

CURRICULUM VITAE

Dr. Darius KAZLAUSKAS

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Education

<i>Year</i>	<i>Institution</i>	<i>Degree</i>
2014	Vilnius University, Lithuania	Biochemistry, PhD
2010	Vilnius University, Lithuania (<i>semester of studies in University of Copenhagen funded by Erasmus scholarship</i>)	Biochemistry, MS
2008	Vilnius University, Lithuania	Molecular biology, BS

Professional experience

<i>Period/Year</i>	<i>Institution</i>	<i>Position</i>
2022-present	EMBL-Partnership institute at Vilnius university Life Science Center	Group Leader
2020-present	Institute of Biotechnology, Vilnius University, Vilnius, Lithuania	Senior Researcher
2016-2020	Institute of Biotechnology, Vilnius University, Vilnius, Lithuania	Researcher
2016,2018,2019	Pasteur Institute, Paris, France	Visiting Researcher
2012-2016	Institute of Biotechnology, Vilnius University, Vilnius, Lithuania	Junior Researcher
2006-2012	Institute of Biotechnology, Vilnius University, Vilnius, Lithuania	Research Assistant

Publications

As of 2022.09.29:

- 21 publications
- 11 presentations at conferences (5 oral presentations)
- H-index 13 (Web of Science)
- Citations 960 (According to Google Scholar)

Research interests

Comparative genomics, virus evolution, protein sequence and structure analysis, protein distant homology detection, protein 3D structure modeling, phylogenetic analysis, CRISPR-Cas systems, Anti-CRISPR proteins, DNA replication.

Honors and awards

2020	Vilnius university Rector's award for scientific achievements
2018	Young scientist scholarship from Lithuanian Academy of Sciences
2015	Laureate of best PhD thesis of 2014 competition held by Lithuanian Society of Young Researchers
2014	Travel Fellowship to attend the ECCB Student Council Symposium in Strasbourg, France
2013	The Research Council of Lithuania scholarship for PhD students actively conducting scientific research
2011	Travel Fellowship to attend the ISMB/ECCB 2011 conference in Vienna, Austria
2011	Outstanding Master's Thesis Award from the Lithuanian Academy of Sciences
2009	ERASMUS/SOCRATES Fellowship to study at the University of Copenhagen

Other academic activities

2018-present	Member of the Federation of European Microbiological Societies (FEMS)
2011-present	Member of the International Society for Computational Biology (ISCB)
2012-present	Member of the International Society for Viruses of Microorganisms (ISVM)
2011-present	Member of Federation of European Biochemical Societies (FEBS)
2012-present	Reviewer for journals „Genome Biology and Evolution“, „PLOS Computational Biology“, “Scientific reports” and “Virus Evolution”

Scientific publications

1. Neri U, Wolf YI, Roux S, Camargo AP, Lee B, **Kazlauskas D**, Chen IM, Ivanova N, Allen LZ, Paez-Espino D, Bryant DA, Bhaya D, RNA Virus Discovery Consortium, Krupovic M, Dolja VV, Kyrpides NC, Koonin EV, and Gophna U (2022) Expansion of the global RNA virome reveals diverse clades of bacteriophages, *Cell* <https://www.sciencedirect.com/science/article/pii/S0092867422011187>
2. Simoliuniene M, Zukauskienė E, Truncaite L, Cui L, Hutinet G, **Kazlauskas D**, Kaupinis A, Skapas M, Crecy-Lagard V, Dedon PC, Valius M, Meskys R, and Simoliunas E. (2021) Pantoea Bacteriophage vB_PagS_MED16-A Siphovirus Containing a 2'-Deoxy-7-amido-7-deazaguanosine-Modified DNA, *Int J Mol Sci* <http://www.ncbi.nlm.nih.gov/pubmed/34298953>
3. Simoliuniene M, **Kazlauskas D**, Zajanckauskaite A, Meskys R, and Truncaite L. (2021) Escherichia coli trxA gene as a molecular marker for genome engineering of felixoviruses, *Biochim Biophys Acta Gen Subj* 1865:129967. <http://www.ncbi.nlm.nih.gov/pubmed/34324954>
4. Liu Y, Demina TA, Roux S, Aiewsakun P, **Kazlauskas D**, Simmonds P, Prangishvili D, Oksanen HM, and Krupovic M. (2021) Diversity, taxonomy, and evolution of archaeal viruses of the class Caudoviricetes, *PLOS Biology* 19:e3001442. <https://doi.org/10.1371/journal.pbio.3001442>
5. Lechuga A, **Kazlauskas D**, Salas M, and Redrejo-Rodriguez M. (2021) Unlimited Cooperativity of Betatectivirus SSB, a Novel DNA Binding Protein Related to an Atypical Group of SSBs From Protein-Primed Replicating Bacterial Viruses, *Front Microbiol* 12:699140. <http://www.ncbi.nlm.nih.gov/pubmed/34267740>
6. Karvelis T, Druteika G, Bigelyte G, Budre K, Zedaveinyte R, Silanskas A, **Kazlauskas D**, Venclovas C, and Siksnys V. (2021) Transposon-associated TnpB is a programmable RNA-guided DNA endonuclease, *Nature* 599:692-696 <http://www.ncbi.nlm.nih.gov/pubmed/34619744>

7. Gasiunas, G., Young, J. K., Karvelis, T., **Kazlauskas, D.**, Urbaitis, T., Jasnauskaite, M., Grusyte, M. M., Paulraj, S., Wang, P. H., Hou, Z., Dooley, S. K., Cigan, M., Alarcon, C., Chilcoat, N. D., Bigelyte, G., Curcuru, J. L., Mabuchi, M., Sun, Z., Fuchs, R. T., Schildkraut, E., Weigele, P. R., Jack, W. E., Robb, G. B., Venclovas, C., & Siksnys, V. (2020). A catalogue of biochemically diverse CRISPR-Cas9 orthologs. *Nat Commun*, *11*(1), 5512. <https://doi.org/10.1038/s41467-020-19344-1>
8. **Kazlauskas, D.**, Krupovic, M., Guglielmini, J., Forterre, P., & Venclovas, C. (2020). Diversity and evolution of B-family DNA polymerases. *Nucleic Acids Res*, *48*(18), 10142-10156. <https://doi.org/10.1093/nar/gkaa760>
9. Wolf, Y. I., Silas, S., Wang, Y., Wu, S., Bocek, M., **Kazlauskas, D.**, Krupovic, M., Fire, A., Dolja, V. V., & Koonin, E. V. (2020). Doubling of the known set of RNA viruses by metagenomic analysis of an aquatic virome. *Nat Microbiol*. <https://doi.org/10.1038/s41564-020-0755-4>
10. Krupovic, M., Varsani, A., **Kazlauskas, D.**, Breitbart, M., Delwart, E., Rosario, K., Yutin, N., Wolf, Y. I., Harrach, B., Zerbini, F. M., Dolja, V. V., Kuhn, J. H., & Koonin, E. V. (2020). Cressdnaviricota: a Virus Phylum Unifying Seven Families of Rep-Encoding Viruses with Single-Stranded, Circular DNA Genomes. *J Virol*, *94*(12). <https://doi.org/10.1128/JVI.00582-20>
11. **Kazlauskas, D.**, Varsani, A., Koonin, E. V., & Krupovic, M. (2019). Multiple origins of prokaryotic and eukaryotic single-stranded DNA viruses from bacterial and archaeal plasmids. *Nat Commun*, *10*(1), 3425. <https://doi.org/10.1038/s41467-019-11433-0>
12. Wolf, Y. I., **Kazlauskas, D.**, Iranzo, J., Lucia-Sanz, A., Kuhn, J. H., Krupovic, M., Dolja, V. V., & Koonin, E. V. (2019). Reply to Holmes and Duchene, "Can Sequence Phylogenies Safely Infer the Origin of the Global Virome?": Deep Phylogenetic Analysis of RNA Viruses Is Highly Challenging but Not Meaningless. *mBio*, *10*(2). <https://doi.org/10.1128/mBio.00542-19>
13. Wolf, Y. I., **Kazlauskas, D.**, Iranzo, J., Lucia-Sanz, A., Kuhn, J. H., Krupovic, M., Dolja, V. V., & Koonin, E. V. (2018). Origins and Evolution of the Global RNA Virome. *mBio*, *9*(6). <https://doi.org/10.1128/mBio.02329-18>
14. **Kazlauskas, D.**, Sezonov, G., Charpin, N., Venclovas, C., Forterre, P., & Krupovic, M. (2018). Novel Families of Archaeo-Eukaryotic Primases Associated with Mobile Genetic Elements of Bacteria and Archaea. *J Mol Biol*, *430*(5), 737-750. <https://doi.org/10.1016/j.jmb.2017.11.014>
15. **Kazlauskas, D.**, Varsani, A., & Krupovic, M. (2018). Pervasive Chimerism in the Replication-Associated Proteins of Uncultured Single-Stranded DNA Viruses. *Viruses*, *10*(4). <https://doi.org/10.3390/v10040187>
16. **Kazlauskas, D.**, Dayaram, A., Kraberger, S., Goldstien, S., Varsani, A., & Krupovic, M. (2017). Evolutionary history of ssDNA bacilladnaviruses features horizontal acquisition of the capsid gene from ssRNA nodaviruses. *Virology*, *504*, 114-121. <https://doi.org/10.1016/j.virol.2017.02.001>
17. **Kazlauskas, D.**, Krupovic, M., & Venclovas, Č. (2016). The logic of DNA replication in double-stranded DNA viruses: insights from global analysis of viral genomes. *Nucleic Acids Res*, *44*(10), 4551-4564. <https://doi.org/10.1093/nar/gkw322>
18. Gudiukaite, R., Gegeckas, A., **Kazlauskas, D.**, & Citavicius, D. (2014). Influence of N- and/or C-terminal regions on activity, expression, characteristics and structure of lipase from *Geobacillus* sp. 95. *Extremophiles*, *18*(1), 131-145. <https://doi.org/10.1007/s00792-013-0605-x>
19. **Kazlauskas, D.**, & Venclovas, Č. (2014). Herpesviral helicase-primase subunit UL8 is inactivated B-family polymerase. *Bioinformatics*, *30*(15), 2093-2097. <https://doi.org/10.1093/bioinformatics/btu204>
20. **Kazlauskas, D.**, & Venclovas, C. (2012). Two distinct SSB protein families in nucleo-cytoplasmic large DNA viruses. *Bioinformatics*, *28*(24), 3186-3190. <https://doi.org/10.1093/bioinformatics/bts626>
21. **Kazlauskas, D.**, & Venclovas, C. (2011). Computational analysis of DNA replicases in double-stranded DNA viruses: relationship with the genome size. *Nucleic Acids Res*, *39*(19), 8291-8305. <https://doi.org/10.1093/nar/gkr564>

Conferences

1. 21st European Conference on Computational Biology (ECCB2022), 2022, Sitges, Kingdom of Spain (poster)
2. Lithuanian Academy of Sciences conference “Biofuture: Prospects of Natural and Life Sciences”, 2020, Vilnius, Lithuania (oral)
3. Lithuanian Academy of Sciences conference “Biofuture: Prospects of Natural and Life Sciences”, 2019, Vilnius, Lithuania (oral)
4. Lithuanian Academy of Sciences conference “Biofuture: Prospects of Natural and Life Sciences”, 2018, Vilnius, Lithuania (oral)
5. Life Sciences Baltics, 2018, Vilnius, Lithuania (poster)
6. Viruses of Microbes, 2018, Wroclaw, Poland (poster)
7. Lithuanian Academy of Sciences conference “Biofuture: Prospects of Natural and Life Sciences”, 2015, Vilnius, Lithuania (oral)
8. European Conference on Computational Biology, 2014, Strasbourg, France (oral and poster)
9. XIIIth International Conference of Lithuanian Biochemical Society, 2014, Birštonas, Lithuania (poster)
10. Meeting of the International Society for Viruses of Microorganisms, 2012, Brussels, Belgium (poster)
11. International Society for Computational Biology / European Conference on Computational Biology, 2011, Vienna, Austria (poster)

International and national projects:

1. EMBL-Partnership institute at Vilnius university Life Science Center “**Function of highly diverged Cas7 homolog (gp87) in phage VpaE1**” (2022-03-2023-09), No. 01.2.2-CVPA-V-716-01-0001. Budget 85000 EUR. Project leader **D. Kazlauskas**
2. COVID-19 R&D Implementation scheme (SMART) “**Expanding the CRISPR toolbox for rapid detection and genomic surveillance of SARS-CoV-2 variants of concern**” (2021-11-2023-09), No. 13.1.1-LMT-K-718-05-0021. Budget 300000 EUR. Project leader **D. Kazlauskas**
3. Researcher groups project “**Search for Anti-CRISPR proteins and research of their action**” (2020-05-2022-11), No. S-MIP-20-39. Budget 150000 EUR. Project leader T. Šinkūnas, secondary project implementer **D. Kazlauskas**
4. Contract-based research project for the CasZyme company „**Sequence analysis of gene editing tools**“ (2019), No. 01.2.1-MITA-T-851-02-0096. Budget 30000 EUR. Project leader Česlovas Venclovas, principal implementer **D. Kazlauskas**.
5. European Social Fund under the No 09.3.3-LMT-K-712 “Development of Competences of Scientists, other Researchers and Students through Practical Research Activities” measure,

- „Development of RNA virus sequence profiles database“** (2019-06-2019-08). No. 09.3.3-LMT-K-712-14-0027. Budget 8000 EUR. Project leader **D. Kazlauskas**.
6. FEBS Short-term Fellowship to conduct research at Institute Pasteur, Paris. **“Diversity and evolution of CRISPR-associated archaeo-eukaryotic primases in bacteria”** (2018-03-2018-05). Budget 4565 EUR. Project leader **D. Kazlauskas**.
 7. European Social Fund activity „Improvement of researchers’ qualification by implementing world-class R&D projects“ **„Computational study of evolutionary relationships, genomic distribution, structural and functional properties of DNA polymerases“** (2018-2021). No: 09.3.3-LMT-K-712-01-0080. Budget 597000 EUR. Project leader Česlovas Venclovas, principal implementer **D. Kazlauskas**.
 8. Bilateral Lithuanian–French program “Gilibert”, **„Archaeo-eukaryotic DNA replication proteins in bacteria and their mobile genetic elements: distribution and diversity“** (2017-2018). No. TAP LZ-17-007. Budget 20000 EUR. Project leader Česlovas Venclovas, principal implementer **D. Kazlauskas**.
 9. EMBO Short-term Fellowship to conduct research at Institute Pasteur, Paris. **“Distribution and diversity of archaeo-eukaryotic DNA replication proteins in bacteria and their mobile genetic elements”** (2016-09-2016-12) No. ASTF-82–2016. Budget 7609 EUR. Project leader **D. Kazlauskas**.
 10. European Social Fund under the Global Grant measure, **„Making use of large-scale biological data for the development of a new method to assess protein models and for studying DNA replication and repair systems in bacteria and viruses“** (2013-2015). No. VP1-3.1-ŠMM-07-K-03-004. Budget 286000 EUR. Project leader Česlovas Venclovas, principal implementer **D. Kazlauskas**.

Teaching experience

Bioinformatics lectures for Ukrainian students at summer school (2022-07)

Conducting biochemistry course seminars for undergraduate students in biochemistry at Vilnius University (2017/2018 academic year)

Teaching of Bioinformatics course for undergraduate students of Biochemistry at Vilnius University (Fall semester 2017)

Supervising/supervised six bachelor, one master student and seven internships (two international internships from Cambridge University and the University of Manchester).