Joseph Matthew Rogers

17th Dec 2020

Joseph 'Joe' Rogers
Department of Drug Design and Pharmacology
Faculty of Health and Medical Sciences
University of Copenhagen
Phone: +45 23 84 00 87
Mail: joseph.rogers@sund.ku.dk
Age: 34
Nationality: British

PROFESSIONAL APPOINTMENTS

2020 - Associate Professor, Department of Drug Design and Pharmacology, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark
2019-2020 Research Scientist II, Vertex Pharmaceuticals, Boston.
2017-2019 Fellow, Vertex Pharmaceuticals, Boston. Industry and drug-discovery program
2013-2017 Post-doc fellow. University of Tokyo, Japan.

EDUCATION

2013 Ph.D. Department of Chemistry, University of Cambridge, UK
2009 M.Sci. B.A. Chemistry, Natural Sciences, University of Cambridge, UK

Book Chapters

2017 **Rogers JM** & Suga H. Molecular technologies for pseudo-natural peptide synthesis and discovery of bioactive compounds against undruggable targets. (Wiley) *Molecular Technologies* (in press)

AWARDS AND HONORS

2019 Vertex VOCAP award (Vertex Outstanding Contributor Award Program) for establishing new technology.
2017 Poster prize. Protein Folding, Evolution and Interactions Symposium, Cambridge.
2016 ACS Chemical Biology poster prize. EMBO Chemical Biology, Heidelberg.
2013 Poster prize. CECAM Intrinsically Disordered Proteins, Zurich.
2009 Top of undergraduate class, Chemistry, University of Cambridge. British Petroleum prize "Most Outstanding Performance"

GRANTS AND FELLOWSHIPS

2019 Hallas-Møller Emerging Investigator Award. Novo Nordisk Fonden. "Massive searches of sequence space to probe diverse protein behaviours" (10,000,000 DKK, ~1,450,000 USD)

2014 Co-wrote JST-ANR, France-Japan, grant 'Molecular technologies for hybrid folded architectures' with H. Suga and I. Huc (Bordeaux). Ranked highest amongst competitors.
2013 Post-doc Fellowship Japan Society for the Promotion of Science (JSPS), long-term award. Nominated by the Royal Society, UK.
2013 Post-doc JSPS Fellowship, short term award (not accepted)

SELECTED TALKS

2020 'Synthesis and analysis of non-proteinogenic peptides by ribosome reprogramming.' Merck, USA. (online)
2019 'Protein & Peptide Drug Discovery' Zealand Pharma. Copenhagen, Denmark.
2018 4th International conference on Circular Proteins and Peptides, Kawasaki, Japan.
2017 63rd Benzon Symposium. New Paradigms of Protein Engineering – applications in modern medicine. Copenhagen, Denmark.

TEACHING EXPERIENCE

2020 Classroom and practical organic chemistry supervision - 3926-E20;Biopharmaceuticals - bioorganisk kemi.
2020 Lectures on drug discovery in industry, and peptides drugs - MIND course in 'Drug Discovery'
2009-2013 Taught ~60 undergraduate students in groups of 1-4; 1st year Chemistry (whole course); 2nd year, Introduction to Chemical Biology; 3rd year, Proteins and Metalloproteins; 4th year MSci, Protein folding, misfolding and disease.

UNIVERSITY SERVICE

2017 Talk. 'Genetic code reprogramming to discovery inhibitory cyclic peptides'. ETH Zurich-Tokyo Joint Symposium of Frontier Chemistry. Tokyo.
2016 Talk. 'Reprogramming the genetic code to discover functional, cyclic, N-methylated peptides: Specific inhibition of a ubiquitin protease' Chemistry department, Cambridge.
2012 Proposed, arranged and chaired 'Biophysics Symposium'. 10x 15 min talks from young researchers in protein science, Chemistry department, Cambridge.
2010 Admissions selection for Corpus Christi College, Cambridge. Attended training and interviewed potential undergraduate chemistry students.
2009 Fund raising for Corpus Christi College, Cambridge. Telephone campaign.

EXTRA TRAINING

2020 PhD supervision: advice, tools, and practices (KU)
2020 PhD supervision: rules and regulations (KU)
2016 MITx 6.00.1x: Introduction to Computer Science and Programming using Python.
MITx 6.00.2x: Introduction to Computational Thinking and Data Science.
UCSD (Coursera): Bioinformatics I; Bioinformatics II

PUBLICATIONS

Refereed Journal Articles

2020 **Rogers JM***, Nawatha M*, Lemma B, Vamisetti BG, Livneh I et al. In vivo modulation of ubiquitin chains by N-methylated non-proteinogenic cyclic peptides. *RSC Chemical Biology.* Advance Article

2020 **Rogers, J. M.** Peptide Folding and Binding Probed by Systematic Non-canonical Mutagenesis. *Frontiers in - Molecular Biosciences* 7, 100. (review)

2020 Tsiamantas C*, **Rogers JM*,** and Suga H. Initiating ribosomal peptide synthesis with exotic building blocks. *Chemical Communications* 56(31). (review)

2020 Tsiamantas, C, Kwon S, **Rogers JM**, Douat C, Huc I, and Suga H. Ribosomal incorporation of aromatic oligoamides as peptide side-chain appendages. *Angewandte Chemie Int Ed Engl.*

2020 Huang Y, Nawatha M, Livneh, I, **Rogers JM**, Sun H., Singh SK, et al. Affinity Maturation of Macrocyclic Peptide Modulators of Lys48-linked Diubiquitin by a Twofold Strategy. *Chemistry A European Journal.*

2019 Nawatha M*, **Rogers JM***, Bonn SM, Livneh I, Lemma B, Mali SM, et al. De novo macrocyclic peptides that specifically modulate Lys48-linked ubiquitin chains. *Nature Chemistry* 11(7), 644-652.

2018 **Rogers JM,** Passioura T & Suga H. Non-proteinogenic deep mutational scanning of linear and cyclic peptides. *Proceeding of the National Academy of Sciences*

2018 **Rogers JM***, Kwon S*, Suga H & Huc I. Ribosomal synthesis and folding of peptide-helical aromatic foldamer hybrids. *Nature Chemistry*

2015 **Rogers JM** & Suga H Discovering functional, non-proteinogenic amino acid containing, peptides using genetic code reprogramming. *Organic & Biomolecular Chemistry* 13:9353-9363. (review)

2014 Huang PS, Oberdorfer G, Xu C, Pei XY, Nannenga BL, **Rogers JM**, DiMaio F, Gonen T, Luisi B & Baker D. High thermodynamic stability of parametrically designed helical bundles. *Science* 346:481-485.

2014 **Rogers JM**, Oleinikovas V, Shammas SL, Wong CT, De Sancho D, Baker CM & Clarke J. Interplay between partner and ligand facilitates the folding and binding of an intrinsically disordered protein. *Proceeding of the National Academy of Sciences* 111:15420-15425.

2014 **Rogers JM**, Wong CT, & Clarke J. Coupled folding and binding of the disordered protein PUMA does not require particular residual structure. *Journal of the American Chemical Society* 136:5197-5200.

2014 Jongkees SAK, Hipolito CJ, **Rogers JM** & Suga H. Model foldamers: applications and structures of stable macrocyclic peptides identified using in vitro selection. *New Journal of Chemistry* 39:3197-3207. (review)

2013 **Rogers JM**, Steward A, & Clarke J. Folding and binding of an intrinsically disordered protein: fast, but not 'diffusion-limited'. *Journal of the American Chemical Society* 135(4):1415-1422.

2012 **Rogers JM***, Shammas SL*, Hill SA* & Clarke J. Slow, reversible, coupled folding and binding of the spectrin tetramerization domain. *Biophysical Journal* 103(10):2203-2214.

2012 Wensley BG, Kwa LG, Shammas SL, **Rogers JM**, Browning S, Yang Z & J Clarke. Separating the effects of internal friction and transition state energy to explain the slow, frustrated folding of spectrin domains. *Proceeding of the National Academy of Sciences* 109(44):17795-17799.

2012 Wensley BG, Kwa LG, Shammas SL, **Rogers JM** & Clarke J. Protein folding: adding a nucleus to guide helix docking reduces landscape roughness. *Journal of Molecular Biology* 423(3):273-283.

2010 Steward A, Chen Q, Chapman RI, Borgia MB, **Rogers JM**, Wojtala A, Wilmanns M & Clarke J. Two immunoglobulin tandem proteins with a linking beta-strand reveal unexpected differences in cooperativity and folding pathways. *Journal of Molecular Biology* 416(1):137-147.

2010 Mallam AL, **Rogers JM** & Jackson SE. Experimental detection of knotted conformations in denatured proteins. *Proceeding of the National Academy of Sciences* 107(18):8189-8194.

*equal contribution