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Tomasz Włodarski

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- born November 6th 1984
- citizen of the Republic of Poland

Education

2008 - 2013	**University of Warsaw,** Warsaw, Poland Inter-Faculty Interdisciplinary Doctoral Studies in Natural Sciences and Mathematics PhD studies in Bioinformatics and Biophysics *Thesis: "Application of computational biophysics and bioinformatics to multiscale biological problems" (advisors: Prof. Paweł Golik and Prof. Marek Niezgódka)*
2003 - 2008	**Jagiellonian University,** Krakow, Poland M. Sc. in Biophysics, 2008 *Thesis: "Study of interactions of fluorescent dyes (Col-F and Sulphorodamine B) with collagens"* *(advisors: Prof. Jerzy Dobrucki and Prof. Marta Pasenkiewicz-Gierula)*

Work Experience

09/2023 - …	**Institute of Biochemistry and Biophysics** Polish Academy of Sciences, Warsaw, Poland
06/2013 - 08/2023	**University College London,** Institute of Structural and Molecular Biology, London, UK
10/2016 - 04/2019	**University of Cambridge,** Chemistry Department, Cambridge, UK

Joint EMBO Postdoctoral Fellow in Prof. John Christodoulou (UCL) and Prof. Michele Vendruscolo (Univ. of Cambridge) groups.

Scientific Experience

11/2011 – 02/2012	**University of Cambridge**, **Chemistry Department**, Cambridge, UK visiting student in Prof. Michele Vendruscolo group *(EMBO Short Term Fellowship)*
07/2011	**Max F. Perutz Laboratories**, Vienna, Austria visiting student in Computational Biophysics of Macromolecules Group *(advisor: Dr. Bojan Zagrovic)*
02/2010	**University of Texas Medical Branch at Galveston,** Galveston, TX, USA visiting student in Bioinformatics and System Biology Group *Project: "Analysis of sequencing data of human fragile sites"* *(advisor: Prof. Maga Rowicka)*
08/2009	**Mediterranean Institute for Life Sciences**, Split, Croatia Summer studentship in Computational Biophysics of Macromolecules Group *Project: "Conformational selection vs induced fit in protein-protein binding"* *(advisor: Dr. Bojan Zagrovic)*
07/2008 – 08/2008	**Mediterranean Institute for Life Sciences**, Split, Croatia FEBS Summer Scholarship in Computational Biophysics of Macromolecules Group *Project: "Conformational selection vs induced fit in protein-protein binding"* *(advisor: Dr. Bojan Zagrovic)*
07/2007 – 08/2007	**University of Illinois in Urbana-Champaign** , Urbana-Champaign, IL, USA Summer studentship in Theoretical and Computational Biophysics Group *Project: "Computational study of solvation and hydrophobic effect around a simple molecular compound"* *(advisor: Prof. Klaus Schulten)*

Research Interest:

- protein folding and missfolding
- computational protein design
- molecular dynamics simulations
- integrative structural biology
- protein structure and dynamics
- structural bioinformatics
- machine learning

Honors and Fellowships:

- EMBO Long Term Fellowship (2013)
- EMBO Short Term Fellowship (2011)
- Foundation for Polish Science Scholarship - START 2011
- FEBS Summer Scholarship (2008)
- FEBS prize for the best Summer Scholarship report in 2008

Research Grants:

- **POLONEZ BIS** grant from the National Science Centre for the project: "Co-translational protein folding in the light of ribosome evolution". (2023-2025)

Computational Grants:

- **LUMI EUROHPC-JU,** Regular Access 2022, EU: Computational microscopy: in-cell co-translational folding and misfolding in health and disease **(co-Principal Investigator)**
- **ARCHER2** HecBiosim Grant 2022, UK: *"Structures of oncogenic Ras protein folding intermediates on the ribosome as novel drug targets"* **(co-Principal Investigator)**
- **EPSRC,** Access to High Performance Computing Call, 2022, UK: "*Atomistic insights into co-translational protein folding on the ribosome using enhanced sampling molecular dynamics simulations"* **(co-Principal Investigator)**
- **ARCHER2** HecBiosim Grant 2022, UK: *"Determining the structural basis of co-translational protein folding by integrating state-of-the-art MD simulations with experimental data."* **(co-Principal Investigator)**
- **EPSRC,** Access to High Performance Computing Call, 2021, UK: *"Computational studies of co-translational protein folding on the ribosome"* **(co-Principal Investigator)**
- **ARCHER2** HecBiosim Grant 2021, UK: **"***Applying coarse-grained molecular dynamics simulations to study ribosome interactions: from nascent polypeptides to small molecule drugs"* **(co-Principal Investigator)**
- **ICM Okeanos** Computational grant, PL (2019 - 2021): "*Studying in atomic details interactions between protein nascent chain and ribosome during protein biosynthesis"* **(Principal Investigator)**
- **ICM Okeanos** - Grand Challenges, PL (2017): *"Integrative structural biology approach to study protein folding and misfolding on the ribosome"* **(Principal Investigator)**
- **ICM Okeanos** - Grand Challenges, PL (2016): *"Studying protein folding and misfolding during biosynthesis on the ribosome using a computational microscope."* **(Principal Investigator)**
- **ARCHER** Leadership Grant, UK (2015-2017): *"Computational studies of co-translational protein folding and mis-folding on the ribosome"* **(co-Principal Investigator)**

Editorial Board:

- Review Editor in Frontiers in Molecular Biosciences (Biological Modeling and Simulation)

Other Experience:

- EMBO Laboratory Leadership Course for Postdocs (2018)
- Polonium Foundation Scientific Content Manager (2017 - 2021)

Publications:

1. Chan, S.H.S., **Włodarski, T.,** Streit, J., Cassaignau, A.M.E., Woodburn, L., Ahn, M., Waudby, C.A., Budisa, N., Cabrita, L.D., Christodoulou, J. 2022 *"The ribosome stabilises partially folded intermediates of a nascent multi-domain protein"* **Nat. Chem.** *14, 1165–1173. https://doi.org/10.1038/s41557-022-01004-0*
2. **Włodarski, T.**, Ahn, M., Mitropoulou A., Chan, S.H.S., Sidhu, H., Plessa, E., Becker, T.A., Waudby, C.A., Beckmann, R., Cassaignau, A.M.E., Cabrita, L.D., Christodoulou, J. 2022 *"Modulating co-translational protein folding by rational design and ribosome engineering"* **Nat. Commun.** *13, 4243. https://doi.org/10.1038/s41467-022-31906-z*
3. **Włodarski, T.**, Deckert, A., Cassaignau, A.M.E., Wang, X., Chan, S.H.S., Waudby, C.A., Kirkpatrick, J.P., Vendruscolo, M., Cabrita, L.D., Christodoulou, J.*, 2021. Common sequence motifs of nascent chains engage the ribosome surface and trigger factor.* ***Proc Natl Acad Sci USA*** *118. doi:10.1073/pnas.2103015118*
4. Cassaignau, A.M.E., **Włodarski, T**., Chan, S.H.S., Woodburn, L.F., Bukvin, I.V., Streit, J.O., Cabrita, L.D., Waudby, C.A., Christodoulou, J.*, 2021. Interactions between nascent proteins and the ribosome surface inhibit co-translational folding.* ***Nat. Chem.*** *13, 1214–1220.. https://doi.org/10.1038/s41557-021-00796-x*
5. Burridge, C., Waudby, C.A., **Włodarski, T.**, Cassaignau, A.M.E., Cabrita, L.D., Christodoulou, J.*, 2021. Nascent chain dynamics and ribosome interactions within folded ribosome-nascent chain complexes observed by NMR spectroscopy.* ***Chem. Sci.*** *12, 13120–13126. doi:10.1039/d1sc04313g*
6. Waudby, C.A., **Włodarski, T**., Karyadi, M.-E., Cassaignau, A.M.E., Chan, S.H.S., Wentink, A.S., Schmidt-Engler, J.M., Camilloni, C., Vendruscolo, M., Cabrita, L.D., Christodoulou, J., 2018. *Systematic mapping of free energy landscapes of a growing filamin domain during biosynthesis*. **Proc Natl Acad Sci USA** *115, 9744–9749. doi:10.1073/pnas.1716252115*
7. Redondo, R.A.F., de Vladar, H.P., **Włodarski, T.**, Bollback, J.P., 2017. *Evolutionary interplay between structure, energy and epistasis in the coat protein of the ϕX174 phage family*. **J. R. Soc. Interface** *14. doi:10.1098/rsif.2016.0139*
8. Deckert, A., Waudby, C.A., **Włodarski, T.**, Wentink, A.S., Wang, X., Kirkpatrick, J.P., Paton, J.F.S., Camilloni, C., Kukic, P., Dobson, C.M., Vendruscolo, M., Cabrita, L.D., Christodoulou, J., 2016. *Structural characterization of the interaction of α-synuclein nascent chains with the ribosomal surface and trigger factor.* **Proc Natl Acad Sci USA** *113, 5012–5017. doi:10.1073/pnas.1519124113*
9. Cabrita, L.D., Cassaignau, A.M.E., Launay, H.M.M., Waudby, C.A., **Włodarski, T**., Camilloni, C., Karyadi, M.-E., Robertson, A.L., Wang, X., Wentink, A.S., Goodsell, L., Woolhead, C.A., Vendruscolo, M., Dobson, C.M., Christodoulou, J., 2016. *A structural ensemble of a ribosome-nascent chain complex during cotranslational protein folding*. **Nat. Struct. Mol. Biol.** *23, 278–285. doi:10.1038/nsmb.3182*
10. **Włodarski, T**., Kutner, J., Towpik, J., Knizewski, L., Rychlewski, L., Kudlicki, A., Rowicka, M., Dziembowski, A., Ginalski, K., 2011. *Comprehensive structural and substrate specificity classification of the Saccharomyces cerevisiae methyltransferome*. **PLoS ONE** *6, e23168. doi:10.1371/journal.pone.0023168*

11. **Włodarski, T.**, Zagrovic, B., 2009. *Conformational selection and induced fit mechanism underlie specificity in noncovalent interactions with ubiquitin*. **Proc Natl Acad Sci USA** *106, 19346–19351. doi:10.1073/pnas.0906966106*

Preprints:

1. Javed, A., **Włodarski, T.**, Cassaignau, AME., Cabrita, LD., Christodoulou, J., Orlova, EV. „*Visualising nascent chain dynamics at the ribosome exit tunnel by cryo-electron microscopy"* doi: https://doi.org/10.1101/722611

Languages

- **Polish** - native
- **English** - fluent
- **Russian –** basic
- **German** – basic