Curriculum Vitae – Klára Hlouchová, Ph.D.

Date of birth	06.08.1981, Třebíč, Czech Republic
Work address	Charles University, Faculty of Science, Hlavova 8, 128 43 Prague 2, Czech Republic
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Career

2017- present	**Junior Group Leader / Assistant Professor** at Charles University Prague
2021	CAREER BREAK (third parental leave)
2016	**Research Associate** at Charles University Prague
2014-2015	CAREER BREAK (second parental leave)
2011 – 2013	**Postdoctoral Research Associate**, University of Colorado Boulder, USA (laboratory of Prof. Shelley Copley, theme: Molecular evolution of enzymes and metabolic pathways)
2009-2010	CAREER BREAK (first parental leave)
2005 – 2009	**PhD student** at IOCB, Czech Academy of Science (lab of Prof. Jan Konvalinka)
2006 & 2008	**Visiting Scientist** at National Cancer Institute, Frederick, USA (two one-month research stays, Macromolecular Crystallography Laboratory, group of Dr. Jacek Lubkowski)

Academic Degrees

2009	**PhD** with Prof. Jan Konvalinka, IOCB, Czech Academy of Science and Charles University, Czech Republic
2005	**MSc** in Biochemistry, Charles University, Prague, Czech Republic

Research Interests

- Design and characterization of proteins/protein libraries from canonical/reduced/unnatural amino acids by methods of synthetic biology
- In vitro forward/reverse protein evolution
- Re/construction of minimal biochemical systems

to study evolution of protein structure and function, early origins of life and RNA/protein coevolution

Grants, distinctions, Invited talks etc.

Grants:
VW Stiftung (2021-2025)
HFSP (2019-2022)
Charles University (2020-2022)
Czech Science Foundation (2017-2019)
CIRES Postdoctoral fellowship (2011-2013)

Editorial Board:
Royal Soc. Interface (2018-present), Scientific Reports (2018-2021)

Invited talks:

May 2022	Potential & Limitations of Evolutionary Processes 2022, Israel
April 2022	Advances in Protein Folding, Evolution and Design 2022, Bayreuth, Germany

March 2022 RIKEN BDR Symposium Emergence in Biological Systems: Challenges to Bridging Hierarchies, Japan
Nov 2021 OIST Symposium „New Proteins by Evolution and Engineering“, Japan (online)
May 2021 IDP seminars (idpseminars.com), online
July 2020 Molecular Origins of Life, Munich, Germany
Jan 2016 GRC Origins of Life, TX, USA

Organization of Scientific meetings:

June 2022 RFA preparation, co-organization and mentoring at Ideas Lab “Bringing Chemistry, Physics and Computing to Life” funded by the John Templeton Foundation, Chateau Stirin, Czech Republic

10 most important publications (19 total)

h-index is 10, papers are cited > 400 times (21 times on average)

Tretyachenko V, Vymetal J, Neuwirthova T, Vondrasek J, Fujishima K, **Hlouchova K**. (2022) Modern and prebiotic amino acids support distinct structural profiles in proteins. *Open Biology 12*: 220040. https://doi.org/10.1098/rsob.220040

Giacobelli VG, Fujishima K, Lepsik M, Tretyachenko V, Kadava T, Bednarova L, Novak P, **Hlouchova K.** (2022) In vitro evolution reveals non-cationic protein – RNA interaction mediated by metal ions. *Molecular Biology and Evolution*, msac032. https://doi.org/10.1093/molbev/msac032.

Fried SD, Fujishima K, Makarov M, Cherepashuk I, **Hlouchova K**. (2022) Peptides before and during the nucleotide world: and origins story emphasizing cooperation between proteins and nucleic acids. *Journal of Royal Society Interface* 19: 20210641. https://doi.org/10.1098/rsif.2021.0641

Bornberg-Bauer E, **Hlouchova K**, Lange A. (2021) Structure and function of naturally evolved de novo proteins. *Current Opinions in Structural Biology*. 68, 175-183. https://doi.org/10.1016/j.sbi.2020.11.010

Makarov M, Meng J, Tretyachenko V, Srb P, Březinová A, Giacobelli VG, Bednárová L, Vondrášek J, Dunker AK and **Hlouchová K.** (2021) Enzyme catalysis prior to aromatic residues: reverse engineering of a dephosphoCoA kinase. *Protein Science* https://doi.org/10.1002/pro.4068

Tretyachenko V, Voráček V, Souček R, Fujishima K, and **Hlouchová K.** (2021) CoLiDe: Combinatorial Library Design tool for probing protein sequence space. *Bioinformatics* https://doi.org/10.1093/bioinformatics/btaa804

Vymětal J, Vondrášek J, and **Hlouchová, K.** (2019). Sequence Versus Composition: What Prescribes IDP Biophysical Properties? *Entropy*, *21*(7), 654.

Tretyachenko V, Vymětal J, Bednárová L, Kopecký V, Hofbauerová K, Jindrová H, Hubálek M, Souček R, Konvalinka J, Vondrášek J, and **Hlouchová K.** (2017) Random protein sequences can form defined secondary structure and are well-tolerated in vivo. *SciRep* **7**, 15449.

Yadid I, Rudolph J, **Hlouchova K**, & Copley SD. (2013) Sequestration of a highly reactive intermediate in an evolving pathway for degradation of pentachlorophenol. *Proc Natl Acad Sci US A*. 110, E2182-90.

Hlouchova K, Rudolph J, Pietari JMH, Behlen LS, & Copley SD (2012) Pentachlorophenol hydroxylase, a poorly functioning enzyme required for degradation of pentachlorophenol by Sphingobium chlorophenolicum. *Biochemistry* **51**, 3848-60.