BIOGRAPHICAL SKETCH

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NAME: MARSHALL, Liam R.

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

POSITION TITLE: Assistant Research Scientist; Baylor University

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)*	Start Date MM/YYYY	Completion Date MM/YYYY	FIELD OF STUDY
University of Sheffield, England	MChem	09/2009	06/2013	Chemistry
University of Sheffield, England	PhD	09/2013	11/2017	Chemistry
Syracuse University, USA	Postdoctoral Associate	04/2018	01/2024	Biochemistry & Biophysics
Baylor University, USA	Assistant Research Scientist	03/2024	Ongoing	Biochemistry & Biophysics

A. Personal Statement

My research interests focus on understanding the molecular basis necessary to design self-assembled peptide structures, for both catalysis and materials applications. My expertise in biochemistry, peptide design, and microscopy are fundamental in my work developing new self-assembling systems. During my training, I have published papers in a range of journals, including *ACS Catalysis, JACS Au,* and *ACS Applied Materials and Interfaces,* as well as cover features in *ChemBioChem* and *Chemistry- A European Journal.*

I also served as Delegate-at-Large for the Central New York Local Section of the American Chemical Society (ACS). I am deeply involved in the mentorship of undergraduate and high-school students that perform research in our lab, as part of both REU and Project SEED programs. I also serve as a reviewer for Catalysis Science and Technology, Scientific Reports and Biotechnology Letters.

B. Positions, Scientific Appointments and Honors

Positions and Employment

2018-2024 Postdoctoral Researcher, Syracuse University, Syracuse, NY
2024- Assistant Research Scientist, Baylor University, Waco TX

Other Experience and Professional Memberships

2013-2018 Royal Society of Chemistry
2014 Executive committee member for RSC Northern Universities Postgraduate Symposium
2018-2020 New York Academy of Sciences
2018-present American Chemical Society (ACS)
2023-present American Peptide Society
2022-2023 Delegate-at-Large, ACS Central New York Local Section

Honors

2019 AAAS/Science Program for Excellence in Science, Syracuse University Department of Chemistry

2023 Dr. Elizabeth Schram Young Investigator Poster Award, American Peptide Society Symposium

C. Contributions to Science

1. **Metal ions vary the assembly behaviors of metastable peptides.** My PhD work under the mentorships of both Barbara Ciani and Richard Jackson focused on an interdisciplinary effort to synthesize unnatural amino acids and incorporate them within *de novo* designed peptides. Palladium catalyzed cross-couplings changed the entire field of synthesis, and using an amino acid synthon developed by the Jackson lab a wide range of unnatural amino acids can be accessed. I subsequently used this to develop the synthesis of 3 isomers of bipyridylalanine. These amino acids were incorporated within a model coiled coil system developed by the Peacock lab in Birmingham, who became our collaborators in this work. I first used this functionalized coiled coil to investigate how metal ion coordination can change the properties of the lanthanide ion within a metallopeptide, identifying nickel-peptide species which show unusual and tunable relaxation behavior when coordinated to gadolinium. I also found some of these assemblies to be metastable, and readily able to switch between fibrous and coiled coil states controlled by metal ions. This work is currently being prepared for publication.
2. **Structure-activity relationships in catalytic amyloids.** My postdoctoral work with Ivan Korendovych focuses on structure-activity relationships in catalytic amyloids. Originally identified as and thought to be only a disease by-product, in 2014 the first work showed that self-assembled amyloids possess extremely high hydrolysis activity, on par by weight with the natural enzymes such as carbonic anhydrase. I subsequently carried out studies on how these amyloids can form stochastic mixtures which display increased activity over the parent peptides. I carried out a series of kinetic studies to map the interactions between all possible combinations of 8 parent peptides, and using these results I created a set of design rules that creates known positive synergy pairs which increase the overall activity of the peptide. These same rules were then demonstrated to be effective in both intramolecular and more complex designs. I also rationally designed a nine-residue peptide Ac-FYFHFHFQF-NH_2 that self-assembles in the presence of zinc to promote CO_2 hydration with a k_{cat}/K_M of 5×10^5 M^{-1} s^{-1} at pH 9.5, exceeding the activity of human carbonic anhydrase III (HCAIII), which to our knowledge is the first time that natural enzymes have been matched by self-assembled peptides. This work is currently being prepared for publication. The complexity required to promote effective catalysis was achieved with a short peptide using only natural amino acid residues. Current work focuses on characterizing the structure of these assemblies to design even more active species.
    a) Marshall, L. R.; Jayachandran, M.; Lengyel-Zhand, Z.; Rufo, C. M.; Kriews, A.; Kim, M.-C.; Korendovych, I. V., Synergistic Interactions Are Prevalent in Catalytic Amyloids. *ChemBioChem* 2020, *21* (18), 2611-2614
    b) Lengyel-Zhand, Z.; Marshall, L. R.; Jung, M.; Jayachandran, M.; Kim, M.-C.; Kriews, A.[¥]; Makhlynets, O. V.; Fry, H. C.; Geyer, A.; Korendovych, I. V., Covalent Linkage and Macrocylization Preserve and Enhance Synergistic Interactions in Catalytic Amyloids. *ChemBioChem* 2021, *22* (3), 585-591

3. **Structure-activity relationships in peptide hydrogels.** In collaboration with Professor Olga Makhlynets, I have characterized self-healing antimicrobial hydrogels reported by their group using transmission and scanning electron microscopy. Most recently, their group reported a short, nine-residue peptide which forms a redox-responsive, antimicrobial copper-containing hydrogel which undergoes morphological changes depending on the redox state of copper within the hydrogel.
    a) D'Souza, A.; Yoon, J. H.; Beaman, H.; Gosavi, P.; Lengyel-Zhand, Z.; Sternisha, A.; Centola, G.; Marshall, L. R.; Wehrman, M. D.; Schultz, K. M.; Monroe, M. B.; Makhlynets, O. V., Nine-Residue Peptide Self-Assembles in the Presence of Silver to Produce a Self-Healing, Cytocompatible, Antimicrobial Hydrogel. *ACS Appl. Mater. Interfaces* 2020, *12* (14), 17091-17099
    b) D'Souza, A.; Marshall, L. R.; Yoon, J; Kulesha, A; Edirisinghe, D. I. U.; Chandrasekaran, S.; Rathee, P.; Prabhakar, R.; Makhlynets, O.V., Peptide hydrogel with self-healing and redox-responsive properties. *Nano Convergence* **9,** 18 (2022)

4. **Enzyme design.** My training in biochemistry has led to several publications and book chapters on the subject of enzyme and catalytic amyloid design.
    a) **Marshall, L. R.**; Zozulia, O.; Lengyel-Zhand, Z.; Korendovych, I. V., Minimalist de Novo Design of Protein Catalysts. *ACS Catal.* 2019, *9* (10), 9265-9275
    b) **Marshall, L. R.**; Korendovych, I. V., Catalytic amyloids: Is misfolding folding? *Curr. Opin. Chem. Biol.* 2021, *64*, 145-153
    c) **Marshall, L. R.*;** Bhattacharya, S.*; Korendoyvch, I. V., Fishing for catalysis: Experimental and computational approaches to narrowing search space in direct evolution of enzymes", J. Am. Chem. Soc. Au.
    d) **Marshall, L. R.**; Korendovych, I. V., "Screening of oxidative behaviours in catalytic amyloid assemblies", Methods in Enzymology, in press
    e) **Marshall, L. R.**; Makhlynets, O. V., "Stopped-flow measurement of CO_2 hydration activity by catalytic amyloids", Methods in Enzymology, in press
    f) **Marshall, L. R.**; Korendovych, I. V., "Avoiding common pitfalls in designing kinetic protocols for catalytic amyloid studies" Methods in Enzymology, accepted

D. Research Support

<u>Ongoing Research Support</u>

NIGMS R35 GM119634 09/01/16 - 05/31/26

National Institute of General Medical Science.

"Understanding Evolution of Protein Function Through Design"

Role: Assistant Research Scientist
PI: Ivan Korendovych

OMB No. 0925-0001 and 0925-0002 (Rev. 03/2020 Approved Through 02-28-2023)

BIOGRAPHICAL SKETCH

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NAME: KORENDOVYCH, Ivan V.

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

POSITION TITLE: Professor of Chemistry and Biochemistry, James R. Schofield Endowed Chair in Biochemistry

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
National Taras Shevchenko U. of Kiev, Kiev, Ukraine	B.S.	06/1999	Chemistry
National Taras Shevchenko U. of Kiev, Kiev, Ukraine	M.S.	06/2000	Inorganic Chemistry
Tufts University, Medford, MA	Ph.D.	11/2006	Chemistry
University of Pennsylvania, Philadelphia, PA	Postdoctoral	08/2011	Biochemistry & Biophysics

A. Personal Statement

The goal of my research program is to advance molecular understanding of protein function and use this fundamental knowledge to create new enzymes for chemical reactions as well as new therapeutics. My expertise in bioinorganic chemistry, spectroscopy, peptide and protein design prepared me to address challenges in basic medical sciences. With the help NIH funding we developed a thriving research program that produced thirty seven papers, including several in high impact journals, such as *Nature*, *Nature Chemistry*, *JACS*, *Angewandte Chemie*, *ACS Nano* and *ACS Catalysis*. Our work was featured in *Chemical and Engineering News*, *New Scientist*, *Chemistry World*, *Air and Space* magazine and presented in many invited talks at various conferences. Prestigious *Humboldt Fellowship for Experienced Researchers* and Japanese *JSPS Invitational Fellowship* allowed me to establish thriving collaborations with leading researchers in Germany and Japan that are critical to the success of the proposed work. As a DAAD Research Ambassador, I promote international cooperation between research in the US and Germany. I am especially proud of our productivity since my career was somewhat disrupted by a birth of my two daughters in 2019 and 2021. With closest family being 4000 miles away in a war torn country and no daycare it was quite a challenge to manage the lab. Now that the children a bit older older I expect even better results coming out of the lab.

I'm engaged in professional organizations and community service at both local and national levels. I'm the Chair of the Central New York Local Section of the American Chemical Society (ACS). I routinely invite ACS project SEED students from inner city Syracuse school district to spend summers doing research in my lab. At the National level I organized five symposia at various ACS meetings. I am a member of the editorial boards of *PLoS ONE* and *Scientific Reports*. I served on the NSF Graduate Research Fellowship panel, NIH K99 study session and the DOE Science Graduate Fellowships panel.

1. Rufo CM, Moroz YS, Moroz OM, Stohr J, Smith TA, Hu Z, DeGrado WF, Korendovych IV* (2014) Short peptides self-assemble to produce catalytic amyloids. Nature Chem, 6, 303-309. PMID: 24651196
2. Remorino A, Korendovych IV, Wu Y, DeGrado WF, Hochstrasser RM (2011) Residue specific vibrational echoes yield three dimensional structures of a transmembrane protein. Science, 332, 1206-1209. PMID:21636774
3. Marshall LR, Jayachandran M, Lengyel-Zhand Z, Rufo CM, Kriews A, Kim M-C, Korendovych IV (2020) Synergistic Interactions Are Prevalent in Catalytic Amyloids. ChemBioChem, Accepted Article, DOI: 10.1002/cbic.202000205 PMID: 32329215
4. Dolan MA, Basa P, Zozulia O, Lengyel Z, Lebl R, Kohn EM, Bhattacharya S, Korendovych IV* (2019) Catalytic Nanoassemblies Formed by Short Peptides Promote Highly Efficient Transfer Hydrogenation. ACS Nano, 133, 9292-9297.

Positions and Employment

1/2024- present Professor and James R. Schofield Endowed Chair in Biochemistry, Department of Chemistry and Biochemistry, Baylor University
5/2021-12/2023 Professor, Department of Chemistry, Syracuse University
5/2017-5/2021 Associate Professor, Department of Chemistry, Syracuse University
8/2011-5/2017 Assistant Professor, Department of Chemistry, Syracuse University
5/2016-present Adjunct Assistant Professor of Radiology, Upstate Medical University
4/2012-present Adjunct Professor of Biology, Syracuse University
3/2013-present Member, Upstate Medical University Cancer Research Institute

Other Experience and Professional Memberships

2001-present American Chemical Society (ACS)
2005-2006 ACS Northeastern Section Younger Chemists Committee Chair (2005-2006)
2008-2010 New York Academy of Sciences
2010-present Protein Society
2012-2013 Biophysical Society
2014-present Member, NSF Graduate Research Fellowship Review panel.
1/2020-12/2020 ACS Central New York Local Section Chair.

Honors

1993, 1995 Ukrainian National Chemistry Olympiad 3rd Prize
1994 Ukrainian National Chemistry Olympiad 2nd Prize
1995, 1996 International Soros Science Educational Program (ISSEP) Student Grants
1999 Award for the best oral presentation at the XLII Scientific Conference of Polish Chemical Society and Society of Engineers of Chemical Industry (among students)
1999 National Academy of Sciences of Ukraine F. D. Ovcharenko fellowship
2002 XXXVth International Conference on Coordination Chemistry Poster Award, Heidelberg, Germany
2003 Tufts University Graduate Student Symposium 1st prize
2004 Tufts University Graduate School of Arts and Sciences Award for Outstanding Academic Performance
2007 Poster competition award at the Inorganic Chemistry Gordon Research Conference
2007 American Chemical Society Division of Inorganic Chemistry Young Investigator Award
2010 Protein Society Young Investigator Travel Award
2013 Ralph E. Powe Junior Faculty Enhancement Award
2014 Humboldt Research Fellowship
2019 Japan Society for Promotion of Science Invitational Fellowship

C. Contribution to Science

1. **Metal containing amyloids can efficiently catalyze chemical reactions.** We showed that small 7-residue amyloid-forming peptides designed from the first principles form efficient catalysts of ester hydrolysis with activity on par with those of the best small molecule and peptide catalysts reported to date. These results provide the first demonstration of substantial catalytic activity in simple peptide amyloids, and from a more practical perspective, open the door to the design of highly stable, robust, and easily varied enzyme-like catalysts. Moreover, by mixing different peptides we were able to observe synergistic interactions that increased activity even further. In the previous grant period we have greatly expanded on this initial finding demonstrating that **C**atalytic **AM**yloid forming **P**eptides (CAMPs) can promote hydrolysis of highly challenging substrates (paraoxon), oxygen and hydrogen peroxide activation, carbene transfer. We showed that CAMPs can be used in devices and can easily promote tandem reactions. We have also found that synergistic interactions are highly prevalent in CAMP mixtures with different sequences. In collaboration with Prof. Mei Hong we were able to determine the molecular structure of a representative CAMP. Perhaps, most significantly, we have rationally designed a 9-residue peptide Ac-FYFHFHFQF-$CONH_2$ that self-assembles in the presence of zinc to promote CO_2 hydration with k_{cat}/K_M of 5.3 x 10^5 M^{-1} s^{-1} at pH 9.5 (work being prepared for publication), exceeding the activity of human carbonic anhydrase III (HCAIII) almost two-fold. Furthermore, introduction of tryptophan into the sequence to yield Ac-FYFHFHFQW-$CONH_2$ results in a drastic reduction in the effective pK_a of the catalyst to pH 8.1 making it at least 100-fold faster than any reported to date artificial catalysts of CO_2 hydration. To our knowledge this is the first time anyone was able to match enzymes in their own game.

This is even more exciting considering that the functional complexity needed to promote efficient catalysis was achieved by supramolecular self-assembly of short peptides containing only natural amino acid residues. Unlike enzymes, catalytic amyloids are extremely robust and can be used under harsh conditions to help promote CO_2 capture and fixation.

a. Makhlynets OV, Gosavi PM, Korendovych IV. (2016) Short Self-Assembling Peptides Are Able to Bind Copper and Activate Oxygen. Angew Chem Int Ed Engl, 55, 917-920. PMID: 27276534

b. Lee M, Wang T, Makhlynets OV, Wu Y, Polizzi NF, Wu H, Gosavi PM, Stöhr J, Korendovych IV, DeGrado WF, Hong M. (2017) Zinc-binding Structure of a Catalytic Amyloid from Solid-State NMR. Proc Natl Acad Sci U S A. 114:6191-6196. PMID: 28566494

c. Lengyel Z, Rufo CM, Moroz YS, Makhlynets OV, Korendovych IV* (2018) Copper-containing Catalytic Amyloids Promote Phosphoester Hydrolysis and Tandem Reactions. ACS Catal, *8*, 59-62 PMID: 30319881

d. Zozulia O, Korendovych IV* (2020) Semi-rationally Designed Short Peptides Self-Assemble and Bind Hemin to Promote Cyclopropanation. Angew Chem Int Ed Engl, 59, 8108-8112 PMID: 32128962

2. **NMR guided directed evolution.** Directed evolution has emerged as a powerful tool for improving protein properties and imparting completely new functionalities onto existing proteins. Nonetheless, it is inherently limited by the astronomical number of possible amino acid sequences to screen. While the currently available methods can predict the locations of the amino acids to be mutated, all of the them rely heavily on structural and/or bioinformatic knowledge that is not always *a priori* available. Even more importantly, all existing algorithms have a poor track record in locating productive mutations away from the active site. Our preliminary data obtained in the previous grant period demonstrates that NMR chemical shift perturbation data obtained from ^{1}H-^{15}N HSQC titration of an enzyme with a competitive inhibitor that structurally closely resembles the substrate correlates with a probability of finding a mutation in that or the neighboring position. This observation was done in a retrospective analysis of previously reported Kemp eliminases of the AlleyCat family (publication a) upon titration with 5-nitrobenzotriazole (5-NBT), a competitive inhibitor of Kemp elimination. This remarkable correlation was then applied prospectively and in three additional mutations away from the active site identified by NMR we were able to further improve the catalytic efficiency of AlleyCat7 by more than 3-fold to reach 4,500 $M^{-1}s^{-1}$. Next we set out to explore whether NMR guided directed evolution could be applied to other proteins and other reaction mechanisms. Recently we discovered that Kemp elimination can be promoted by a redox mechanism in cytochrome P450BM3 (publication b), so we tested whether myoglobin (Mb), a small non-enzymatic protein can be evolved to become a Kemp eliminase. NMR titration of Mb-H64V, in which the distal histidine 64 was removed to provide access for substrates to the metal, with 5-NBT identified several regions of high chemical shift. Subsequent saturation mutagenesis in those positions yielded a triple mutant Mb-H64G/H68A/L29I that shows catalytic efficiency of $1.5x10^{7}$ $M^{-1}s^{-1}$ that is only 1-2 orders away from the diffusion limit. Given the ease such drastic increase in efficiency in just one round of directed evolution we are confident that our approach will be broadly applicable.

a. Moroz OV, Moroz YS, Wu Y, Olsen AB, Cheng H, Mack KL, McLaughlin JM, Raymond EA, Zhezherya K, Roder H, Korendovych IV* (2013) A Single Mutation in a Regulatory Protein Produces Evolvable Allosterically Regulated Catalyst of Unnatural Reaction. Angew Chem Int Ed, 52, 6246-6249. PMID: 23630096

b. Li A, Wang B, Ilie A, Dubey KD, Bange G, Korendovych IV, Shaik S, Reetz MT (2017) A redox-mediated Kemp Eliminase Nat Commun, 8, 14876. PMID: 28348375.

c. Bhattacharya S, Margheritis EG, Takahashi K, Kulesha A, D'Souza A, Kim I, Yoon JH, Tame JRH, Volkov AN, Makhlynets OV, Korendovych IV. NMR-guided directed evolution. Nature. 2022;610(7931):389- 93.

3. **Minimalist design of protein catalysts.** Design of a new catalytic function in proteins, apart from its inherent practical value, is important for fundamental understanding of enzymatic activity. We developed a computationally inexpensive, minimalistic approach that focuses on introducing a single highly reactive residue into proteins to achieve catalysis. We showed that this method can be easily generalized to various chemical transformations, such as the retroaldol reaction, Kemp elimination and ester hydrolysis. Directed evolution allowed for further improvement of protein's catalytic efficiency. Despite the seeming simplicity, the catalysts produced by this approach are highly active. AlleyCat7, an evolved catalyst of Kemp elimination, shows the k_{cat} value that is ca. 5-fold higher than that of a catalytic antibody for Kemp

elimination and the corresponding k_{cat}/k_{uncat} value of more than 10^6. The catalytic efficiency of AlleyCatE (publication a), a stereoselective, allosterically regulated esterase, is higher than that of any previously reported *de novo* designed esterases and is on par with that of catalytic antibodies. The catalytic efficiency of AlleyCatR, an allosterically regulated retroaldolase is on par with that of other designed retroaldolases. The simplicity of our design protocol should complement and expand the capabilities of current state-of-art approaches to protein design and engineering. Moreover, we have demonstrated that *de novo* designed proteins of the AlleyCat family can be utilized practically to posttranslationally selectively modify calmodulin-binding peptides (publication b) opening the path to using AlleyCats in chemical biology applications. The promiscuous nature of *de novo* designed proteins allows for a large substrate variability: we have shown that AlleyCat2 can efficiently convert leflunomide, a immunomodulatory pharmaceutical, into its active form, teriflunomide (publication c) suggesting that proteins evolved for model reactions can be used as starting points for subsequent specialization for practically important reactions/substrates.

Metal-based allostery in AlleyCats allows for development of catalytically amplified, genetically encoded sensors for metal ions. Mutating a single residue in each EF-hand of the allosterically regulated Kemp eliminase AlleyCat to introduce an additional negative charge and/or longer side chain (i.e. Asp to Glu) results in a reversal of metal binding preferences (publication d) making it suitable for directed evolution via a colorimetric, catalytically amplified readout that is linked to lanthanide binding.

a. Moroz YS, Dunston TT, Makhlynets OV, Moroz OV, Wu Y, Yoon JH, Olsen AB, McLaughlin JM, Mack KL, Gosavi PM, van Nuland NAJ, Korendovych IV (2015) New Tricks for Old Proteins: Single Mutations in a Nonenzymatic Protein Give Rise to Various Enzymatic Activities. J Am Chem Soc, *137*, 14905. PMID: 26555770

b. Gosavi PM, Jayachandran M, Rempillo JJL, Makhlynets OV, Korendovych IV (2018) Designed Enzyme Promotes Selective Post-translational Acylation. ChemBioChem, 19, 1605-1608 PMID: 29756279.

c. Caselle EA, Yoon JH, Bhattacharya S, Rempillo JJL, Lengyel Z, D'Souza A, Moroz YS, Tolbert PL, Volkov AN, Forconi M, Castaneda CA, Makhlynets OV, Korendovych IV (2019) Kemp Eliminases of the AlleyCat Family Possess High Substrate Promiscuity. ChemCatChem, 11, 1425-1430. PMID: 31788134

d. Mack KL, Moroz OV, Moroz YS, Olsen AB, McLaughlin JM, Korendovych IV* (2013) Reprogramming EF-hands for Design of Catalytically Amplified Lanthanide Sensors. J Biol Inorg Chem, 18, 411-418 PMID: 23420322.

4. **Development of a novel fluorescence probe.** Tryptophan's intrinsic fluorescence provides invaluable information about protein folding, dynamics, and structure. One of tryptophan's strengths is dependence of its fluorescence on local microenvironment. The very same dependence is its Achilles' heel: large shifts of quantum yields and fluorescence maxima positions could potentially change FRET and quenching efficiencies. We discovered that, unlike the previously developed tryptophan mimics, β-(1-Azulenyl)-L-Alanine (AzAla), a fluorescent pseudoisosteric analog of tryptophan has very little dependence on its local microenvironment. AzAla can be selectively excited at 342 nm, far away from most intrinsic fluorophores. AzAla shows a single exponential fluorescence decay that allows for easy deconvolution of fluorescence lifetime data. Weak environmental dependence of AzAla fluorescence allows for the use of even weak intrinsic quenchers, such as methionines and histidines to monitor protein-protein interactions while not perturbing them in both aqueous and membrane environments (publications a-b). These unique properties of AzAla together with its simple photophysics suggest great promise for this tryptophan mimic as a chemical biology tool. We have incorporated AzAla into the influenza A virus M2 proton channel without perturbing protein's function (publication c). AzAla's sensitivity to protonation state of the nearby histidines and the lack of environmental fluorescence dependence allowed us for direct and straightforward determination of histidine pK_a values in ion channels. In collaboration with the group of Prof. Broos (U. of Groningen) we used a tryptophan auxotroph of the gram-positive bacterium *Lactococcus lactis* to incorporate AzAla into proteins *in vivo* with excellent efficiency (publication d). *L. lactis* is an attractive host for recombinant production of proteins including membrane proteins.

a. Moroz, Y.S., Binder, W., Nygren, P., Caputo, G.A., Korendovych, I.V.* (2013) Painting Proteins Blue: ß-(1-Azulenyl)-L-Alanine as a Tryptophan Mimic for Studying Protein-Protein interactions. Chem. Commun. 49, 490-492. PMID: 23207368

b. Ridgeway, Z., Picciano, A.L., Gosavi, P.M., Moroz, Y.S., Angevine, C.E., Chavis, A.E., Reiner, J., Korendovych* I.V., Caputo, G.A.* (2015) Functional Characterization of a Melittin Analog Containing a Non-natural Tryptophan Analog. Peptide Sci. 24, 561-570. PMID: 25670241
c. Gosavi, P.M., Moroz Y.S., Korendovych, I.V.* (2015) ß-(1-Azulenyl)-L-Alanine - a Functional Probe Studies of Membrane Proteins. Chem. Commun., 51, 5347-5350. PMID: 25645241
d. J. Shao, I.V. Korendovych, J. Broos (2015) Biosynthetic Incorporation of the Azulene Moiety in Proteins with High Efficiency. Amino Acids, 47, 213-216. PMID: 25399056

My Bibliography link to complete list of publications:
http://www.ncbi.nlm.nih.gov/sites/myncbi/ivan.korendovych.1/bibliography/47575991/public/?sort=date&direction=ascending

D. Research Support.
Ongoing Research Support

NIGMS R35 GM119634 09/01/16 - 05/31/26
National Institute of General Medical Science.
"Understanding Evolution of Protein Function Through Design"
Role: PI

Completed Research Support

OISE-17-63891-0 04/01/18 - 09/30/18
CRDF GLOBAL
"Metallopeptide assemblies for pesticide remediation"
Role: PI

Nappi Family Award 01/01/16 - 12/31/17
Sponsor: Sam Nappi Family.
"*Development of novel ^{18}F-based highly specific radiotracer for early noninvasive in vivo detection of hepatocellular carcinoma using Positron Emission Tomography*"
Role: PI

NSF 1332349 08/01/13 - 08/21/17
NSF Emerging Frontiers in Research and Innovation (EFRI) Program
"*Continuous Liquid Fuel Production via Scalable Biosynthesis of Enzyme-Quantum Dot Hybrid Photocatalysts*"
Role: co-PI