMC5743206</u>.
- 3. Saotome K, Singh AK, Yelshanskaya MV, Sobolevsky AI. Crystal structure of the epithelial calcium channel TRPV6. **Nature**. 2016 Jun 23;534(7608):506-11. PubMed PMID: <u>27296226</u>; PubMed Central PMCID: PMC4919205.
- Yelshanskaya MV, Li M, Sobolevsky AI. Structure of an agonist-bound ionotropic glutamate receptor. Science. 2014 Aug 29;345(6200):1070-4. PubMed PMID: <u>25103407</u>; PubMed Central PMCID: PMC4383034.

# **B. Positions and Honors**

# **Positions and Employment**

1993 - 1996	Pre-diploma Research Fellow, Moscow Institute of Physics and Technology, Moscow
1996 - 1999	Pre-doctoral Research Fellow, Moscow Institute of Physics and Technology, Moscow
2000 - 2004	Post-doctoral Research Fellow, Stony Brook University, Stony Brook, NY
2004 - 2005	Post-doctoral Research Fellow, Columbia University, New York, NY
2005 - 2010	Post-doctoral Research Fellow, Vollum Institute, Oregon Health and Science University, Portland, OR
2010 - 2017	Assistant Professor, Columbia University, New York, NY
2017 -	Associate Professor, Columbia University, New York, NY

# Other Experience and Professional Memberships

2013 -	Member, American Heart Association
2017 -	Member, Biophysical Society
2017 -	Member, American Chemical Society
2018 -	Member, Society for Neuroscience

# **Honors**

1998	International Soros Science Education Program Grant, Soros Foundation
1998	Travel Grant for participation in the 29th Annual Meeting of the Society for Neuroscience,
	International Brain Research Organization
1999	International Soros Science Education Program Grant, Soros Foundation
2000	Travel Grant for participation in the 31st Annual Meeting of the Society for Neuroscience,
	International Brain Research Organization
2002	Postdoctoral Travel Award for participation in the 32nd Annual Meeting of the Society for
	Neuroscience, Burroughs Wellcome Fund
2011	Klingenstein Fellowship Award in the Neurosciences, Esther A. & Joseph Klingenstein Fund
2012	Schaefer Research Scholar Award, Dr. Ludwig Schaefer Fund
2013	Pew Scholar Award, Pew Charitable Trusts
2015	Irma T. Hirschl Career Scientist Award, Irma T. Hirschl Trust
2017	Amgen Young Investigator Award, Amgen

## C. Contribution to Science

- 1. N-methyl-D-aspartate (NMDA) receptors are a subtype of ionotropic glutamate receptors that is critical to neuronal development and synaptic plasticity, associated with memory formation and learning and implicated in acute and chronic neuronal death, associated with brain trauma and neurological disorders. Ion channel blockers of NMDA receptors therefore have an enormous drug potential. We have been among the first research groups to study the mechanism of ion channel block of NMDA receptors by various derivatives of aminoadamantane, one of which, Memantine (NAMENDA), have become the first and so far the only drug acting at NMDA receptors that has been approved by FDA for treatment of moderate to severe Alzheimer's disease. We developed a set of new kinetic criteria to analyze the mechanism of blocker interaction with ion channel gating machinery. Using this set, we were the first to discover that Mg2+ interacts with NMDA receptors via the trapping block mechanism. The discovery of the trapping block of NMDA receptor channels by Mg2+ led to reevaluation of the role of Mg2+ and NMDA receptors in neurotransmission across excitatory synapses in the brain.
  - a. Sobolevsky AI, Yelshansky MV. The trapping block of NMDA receptor channels in acutely isolated rat hippocampal neurones. J Physiol. 2000 Aug 1;526 Pt 3:493-506. PubMed PMID: <u>10922002</u>; PubMed Central PMCID: <u>PMC2270033</u>.
  - b. Sobolevsky AI, Koshelev SG, Khodorov BI. Probing of NMDA channels with fast blockers. **J Neurosci.** 1999 Dec 15;19(24):10611-26. PubMed PMID: 10594045.

- c. Sobolevsky AI, Koshelev SG, Khodorov BI. Interaction of memantine and amantadine with agonist-unbound NMDA-receptor channels in acutely isolated rat hippocampal neurons. **J Physiol.** 1998 Oct 1;512 ( Pt 1):47-60. PubMed PMID: 9729616; PubMed Central PMCID: PMC2231181.
- d. Sobolevsky A, Koshelev S. Two blocking sites of amino-adamantane derivatives in open N-methyl-D-aspartate channels. **Biophys J.** 1998 Mar;74(3):1305-19. PubMed PMID: <u>9512028</u>; PubMed Central PMCID: <u>PMC1299478</u>.
- 2. Before the structures of the full length iGluR become available, one could only guess what are the structural organization of the iGluR channel and the mechanisms of pore opening and closure. To gain insights into the structure of the NMDA receptor ion channel pore and the structural rearrangements during gating, we used the substituted cysteine accessibility method (SCAM). The NMDA receptor is an obligate heterotetramer composed of two or more different subunits. We individually mutated residues in the transmembrane portion of the two major subtypes of NMDA receptor subunits, NR1 and NR2. We identified the boundaries and the pore-facing surfaces of the transmembrane domains, their relative contribution to the ion channel pore and gating and the amino acid residues in the pore involved into receptor activation and desensitization as well as binding of the channel blockers. We were among the first to discover the asymmetrical contribution of the NR1 and NR2 subunits to channel pore structure and gating and the central role of the M3 segment in NMDA receptor gating.
  - a. Sobolevsky AI, Prodromou ML, Yelshansky MV, Wollmuth LP. Subunit-specific contribution of pore-forming domains to NMDA receptor channel structure and gating. J Gen Physiol. 2007 Jun;129(6):509-25. PubMed PMID: <u>17504910</u>; PubMed Central PMCID: <u>PMC2151626</u>.
  - b. Wollmuth LP, Sobolevsky AI. Structure and gating of the glutamate receptor ion channel. **Trends Neurosci.** 2004 Jun;27(6):321-8. PubMed PMID: 15165736.
  - c. Sobolevsky AI, Rooney L, Wollmuth LP. Staggering of subunits in NMDAR channels. **Biophys J.** 2002 Dec;83(6):3304-14. PubMed PMID: 12496098; PubMed Central PMCID: PMC1302406.
  - d. Sobolevsky AI, Beck C, Wollmuth LP. Molecular rearrangements of the extracellular vestibule in NMDAR channels during gating. **Neuron**. 2002 Jan 3;33(1):75-85. PubMed PMID: <u>11779481</u>.
- 3. We used SCAM and patch-clamp recordings to study structure and function of homotetrameric AMPA subtype iGluRs. We identified pore-forming elements and residues involved in AMPA receptor gating. We discovered mutations outside the ligand binding domain (LBD) in the linkers connecting the LBD to the ion channel that resulted in either enhancement or nearly complete oblation of AMPA receptor desensitization. We found that AMPA receptors are unique compared to other tetrameric ion channels and that despite the subunit assembly is homomeric, contribution of individual subunits to the ion channels pore is different leading to the overall two- rather than four-fold rotation symmetry of the ion channel in the active state.
  - a. Sobolevsky AI, Yelshansky MV, Wollmuth LP. State-dependent changes in the electrostatic potential in the pore of a GluR channel. **Biophys J.** 2005 Jan;88(1):235-42. PubMed PMID: <u>15516523</u>; PubMed Central PMCID: <u>PMC1305001</u>.
  - b. Yelshansky MV, Sobolevsky AI, Jatzke C, Wollmuth LP. Block of AMPA receptor desensitization by a point mutation outside the ligand-binding domain. **J Neurosci.** 2004 May 19;24(20):4728-36. PubMed PMID: 15152033.
  - c. Sobolevsky AI, Yelshansky MV, Wollmuth LP. The outer pore of the glutamate receptor channel has 2-fold rotational symmetry. **Neuron**. 2004 Feb 5;41(3):367-78. PubMed PMID: 14766176.
  - d. Sobolevsky AI, Yelshansky MV, Wollmuth LP. Different gating mechanisms in glutamate receptor and K+ channels. **J Neurosci.** 2003 Aug 20;23(20):7559-68. PubMed PMID: 12930794.
- 4. The transient receptor potential (TRP) channels are a superfamily of cation permeable ion channels that are widely known for their role as transducers of sensory modalities, including temperature, taste, olfaction, vision, hearing and touch. TRP channels are also crucial for a diverse range of physiological processes, such as neurite outgrowth, hormone secretion and control of vascular tone. Accordingly, mutations or malfunction of TRP channels are associated with numerous human diseases, including cardiovascular, renal, nociceptive and metabolic disorders. We solved the first crystal structure of TRP channel, Ca2+-

selective channel TRPV6 that plays vital roles in calcium homeostasis as a Ca2+ uptake channel in epithelial tissues and is implicated in development and progression of numerous forms of cancer. We also determined the structural bases of TRPV6 allosteric regulation and calcium-induced calmodulin-mediated inactivation. We also solved the first structure of TRPV3 and determined structural beses of TRPV3 activation. Our results provide a structural foundation to understand the regulation of epithelial Ca2+ uptake and its role in pathophysiology and provide information necessary for drug design.

- a. Singh AK, McGoldrick LL, Sobolevsky AI. Structure and gating mechanism of the transient receptor potential channel TRPV3. Nat Struct Mol Biol. 2018 Sep;25(9):805-813. PubMed PMID: 30127359; PubMed Central PMCID: PMC6128766.
- b. Singh AK, Saotome K, McGoldrick LL, Sobolevsky AI. Structural bases of TRP channel TRPV6 allosteric modulation by 2-APB. **Nat Commun.** 2018 Jun 25;9(1):2465. PubMed PMID: <u>29941865</u>; PubMed Central PMCID: <u>PMC6018633</u>.
- c. McGoldrick LL, Singh AK, Saotome K, Yelshanskaya MV, Twomey EC, Grassucci RA, Sobolevsky AI. Opening of the human epithelial calcium channel TRPV6. **Nature**. 2018 Jan 11;553(7687):233-237. PubMed PMID: 29258289; PubMed Central PMCID: PMC5854407.
- d. Saotome K, Singh AK, Yelshanskaya MV, Sobolevsky AI. Crystal structure of the epithelial calcium channel TRPV6. **Nature**. 2016 Jun 23;534(7608):506-11. PubMed PMID: <u>27296226</u>; PubMed Central PMCID: PMC4919205.
- 5. High resolution structural information about ionotropic glutamate receptors opens new horizons to understanding their gating mechanism and regulation at the molecular level as well as makes iGluRs a novel pharmacological platform for characterizing new compounds with diverse activities for use as therapies in neurological diseases. My lab has solved the first crystal structure of the full length AMPA receptor in complex with agonist, crystallographically discovered novel binding sites of antiepileptic drugs, obtained the first cryo-EM structures of AMPA receptor complexes with the auxiliary subunits stargazin and GSG1L, and solved the first structures of AMPA receptor in the open and desensitized states.
  - a. Twomey EC, Yelshanskaya MV, Grassucci RA, Frank J, Sobolevsky AI. Channel opening and gating mechanism in AMPA-subtype glutamate receptors. **Nature**. 2017 Sep 7;549(7670):60-65. PubMed PMID: 28737760; PubMed Central PMCID: PMC5743206.
  - b. Yelshanskaya MV, Singh AK, Sampson JM, Narangoda C, Kurnikova M, Sobolevsky AI. Structural Bases of Noncompetitive Inhibition of AMPA-Subtype Ionotropic Glutamate Receptors by Antiepileptic Drugs. **Neuron**. 2016 Sep 21;91(6):1305-1315. PubMed PMID: <u>27618672</u>; PubMed Central PMCID: PMC5033713.
  - c. Twomey EC, Yelshanskaya MV, Grassucci RA, Frank J, Sobolevsky AI. Elucidation of AMPA receptor-stargazin complexes by cryo-electron microscopy. **Science**. 2016 Jul 1;353(6294):83-6. PubMed PMID: 27365450; PubMed Central PMCID: PMC5125255.
  - d. Yelshanskaya MV, Li M, Sobolevsky AI. Structure of an agonist-bound ionotropic glutamate receptor. Science. 2014 Aug 29;345(6200):1070-4. PubMed PMID: <u>25103407</u>; PubMed Central PMCID: PMC4383034.

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

# Ongoing Research Support

R01 NS083660, NIH/NINDS Sobolevsky, Alexander (PI) 09/30/13-06/30/23

Structure and Function of AMPA subtype ionotropic glutamate receptors

The major goal of this project is to study mechanisms of desensitization and ion channel block in ionotropic glutamate receptors.

Irma T. Hirschl Career Scientist Award, the Irma T. Hirschl Trust

Alexander Sobolevsky (PI)

07/01/15-06/30/20

Molecular mechanisms of ionotropic glutamate receptor gating, assembly and regulation

The major goal of this project is to study structural mechanisms of ionotropic glutamate receptor gating, assembly and regulation by auxiliary subunits.

R01CA206573, NIH/NCI

Sobolevsky, Alexander (PI)

01/12/17-12/31/21

Structure and Function of Transient Receptor Potential channels

The major goal of this project is to study molecular mechanisms of TRP channel gating and regulation by calcium and various small molecules.

R01NS107253, NIH/NINDS

Sobolevsky, Alexander (PI)

08/01/18-05/31/23

Single-particle cryo-EM characterization of AMPA receptor functional states

The major goal of this project is to study structure and function of AMPA-subtype ionotropic glutamate receptors using advances in single-particle cryo-electron microscopy.

# Oleg V. Klykov, Ph.D.

Born in Chelyabinsk region, USSR, 26th November 1989.

#### **EDUCATION**

• 10/2015 — 10/2019. Ph.D. degree, Utrecht University, Utrecht, The Netherlands.

Promotor: Prof. Dr. Albert J. R. Heck. Copromotor: Dr. Richard A. Scheltema

Biomolecular Mass Spectrometry and Proteomics Group.

Dissertation Title: Advancing Crosslinking Mass Spectrometry as a tool for deciphering the spatial organization of protein assemblies: from molecular machines to biopolymers.

• 09/2007-07/2012. Diploma degree (distinction). Lomonosov Moscow State University, Moscow, Russia.

Supervised by Prof. Dr. Albert T. Lebedev.

Department of Organic Chemistry, Laboratory of Organic Analysis, Mass Spectrometry Division

Diploma Title: Mass-spectrometric monitoring of changes in the Composition of the grass frog skin peptidome caused by bacteria *Micrococcus lutes* and *Staphylococcus aureus*.

#### RESEARCH EXPERIENCE

• BAM Federal Institute for Materials Research and Testing. Berlin, Germany. 09/2012-09/2015.

Supervised by Dr. Michael G. Weller, Division 1.5 Protein Analysis. Research assistant.

Project title: Developing of high-performance affinity methods based on nanoparticles for the analysis of complex protein samples. Major responsibilities: development of HPLC techniques for analysis of different biological samples, development of affinity chromatography techniques based on human IgG antibodies, antibody purification, synthesis and characterization of derivatives of nanodiamond particles and their application in affinity chromatography.

• Columbia University Irving Medical Center. Since 01/2020.

Supervised by Dr. Alexander I. Sobolevsky, Department of Biochemistry and Molecular Biophysics.

### **Postdoctoral Scientist**

Project title: Structural basis for the function and modulation of the Kainate receptors.

#### **INTERNSHIPS**

• University of Munster, Munster, Germany. 05/2011-07/2011.

Supervised by Prof. Luisa De Cola. Organic Synthesis lab. Short-term intern.

Project title: Synthesis and characterization of Aluminum-containing Zeolite materials. Major responsibilities: synthesis of zeolite materials with their further analysis by low-resolution EM methods.

University of North Dakota, Grand Forks, ND, USA. 06/2010-09/2010.

Supervised by Dr. Prof. Kozliak and Dr. Prof. Alena Kubatova.

Physical Chemistry and Analytical Chemistry labs. Short-term intern.

Project title: Developing and modification of methods for determining trace amounts of Arsenic, Antimony, and Selenium in the air. Major responsibilities: experiments on the state-of-art Graphite Atomic Absorption Spectrometer, data processing.

## TEACHING AND ORGANIZATIONAL EXPERIENCE

- Teaching Assistant. Department of Chemistry. 12/2016-01/2018.
- Organizing Committee, 10/2018. 1st Integrative Structural Biology Autumn School, Utrecht University
- Sebastiaan C. de Graaf, Master Student. 02/2018-08/2018 Project title: Developing of Data Visualization
   Platforms for Crosslinking Mass Spectrometry Data.
- Tim Veth, **Master Student.** 05/2017-11/2017. **Project title:** Novel approaches for in vivo crosslinking with lysine-targeting reagents.
- Olympia Hoffman, **Bachelor Student.** 09/2016-02/2017. **Project Title:** Optimization of peptide dimethyl labeling for quantitative proteomics.

#### **AWARDS**

- 2008 Undergraduate Annual Thesis Competition on Analytical Chemistry at the Lomonosov University,
   Winner
- 2018 American Society for Mass Spectrometry (ASMS) Sanibel, Travel Grant
- 2018 Utrecht Institute of Pharmaceutical Scinces, shortlisted for Best PhD Publication Award
- 2019 Netherlands Society for Mass Spectrometry (NVMS) Conference, Travel Fund Award
- 2019 EMBO Practical Course: Integrative and cellular structural Biology, Travel Award

#### **CONFERENCE TALKS AND POSTER PRESENTATIONS**

### **Oral Presentations:**

- Mar 31-Apr 02, **2019**. **Klykov O.**, van der Zwaan C., Meijer A. B., Heck A. J. R., Scheltema R. A. S. **Talk title:** Molecular Architecture of Fibrin Clots by *in situ* Crosslinking Mass Spectrometry. 4<sup>th</sup> NVMS-BSMS conference on Mass Spectrometry, Kerkrade, The Netherlands.
- Jan 24-27, **2019**. **Klykov O.**, van der Zwaan C., Meijer A. B., Heck A. J. R., Scheltema R. A. S. **Flash talk title**: High-resolution structural model of fibrin clots with *in-situ* Crosslinking Mass Spectrometry. ASMS Sanibel, St. Petersburg, FL, USA
- Nov 17-18, **2016**. **Klykov, O.**, Fagerlund, R.D., Wilkinson, M.E., Barendregt, A., Pearce, F.G., Kieper, S.N., Maxwell, H.W.R., Capolupo, A., Heck, A.J.R., Krause, K.L., Bostina, M., Staals, R.H.J., Fineran, P.C. and Scheltema, R.A. **Talk title:** Type I-F Cas1:Cas2-3 CRISPR Adaptation Complex. Structural Proteomics Symposium, Dortmund, Germany.

### **Poster Presentations:**

- EMBO Integrative structural and cellular biology, Paris 2018
- Jan 24-27, **2019**. **Klykov O.**, van der Zwaan C., Meijer A. B., Heck A. J. R., Scheltema R. A. S. **Poster title**: High-resolution structural model of fibrin clots with *in-situ* Crosslinking Mass Spectrometry. ASMS Sanibel, St. Petersburg, FL, USA
  - Jul 02-06, 2018. **Klykov O.,** Fagerlund R.D., Wilkinson M.E., Barendregt A., Pearce F.G., Kieper S.N., Maxwell H.W.R., Capolupo A., Heck A.J.R., Krause K.L., Bostina M., Staals R.H.J., Fineran P.C. and Scheltema R.A. **Poster title:** Molecular Architecture and Spacer Acquisition in Type I-F Cas1:Cas2-3 CRISPR Complex by Structural Mass Spectrometry. EMBO Course: Integrative Modelling of Biomolecular Interactions, Barcelona, Spain.
  - Apr 23-24, 2018. **Klykov, O.,** Fagerlund, R.D., Wilkinson, M.E., Barendregt, A., Pearce, F.G., Kieper, S.N., Maxwell, H.W.R., Capolupo, A., Heck, A.J.R., Krause, K.L., Bostina, M., Staals, R.H.J., Fineran, P.C. and Scheltema, R.A. **Poster title:** Molecular Architecture and Spacer Acquisition in Type I-F Cas1:Cas2-3 CRISPR Complex by Structural Mass Spectrometry. Bijvoet Symposium, Utrecht, The Netherlands.
  - Mar 8-11, 2018. Mayr C. H., **Klykov O.,** Scheltema R.A., Schiller H.B. **Poster title:** Interaction Proteomics of the Pulmonary Extracellular Matrix. 16th ERS Lung Science Conference, Estoril, Portugal.
  - Aug 6-11, 2017. Fagerlund, R.D., Wilkinson, M.E., **Klykov, O.**, Barendregt, A., Pearce, F.G., 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. and Fineran, P.C. **Poster title:** Spacer capture and integration by a type I-F Cas1:Cas2-3 CRISPR adaptation complex. 22nd Biennial Evergreen International Phage Biology Meeting, Olympia, WA, USA.
  - Jun 8-11, 2017. Fagerlund, R.D., Wilkinson, M.E., **Klykov, O.**, Barendregt, A., Pearce, F.G., 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. and Fineran, P.C. **Poster title:** Spacer capture and integration by a type I-F Cas1:Cas2-3 CRISPR adaptation complex. CRISPR 2017, Big Sky, MO, USA.
  - Oct 28, 2016. **Klykov, O.,** Fagerlund, R.D., Wilkinson, M.E., Barendregt, A., Pearce, F.G., Kieper, S.N., Maxwell, H.W.R., Capolupo, A., Heck, A.J.R., Krause, K.L., Bostina, M., Staals, R.H.J., Fineran, P.C. and Scheltema, R.A. **Poster title:** Molecular Architecture and SpacerAcquisition in Type I-F Cas1:Cas2-3 CRISPR Complex by Structural Mass Spectrometry. UIPS symposium, Fort Voordorp, The Netherlands
  - Jul 04-08, 2016. **Klykov O.,** Heck A.J.R., Scheltema R. A. **Poster title**: Extended Shotgun Proteomics Approach for the characterization of human Monocyte Cells. 9th Max Quant Summer School, Oxford, UK.
  - Apr 17-19, 2016. **Klykov O.,** Heck A.J.R., Scheltema R. A. **Poster title:** Extended Shotgun Proteomics Approach for the characterization of human Monocyte Cells. 3rd NVMS-BSMS conference on Mass

Spectrometry, Kerkrade, The Netherlands.

• Jul 8-14, 2012. **Klykov O.,** Samguina T. Yu., Lebedev A. T. **Poster title:** Mass-spectrometric monitoring of changes in the Composition of the grass frog skin peptidome caused by bacteria Micrococcus lutes and Staphylococcus aureus. Mass-spectrometry in Biotechnology and Medicine, Dubrovnik, Croatia.

#### LIST OF PUBLICATIONS

- **Klykov O.,** van der Zwaan C., Heck A.J.R., Meijer A.B., Scheltema R.A. Missing regions within the molecular architecture of human fibrin clots structurally resolved by XL-MS and integrative structural modeling. Proc Natl Acad Sci 117 (4), 2020, 1976-1987.
- Iacobucci C., Piotrowski C., Aebersold R., Amaral B.C., Andrews P., Bernfur K., Borchers C., Brodie N.I., Bruce J.E., Cao Y., Chaignepain S, Chavez J.D., Claverol S., Cox J., Davis T., Degliesposti G., Dong M.Q., Edinger N., Emanuelsson C., Gay M., Goetze M., Gomes-Neto F., Gozzo F.C., Gutierrez C., Haupt C., Heck A.J.R., Herzog F., Huang L., Hoopmann M.R., Kalisman N., Klykov O., Kukacka Z., Liu F., MacCoss M.J., Mechtler K., Mesika R., Moritz R.L., Nagaraj N., Nesati V., Neves-Ferreira A.G.C., Ninnis R., Novák P., O'Reilly F.J., Pelzing M., Petrotchenko E., Piersimoni L., Plasencia M., Pukala T., Rand K.D., Rappsilber J., Reichmann D., Sailer C., Sarnowski C.P., Scheltema R.A., Schmidt C., Schriemer D.C., Shi Y., Skehel J.M., Slavin M., Sobott F., Solis-Mezarino V., Stephanowitz H., Stengel F., Stieger C.E., Trabjerg E., Trnka M., Vilaseca M., Viner R., Xiang Y., Yilmaz S., Zelter A., Ziemianowicz D., Leitner A., Sinz A. First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. Anal Chem, 91, 2019, 6953-6961.
- de Graaf S.C\*, **Klykov O.**\*, van den Toorn H., Scheltema R.A.S. Cross-ID: Analysis and Visualization of Complex XL–MS-Driven Protein Interaction Networks. Journal of Proteome Research, 2, 2019, 642-651.

  \*\*featured on the journal cover\*\*
- **Klykov O.,** Steigenberger B., Pektas S., Fasci D., Heck A.J.R., Scheltema R.A.S. Efficient and robust proteome-wide approaches for crosslinking mass spectrometry. Nature Protocols, 12, 2018, 2964-2990.
- Stucchi R., Plucinska G., Hummel J.J.A., Zahavi E.E., San Juan I.G., **Klykov O.,** Scheltema R.A.S., Altelaar M.A.F., Hoogenraad C.C. Regulation of KIF1A-Driven Dense Core Vesicle Transport: Ca2+/CaM Controls DCV Binding and Liprin-α/TANC2 Recruits DCVs to Postsynaptic Sites. Cell Reports, 3, 2018, 685-700.
- Fagerlund, R.D.\*, Wilkinson, M.E.\*, **Klykov, O.\*,** Barendregt, A., Pearce, F.G., 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. and Fineran, P.C. Spacer capture and integration by a type I-F Cas1:Cas2-3 CRISPR adaptation complex. Proceedings of the National Academy of Sciences of the United States of America, 26, 2017, 5122-5128.
- Klykov O., Weller M. G., Quantification of N-hydroxysuccinimide and N-hydroxysulfosuccinimide by

hydrophilic interaction chromatography (HILIC), Analytical Methods, 7, 2015, 6443-6448.

- Samgina T., Gorshkov V., Artemenko A., Vorontsov E., **Klykov O.**, Ogurtsov S., Zubarev R., Lebedev A., LC-MS/MS with 2D mass mapping of skin secretions' peptides as a reliable tool for interspecies identification inside Rana esculenta complex. Peptides, 34, 2012, 296-302.
- Raeva A., **Klykov O.**, Kozliak E., Pierce D., Seames W., 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, 2011, 4290-4298.

<sup>\*—</sup> equal contribution