



Kira S. Makarova

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Kira S. Makarova was graduated from Novosibirsk State University, Department of Natural Sciences in 1991 and received her PhD in genetics from the Institute of Cytology and Genetics, Novosibirsk, Russia in 1996. She has been working in the field of Computational Biology and Comparative Genomics since 1989. Dr. Makarova moved to the US in 1997, first, as a Visiting Scientist in Pathology Department at Uniformed Services University of the Health Sciences, Bethesda, MD and then, since 2001, as a Staff Scientist at the National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD. She works in Computational Biology Branch in Dr. Koonin's group focusing her research in many areas of comparative genomics and analysis of structure, function and evolution of protein families. Dr. Makarova received National Institute of Health Director's Award for prediction of novel CRISPR-Cas systems in 2016. She is elected Fellow of the American Academy of Microbiology since 2017. She is a leading expert in classification and protein sequence analysis of CRISPR-Cas systems and has been an invited speaker at many meetings related to CRISPR research. Overall Dr. Makarova has contributed to over 190 scientific papers with over 30,000 citations and an h-index of 62 (Google Scholar).

Abstract: Comparative Genomics Perspective on Discovery and Functional Diversity of CRISPR-Cas Systems

Computational biology and comparative genomics play a dominant role in identification of novel CRISPR-Cas systems. Over the five recent years one new type and twelve new subtypes have been added to the two types and four subtypes known in 2015 for Class 2 (single protein effector) CRISPR-cas systems. Furthermore, multiple variants of Class 1 (multi-subunit effector complexes) systems were found lacking the interference capacity and therefore are predicted to perform functions, distinct from adaptive immunity in the narrow sense. In the first part of my talk I will present the timeline of discovery of new CRISPR-Cas systems and tell about computational biology approaches employed in those studies. The second part of my talk will be focused on evolutionary classification and origin of the CRISPR-cas systems and on further perspectives on discovery of new CRISPR-cas systems and their roles in microbial cells.