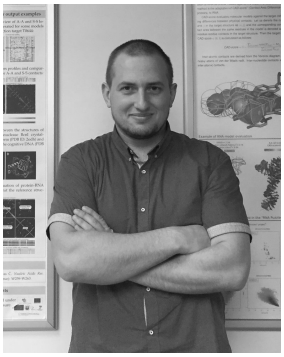
Dr. Kliment Olechnovič

Updated on 2025-09-01.
Latest CV online: https://www.kliment.lt | pdf.



General information

Occupation	Senior Researcher at Vilnius University Life Sciences Center
Email	kliment.olechnovic@bti.vu.lt
GitHub	https://github.com/kliment-olechnovic
Google Scholar	https://scholar.google.lt/citations?user=uT_t5ewAAAAJ
ORCID	https://orcid.org/0000-0003-4918-9505
Semantic Scholar	https://www.semanticscholar.org/author/2671554
Bluesky	https://bsky.app/profile/kliment-olechnovic.bsky.social

Education

2012–2017	Ph.D. Computer Science, Vilnius University
2010–2012	M.S. Computer Science, Vilnius University (*Magna Cum Laude*)
2005–2009	B.S. Bioinformatics, Vilnius University

Work experience

2025–now	Senior Researcher, permanent (Vilnius University / Life Sciences Center / Institute of Biotechnology)
2025	Visiting Researcher, for 8 weeks (EPFL LPDI, Lausanne, Switzerland)
2023–2025	MSCA Postdoctoral Fellow, for 2 years (CNRS Laboratoire Jean Kuntzmann, Grenoble, France)
2020–2023	Senior Researcher (Vilnius University / Life Sciences Center / Institute of Biotechnology)
2021–2023	Visiting Researcher, for 28 weeks in total (CNRS Laboratoire Jean Kuntzmann, Grenoble, France)
2017–2020	Researcher (Vilnius University / Life Sciences Center / Institute of Biotechnology)
2019–2020	Visiting Researcher, for 9 weeks (Inria, Grenoble, France)
2013–2017	Junior Researcher (Vilnius University / Institute of Biotechnology)
2010–2013	Research Engineer (Vilnius University / Institute of Biotechnology)
2009–2010	Research Engineer (Institute of Biotechnology, Vilnius)
2007–2008	C++ software developer (4Team Corporation, Vilnius)

Publications

Research papers

1. Voronota-LT: efficient, flexible and solvent-aware tessellation-based analysis of atomic interactions.
   Olechnovič K, Grudinin S.
   J Comput Chem. 2025 Jul;46(19):e70178.
   doi:10.1002/jcc.70178
   PMID:40632668.
   Zenodo doi:10.5281/zenodo.15877514.

2. FTDMP: A Framework for Protein-Protein, Protein-DNA, and Protein-RNA Docking and Scoring.
   Olechnovič K, Banciul R, Dapkūnas J, Venclovas Č.
   Proteins. 2025 Jan 2.
   doi:10.1002/prot.26792.
   PMID:39748638.

3. PPI3D: a web server for searching, analyzing and modeling protein-protein, protein-peptide and protein-nucleic acid interactions.
Dapkūnas J, Timinskas A, **Olechnovič K**, Tomkuvienė M, Venclovas Č.
Nucleic Acids Res. 2024 Apr.
doi:10.1093/nar/gkae278.
PMID:38619046.

4. TemStaPro: protein thermostability prediction using sequence representations from protein language models.
Pudžiuvelytė I, **Olechnovič K**, Godliauskaite E, Sermokas K, Urbaitis T, Gasiunas G, Kazlauskas D.
Bioinformatics. 2024 Apr 4.
doi:10.1093/bioinformatics/btae157.
PMID:38507682.

5. VoroIF-GNN: Voronoi tessellation-derived protein-protein interface assessment using a graph neural network.
Olechnovič K, Venclovas Č.
Proteins. 2023 Jul 21.
doi:10.1002/prot.26554.
PMID:37482904.

6. Prediction of protein assemblies by structure sampling followed by interface-focused scoring.
Olechnovič K, Valančauskas L, Dapkūnas J, Venclovas Č.
Proteins. 2023 Aug 14.
doi:10.1002/prot.26569.
PMID:37578163.

7. Impact of AlphaFold on Structure Prediction of Protein Complexes: The CASP15-CAPRI Experiment.
Lensink M, Brysbaert G, Raouraoua N, Bates P, Giulini M, Vargas Honorato R, van Noort C, Teixeira J, MJJ Bonvin A, Kong R, Shi H, Lu X, Chang S, Liu J, Guo Z, Chen X, Morehead A, Roy R, Wu T, Giri N, Quadir F, Chen C, Cheng J, Del Carpio C, Ichiishi E, Fernández-Recio J, Harmalkar A, Chu L, Canner S, Smanta R, Gray J, Li H, Lin P, He J, Tao H, Huang S, Roel J, Jimenez-Garcia B, Christoffer C, Jain A, Kagaya Y, Kannan H, Nakamura T, Terashi G, Verburgt J, Zhang Y, Zhang Z, Fujuta H, Sekijima M, Kihara D, Khan O, Kotelnikov S, Ghani U, Padhorny D, Beglov D, Vajda S, Kozakov D, Negi S, Ricciardelli T, Barradas-Bautista D, Cao Z, Chawla M, Cavallo L, Oliva R, Yin R, Cheung M, Guest J, Lee J, Pierce B, Shor B, Cohen T, Halfon M, Schneidman-Duhovny D, Zhu S, Yin R, Sun Y, Shen Y, Maszota-Zieleniak M, Bojarski K, Lubecka E, Marcisz M, Danielsson A, Dziadek L, Gaardlos M, Giełdoń A, Liwo J, Samsonov S, Slusarz R, Zieba K, Sieradzan A, Czaplewski C, Kobayashi S, Miyakawa Y, Kiyota Y, Takeda-Shitaka M, **Olechnovič K**, Valančauskas L, Dapkūnas J, Venclovas C, Wallner B, Yang L, Hou C, He X, Guo S, Jiang S, Ma X, Duan R, Qiu L, Xu X, Zou X, Velankar S, Wodak S.
Proteins. 2023 Oct 31.
doi:10.1002/prot.26609.
PMID:37905971.

8. Discriminating Physiological from Non-Physiological Interfaces in Structures of Protein Complexes: A Community-Wide Study.
Schweke H, Xu Q, Tauriello G, Pantolini L, Schwede T, Cazals F, Lhéritier A, Fernandez-Recio J, Rodríguez-Lumbreras LÁ, Schueler-Furman O, Varga JK, Jiménez-García B, Réau MF, Bonvin A, Savojardo C, Martelli P-L, Casadio R, Tubiana J, Wolfson H, Oliva R, Barradas-Bautista D, Ricciardelli T, Cavallo L, Venclovas Č, **Olechnovič K**, Guerois R, Andreani J, Martin J, Wang X, Kihara D, Marchand A, Correia B, Zou X, Dey S, Dunbrack R, Levy E, Wodak S.
Proteomics. 2023 Jun 27.
doi:10.1002/pmic.202200323.
PMID:37365936.

9. Modeling SARS-CoV2 proteins in the CASP-commons experiment.
Kryshtafovych A, Moult A, Billings WM, Della Corte D, Fidelis K, Kwon S, **Olechnovič K**, Seok C, Venclovas Č, Won J, et al.
Proteins. 2021 Aug 30.
doi:10.1002/prot.26231.
PMID:34462960.

10. Prediction of protein assemblies, the next frontier: The CASP14-CAPRI experiment.
Lensink MF, Brysbaert G, Mauri T, Nadzirin N, Velankar S, Chaleil RAG, Clarence T, Bates PA, Kong R, Liu B, Yang G, Liu M, Shi H, Lu X, Chang S, Roy RS, Quadir F, Liu J, Cheng J, Antoniak A, Czaplewski C, GiełdoŃ A, Kogut M, Lipska AG, Liwo A, Lubecka EA, Maszota-Zieleniak M, Sieradzan AK, Ślusarz R, Wesołowski PA, ZiĘba K, Del Carpio Muñoz CA, Ichiishi E, Harmalkar A, Gray JJ, Bonvin AMJJ, Ambrosetti F, Honorato RV, Jandova Z, Jiménez-García B, Koukos PI, Van Keulen S, Van Noort CW, Réau M, Roel-Touris J, Kotelnikov S, Padhorny D, Porter KA, Alekseenko A, Ignatov M, Desta I, Ashizawa R, Sun Z, Ghani U, Hashemi N, Vajda S, Kozakov D, Rosell M, Rodríguez-Lumbreras LA, Fernandez-Recio J, Karczynska A, Grudinin S, Yan Y, Li H, Lin P, Huang SY, Christoffer C, Terashi G, Verburgt J, Sarkar D, Aderinwale T, Wang X, Kihara D, Nakamura T, Hanazono Y, Gowthaman R, Guest JD, Yin R, Taherzadeh G, Pierce BG, Barradas-Bautista D, Cao Z, Cavallo L, Oliva R, Sun Y,

Zhu S, Shen Y, Park T, Woo H, Yang J, Kwon S, Won J, Seok C, Kiyota Y, Kobayashi S, Harada Y, Takeda-Shitaka M, Kundrotas PJ, Singh A, Vakser IA, Dapkūnas J, **Olechnovič K**, Venclovas Č, Duan R, Qiu L, Zhang S, Zou X, Wodak SJ.
Proteins. 2021 Aug 28.
doi:10.1002/prot.26222.
PMID:34453465.

11. Modeling of protein complexes in CASP14 with emphasis on the interaction interface prediction.
Dapkūnas J, **Olechnovič K**, Venclovas Č.
Proteins. 2021 Jun 27.
doi:10.1002/prot.26167.
PMID:34176161.

12. VoroContacts: a tool for the analysis of interatomic contacts in macromolecular structures.
Olechnovič K, Venclovas Č.
Bioinformatics. 2021 Jun 16. pdf.
doi:10.1093/bioinformatics/btab448.
PMID:34132767.

13. VoroCNN: Deep convolutional neural network built on 3D Voronoi tessellation of protein structures.
Igashov I, **Olechnovič K**, Kadukova M, Venclovas Č, Grudinin S.
Bioinformatics. 2021 Feb 23.
doi:10.1093/bioinformatics/btab118.
PMID:33620450.

14. Template-based modeling of diverse protein interactions in CAPRI rounds 38-45.
Dapkūnas J, Kairys V, **Olechnovič K**, Venclovas Č.
Proteins. 2020 Aug;88(8):939-947. pdf.
doi:10.1002/prot.25845.
PMID:31697420.

15. Blind prediction of homo- and hetero-protein complexes: The CASP13-CAPRI experiment.
Lensink MF, Brysbaert G, Nadzirin N, Velankar S, Chaleil RAG, Gerguri T, Bates PA, Laine E, Carbone A, Grudinin S, Kong R, Liu RR, Xu XM, Shi H, Chang S, Eisenstein M, Karczynska A, Czaplewski C, Lubecka E, Lipska A, Krupa P, Mozolewska M, Golon Ł, Samsonov S, Liwo A, Crivelli S, Pagès G, Karasikov M, Kadukova M, Yan Y, Huang SY, Rosell M, Rodríguez-Lumbreras LA, Romero-Durana M, Díaz-Bueno L, Fernandez-Recio J, Christoffer C, Terashi G, Shin WH, Aderinwale T, Maddhuri Venkata Subraman SR, Kihara D, Kozakov D, Vajda S, Porter K, Padhorny D, Desta I, Beglov D, Ignatov M, Kotelnikov S, Moal IH, Ritchie DW, Chauvot de Beauchêne I, Maigret B, Devignes MD, Ruiz Echartea ME, Barradas-Bautista D, Cao Z, Cavallo L, Oliva R, Cao Y, Shen Y, Baek M, Park T, Woo H, Seok C, Braitbard M, Bitton L, Scheidman-Duhovny D, Dapkūnas J, **Olechnovič K**, Venclovas Č, Kundrotas PJ, Belkin S, Chakravarty D, Badal VD, Vakser IA, Vreven T, Vangaveti S, Borrman T, Weng Z, Guest JD, Gowthaman R, Pierce BG, Xu X, Duan R, Qiu L, Hou J, Ryan Merideth B, Ma Z, Cheng J, Zou X, Koukos PI, Roel-Touris J, Ambrosetti F, Geng C, Schaarschmidt J, Trellet ME, Melquiond ASJ, Xue L, Jiménez-García B, van Noort CW, Honorato RV, Bonvin AMJJ, Wodak SJ.
Proteins. 2019 Dec;87(12):1200-1221.
doi:10.1002/prot.25838.
PMID:31612567.

16. Structural modeling of protein complexes: Current capabilities and challenges.
Dapkūnas J, **Olechnovič K**, Venclovas Č.
Proteins. 2019 Dec;87(12):1222-1232.
doi:10.1002/prot.25774.
PMID:31294859.

17. Estimation of model accuracy in CASP13.
Cheng J, Choe MH, Elofsson A, Han KS, Hou J, Maghrabi AHA, McGuffin LJ, Menéndez-Hurtado D, **Olechnovič K**, Schwede T, Studer G, Uziela K, Venclovas Č, Wallner B.
Proteins. 2019 Dec;87(12):1361-1377.
doi:10.1002/prot.25767.
PMID:31265154.

18. VoroMQA web server for assessing three-dimensional structures of proteins and protein complexes.
Olechnovič K, Venclovas Č.
Nucleic Acids Res. 2019 Jul 2;47(W1):W437-W442.
doi:10.1093/nar/gkz367.

PMID:31073605.

19. Comparative analysis of methods for evaluation of protein models against native structures.
Olechnovič K, Monastyrskyy B, Kryshtafovych A, Venclovas Č.
Bioinformatics. 2019 Mar 15;35(6):937-944.
doi:10.1093/bioinformatics/bty760.
PMID:30169622.

20. Modeling of protein complexes in CAPRI Round 37 using template-based approach combined with model selection.
Dapkūnas J, **Olechnovič K**, Venclovas Č.
Proteins. 2018 Mar;86 Suppl 1:292-301.
doi:10.1002/prot.25378.
PMID:28905467.

21. VoroMQA: Assessment of protein structure quality using interatomic contact areas.
Olechnovič K, Venclovas Č.
Proteins. 2017 Jun;85(6):1131-1145.
doi:10.1002/prot.25278.
PMID:28263393.

22. The PPI3D web server for searching, analyzing and modeling protein-protein interactions in the context of 3D structures.
Dapkūnas J, Timinskas A, **Olechnovič K**, Margelevičius M, Diciunas R, Venclovas Č.
Bioinformatics. 2017 Mar 15;33(6):935-937.
doi:10.1093/bioinformatics/btw756.
PMID:28011769.

23. The CAD-score web server: contact area-based comparison of structures and interfaces of proteins, nucleic acids and their complexes.
Olechnovič K, Venclovas Č.
Nucleic Acids Res. 2014 Jul;42(Web Server issue):W259-63.
doi:10.1093/nar/gku294.
PMID:24838571.

24. The use of interatomic contact areas to quantify discrepancies between RNA 3D models and reference structures.
Olechnovič K, Venclovas Č.
Nucleic Acids Res. 2014 May;42(9):5407-15.
doi:10.1093/nar/gku191.
PMID:24623815.

25. Voronota: A fast and reliable tool for computing the vertices of the Voronoi diagram of atomic balls.
Olechnovič K, Venclovas Č.
J Comput Chem. 2014 Mar 30;35(8):672-81.
doi:10.1002/jcc.23538.
PMID:24523197.

26. CAD-score: a new contact area difference-based function for evaluation of protein structural models.
Olechnovič K, Kulberkytė E, Venclovas Č.
Proteins. 2013 Jan;81(1):149-62.
doi:10.1002/prot.24172.
PMID:22933340.

27. Voroprot: an interactive tool for the analysis and visualization of complex geometric features of protein structure.
Olechnovič K, Margelevičius M, Venclovas Č.
Bioinformatics. 2011 Mar 1;27(5):723-4.
doi:10.1093/bioinformatics/btq720.
PMID:21186248.

Book chapters

- Contact Area-Based Structural Analysis of Proteins and Their Complexes Using CAD-Score.
Olechnovič K, Venclovas Č.
In: *Zoltán Gáspári (eds) Structural Bioinformatics: Methods and Protocols, Methods in Molecular Biology, vol. 2112*. Springer. 2020.

- In Silico Modeling of Inhibitor Binding to Carbonic Anhydrases.
  Kairys V, **Olechnovič K**, Raškevičius V, Matulis D.
  In: *Matulis D. (eds) Carbonic Anhydrase as Drug Target*. Springer, Cham. 2019.

Doctoral dissertation

- Methods for the analysis and assessment of the three-dimensional structures of proteins and nucleic acids: development and applications.
  Olechnovič K.
  Doctoral dissertation, Vilnius University, 2017.

- Baltymų ir nukleorūgščių erdvinių struktūrų analizės ir vertinimo metodai: kūrimas ir taikymas.
  Olechnovič K.
  Doctoral dissertation summary in Lithuanian, Vilnius University, 2017.

Other publications

- Kompiuteriai padeda pažinti sudėtingą baltymų pasaulį.
  Dapkūnas J, **Olechnovič K**.
  Popular science article in *SPECTRUM*. 2017 1(26), ISSN 1822-0147.

- Journal cover image based on the article *"VoroMQA: Assessment of protein structure quality using interatomic contact areas"*.
  Olechnovič K, Venclovas Č.
  Cover Image for *Proteins*. 2019 Volume 85, Issue 6.
  doi:10.1002/prot.25129.

Presentations and posters

Oral presentations at international conferences

- PSB Symposium on Machine Learning in Cellular Structural Biology, Grenoble, France (2025)
- ELIXIR 3DBioinfo Annual General Meeting | ISCB 3DSig 2025, Barcelona, Spain (2025)
- MASIM (Algorithmic Methods for Macromolecular Structures and Interactions), Paris, France (2025)
- Beyond the structural frontier: Modeling the dynamics of biomolecular interfaces, Paris, France (2024)
- 2nd ML4NGP Meeting on Machine Learning and Non-globular proteins, Thessaloniki, Greece (2024)
- Joint ICB Workshop and 8th CAPRI Assessment Meeting, Grenoble, France (2024)
- CASP15 meeting, Turkey, Antalya (2022)
- AI at CIRM, France, Marseille (2021)
- CASP14 meeting, Virtual (2020)
- COINS, Lithuania, Vilnius (2019), *keynote presentation*
- CASP13 meeting, Mexico, Riviera Maya (2018)
- VitaScientia, Lithuania, Vilnius (2018)
- CASP12 meeting, Italy, Gaeta (2016)
- CASP10 meeting, Italy, Gaeta (2012)

Poster presentations at international conferences

- PSB Symposium on Machine Learning in Cellular Structural Biology, Grenoble, France (2025), poster
- ML4NGP meeting, Vilnius, Lithuania (2025), poster
- CASP16 meeting, Punta Cana, Dominican Republic (2024), poster
- NCSB meeting, Nancy, France (2024), poster
- CASP15 meeting, Antalya, Turkey (2022), poster
- AI at CIRM, France, Marseille (2021), poster
- PDB50, Virtual (2021), poster
- CASP14 meeting, Virtual (2020), poster
- ISMB, Switzerland, Basel (2019), poster
- CASP13 meeting, Mexico, Riviera Maya (2018), poster
- CASP12 meeting, Italy, Gaeta (2016), poster
- ECCB, Netherlands, Hague (2016), poster
- CASP11 meeting, Mexico, Riviera Maya (2014), poster
- ECCB, France, Strasbourg (2014), poster
- ISMB, Germany, Berlin (2013), poster

- SocBiN, Poland, Torun (2013), poster
- CASP10 meeting, Italy, Gaeta (2012), poster
- ECCB, Switzerland, Basel (2012), poster
- SAGA, Lithuania, Vilnius (2011), poster
- ISMB, Austria, Vienna (2011), poster
- ECCB, Belgium, Ghent (2010), poster
- VizBi, Germany, Heidelberg (2010), poster

Gallery of posters: www.kliment.lt/posters

Main published software

Developed by me

- **Voronota**: a standalone software package of various tools for analyzing three-dimensional structures of biological macromolecules using the Voronoi diagram of atomic balls (includes the latest versions of CAD-score and VoroMQA methods).
https://kliment-olechnovic.github.io/voronota

- **Voronota-JS**: an expansion of the core Voronota software. Voronota-JS provides a way to write JavaScript scripts for the comprehensive analysis of macromolecular structures, including the Voronoi tesselation-based analysis.
https://kliment-olechnovic.github.io/voronota/expansion_js/

- **Voronota-LT**: an expansion of the core Voronota software. Voronota-LT (pronounced ‘voronota lite’) is an alternative, significantly faster version of Voronota for constructing tessellation-derived atomic contact areas and volumes.
https://kliment-olechnovic.github.io/voronota/expansion_lt/

- **Voronota-GL**: a visual tool for the comprehensive interactive analysis of macromolecular structures, including the Voronoi tesselation-based analysis.
https://kliment-olechnovic.github.io/voronota/expansion_gl/

- **VoroMarmotte**: a method to predict whether Voronoi tessellation-derived contact areas observed in a single conformation of a protein are likely to persist (remain stable) in an ensemble of multiple conformations of the same protein.
https://github.com/kliment-olechnovic/voromarmotte-app

- **VoroChipmunk**: a method to calculate area statistical pseudo-energy of interfaces in protein complexes, based on the observed probabilities of atom-atom contact areas to occur and persist in structural ensembles from PDB.
https://github.com/kliment-olechnovic/vorochipmunk-app

- **VoroNikon**: a method to calculate area statistical pseudo-energy of interfaces for protein complexes with peptides that can contain non-canonical amino acid residues.
https://github.com/kliment-olechnovic/voronikon-app

- **VoroPadding**: a method to calculate how much space is available for atoms to occupy around a selected part of the molecular structure (e.g. a ligand).
https://github.com/kliment-olechnovic/voropadding-app

- **VoroIF-GNN-v2**: a new version of the VoroIF-GNN, uses tessellation contact area-based pseudoenergy descriptors based on the observed and expected probabilities of contacts to occur and persist in folded conformations.
https://github.com/kliment-olechnovic/voroif-gnn-v2-app

- **FTDMP**: a software system for running docking experiments and scoring/ranking multimeric models (includes VoroIF-jury and VoroIF-GNN methods).
  https://kliment-olechnovic.github.io/ftdmp/
- **VoroMQA web server** for the assessment of protein structure quality using interatomic contact areas.
  https://bioinformatics.lt/wtsam/voromqa
- **VoroContacts web server** for the computation and interactive querying of Voronoi tessellation-derived contacts.
  https://bioinformatics.lt/wtsam/vorocontacts
- **CAD-score web server** for contact area-based comparison of structures and interfaces of proteins, nucleic acids and their complexes.
  https://bioinformatics.lt/cad-score/
- **Voroprot**: an interactive tool for exploring some tesselation-derived features of protein structures (no longer maintained).
  https://bioinformatics.lt/software/voroprot

Developed under my supervision

- **TemStaPro**: a standalone software for protein thermostability prediction using sequence representations from protein language models.
  https://github.com/ievapudz/TemStaPro.
  TemStaPro was mainly developed by Ieva Pudžiuvelytė.

Achievements and awards

Achievements in CASP and CAPRI experiments

CASP (Critical Assessment of Techniques for Protein Structure Prediction) and CAPRI (Critical Assessment of PRedicted Interactions) are world-wide experiments focused on the blind testing of methods for protein structural bioinformatics.

2024	Top performance (ranked 1st in the CAPRI assessment of scoring groups) in the CASP16-CAPRI scoring experiment. Group “Olechnovic”.
2024	Contributed to the top performance (ranked 1st) in modeling structures of protein complexes in the CAPRI experiment rounds 47–55. Group “Venclovas”, members: Dapkūnas J, Olechnovič K, Venclovas Č.
2022	Contributed to one of the top performances in modeling structures of protein complexes in CASP15 and CASP15-CAPRI experiments (ranked 2nd in CASP, ranked 1st in CAPRI). Group “Venclovas”, members: Olechnovič K, Valančauskas L, Dapkūnas J, Venclovas Č.
2022	One of the top performances in EMA (estimation of model accuracy) in CASP15 experiment (and ranked 1st in CASP15-CAPRI scoring experiment). Groups “Venclovas” and “VoroIF”.
2020	Contributed to one of the top performances in modeling structures of protein complexes in CASP14 and CASP14-CAPRI experiments (ranked 2nd in CASP, ranked 1st in CAPRI jointly with two other groups). Group “Venclovas”, members: Olechnovič K, Dapkūnas J, Venclovas Č.
2019	Contributed to one of the top performances (ranked 3rd) in modeling structures of protein complexes in the CAPRI experiment rounds 38–45. Group “Venclovas”, members: Dapkūnas J, Kairys V, Olechnovič K, Venclovas Č.
2018	Contributed to the best results (ranked 1st) in modeling structures of protein complexes in CASP13 and CASP13-CAPRI experiments. Group “Venclovas”, members: Dapkūnas J, Olechnovič K, Venclovas Č.
2018	One of the top performances in EMA (estimation of model accuracy) in CASP13 experiment (ranked 1st in prediction of unreliable regions). Groups “VoroMQA-A” and “VoroMQA-B”.
2016	Contributed to the best results (ranked 1st) in modeling structures of protein complexes in CASP12-CAPRI experiment. Group “Venclovas”, members: Dapkūnas J, Olechnovič K, Venclovas Č.
2016	One of the top performances in protein structure prediction in CASP12 experiment. Group “VoroMQA-select”.

National awards

2025	Lithuanian Science Prize 2024, awarded to the group of scientists: Justas Dapkūnas, Darius Kazlauskas, **Kliment Olechnovič**, and Česlovas Venclovas for the cycle of studies “Development and application of protein structural bioinformatics methods (2010–2023)”
2019	Lithuanian Academy of Sciences scholarship for young scientists

2018	Laureate of the “Best doctoral dissertation of 2017 in Lithuania” contest
2015	Lithuanian Academy of Sciences award for the best works by young researchers in 2014
2013–2014	The Research Council of Lithuania scholarship for PhD students actively conducting scientific research
2013	INFOBALT incentive scholarship for young scientists

Conference awards

2019	ISCB Art in Science Award Winner at “ISMB/ECCB 2019”. Work title: “Disassembled tessellation”.
2016	Poster selected for an oral presentation at “12th Community Wide Experiment on the Critical Assessment of Techniques for Protein Structure Prediction (CASP12 meeting)”. Poster title: *VoroMQA: assessment of protein structure quality using interatomic contact areas derived from the Voronoi tessellation of atomic balls*.
2013	Best poster award at “Society for Bioinformatics in Northern European countries (SocBiN)”. Poster title: *The use of interatomic contact areas for the assessment of RNA 3D structural models*.
2012	Poster selected for an oral presentation at “EMBO Conference on Critical Assessment of Protein Structure Prediction (CASP10 meeting)”. Poster title: *CAD-score: a new method for the evaluation of protein structural models*.

Other achievements

2018	Judo champion of Lithuania, judo black belt.
2018	Sambo champion of Lithuania.