Dr. Vladimir B Teif

CONTACTS:

School of Life Sciences, University of Essex, Wivenhoe Park, Colchester, CO4 3SQ, UK
Faculty profile: https://www.essex.ac.uk/people/teifv75808
Community/lab web site: https://generegulation.org
E-mail: vteif@essex.ac.uk

ACADEMIC QUALIFICATIONS:

2017: Fellow of the Higher Education Academy, UK (FHEA)
2004: PhD, *summa cum laude*
CEA/Saclay, French Commission for Atomic Energy,
joint program with the Belarus National Academy of Sciences:
INTAS PhD Fellowship (http://cordis.europa.eu/programme/rcn/493_en.html)
Supervisors: Dr. Jean-Louis Sikorav and Prof. Dmitry Lando
2000: MSc (Diploma), *honors*, Belarus State University, Minsk

PROFESSIONAL APPOINTMENTS:

2015 – current: School of Life Sciences, University of Essex, UK
- 2021 – current: *Senior Lecturer*
  - *2024 - current: Genomics Group Lead (https://genomics.essex.ac.uk)*
  - *2022-2023: Director of Employability Development*
  - 2021-2022: *Director of BSc Genetics and MSc Health Genomics programs*
- 2015 – 2021: *Lecturer*
  - 2019-2022: *Academic Offences Officer* for the School of Life Sciences

2008 – 2015: German Cancer Research Center (DKFZ) and BioQuant, Heidelberg, Germany
- 2011 – 2015: BIOMS Postdoctoral Fellowship (www.bioms.de)
- 2009 – 2011: Fellow of the Cellnetworks Cluster of Excellence (www.cellnetworks.de)
- 2008 – 2009: DKFZ Guest Scientist (www.dkfz.de), Group of Prof. Karsten Rippe.

2004 – 2010: Belarus National Academy of Sciences, Institute of Bioorganic Chemistry, Minsk
- 2009 – 2010: Senior Research Scientist (affiliated, while working full-time in Germany).
- 2004 – 2008: Research Scientist (affiliated, while visiting scientist in Israel and USA).

VISITING SCIENTIST POSITIONS:

02/2008 – 06/2008: University of California San Diego, Centre of Theoretical Biological Physics
(CTBP Visiting Scientist Fellowship, working in the group of Prof. Terry Hwa).
03/2008: Institute of Complex Systems, Santa Fe, NM, USA
09/2007: International Center of Theoretical Physics, Trieste, Italy (UNESCO Fellow)
04/2007 – 05/2007, 11/2005 – 02/2006: Hebrew University, Jerusalem
(FEBS Fellowship, groups of Prof. Avinoam Ben-Shaul and Dr. Daniel Harries)

RESEARCH GRANTS

1) Pancreatic Cancer UK, 2024-2027, "Next-generation liquid biopsies for early detection of pancreatic cancer based on cell-free DNA nucleosomics", **lead PI, £499,890**; co-PI with Andrea Mohr, Ralf Zwacka, Greg Brooke.
2) BBSRC Impact Acceleration Account, 2023, "Next Generation Liquid Biopsies for AI-Guided Monitoring of Ageing", **PI**, **£20,289**
3) University of Essex, Commercial Enterprise Grant, 2023, "Improve patient stratification and the monitoring of therapy response in cancer", **PI, £35,000.**
4) Cancer Research UK, 2023, "Nucleosomics for liquid biopsies", **PI**, **£70,000**.
5) Cancer Research UK, 2022, "Early cancer diagnostics & stratification based on nucleosome positioning reconstructed from cell-free DNA", **co-PI** with Dr Paul Brennan, **£100,000**.

6) BBSRS Responsive Mode Grant, 2021-2024, “Integrating cellular space and time: interplays between subcellular organisation and lifespan”, **co-I** with Dr Charalampos Rallis, **£709,156.89**.

7) Wellcome Trust Seed Award, 2016-2018. “Nucleosome repositioning as a mechanism for cell memory in cancer transitions”, **PI. £85,432**

8) @RAction grant, ANR (France), 2015. “Deciphering and modifying epigenetic mechanisms of stem cell development”, **PI**. **€870,000**.

9) Merck grant "Chaire Junior Fondagen", 2015, **PI**. **€275,000**

10) Sonata-BIS-4 grant, NCN (Poland), 2015, "Predicting differential transcription factor binding in chromatin", **PI**. **€500,000**

11) Intramural Grant of the German Cancer Research Center, 2012-2014, “Calculating transcription factor binding maps in chromatin”, **PI. €120,000**

12) Intramural Grant of the German Cancer Research Center, 2012-2013, “Developing a software suite for the analysis of epigenetic regulation from high-throughput sequencing data”, **Co-PI** with Dr Yevhen Vainshtein. **€20,000**

13) Belarus National Foundation of Fundamental Research, Young Scientist Grant #B10M-060, “Investigation of chromatin rearrangements in tumor and normal tissues”, 2010, **PI, €10,000**

14) Belarusian Program “Bio-rational Pesticides-II”, “Study of synergistic effects of pesticide combinations using statistical analysis”, 2009, **co-PI** with Prof Dmitry Lando. **€10,000**

15) Belarus National Foundation of Fundamental Research, Young Scientist Grant #B06M-127 “Biomolecular interactions with condensed DNA”, 2006-2008, **PI**. **€10,000**

16) Belarus National Foundation of Fundamental Research, #B02M-091 “Influence of anticancer and carcinogenic metal complexes on DNA condensation”, 2002-2004, **PI**. **€10,000**

GRANTS FOR OUTREACH, NETWORKING AND TEACHING

17) Four grants to provide summer studentships to undergraduate students, funded by the Genetics Society and Wellcome Trust (**~£3k each**).

18) Three Proficio grants to develop new graduate courses in the University of Essex, 2016, 2020, 2021, **PI**, **£3,200**.

19) Two grants of the Global Challenges Research Fund (GCRF) (**£2,616** and **£1,750**) to establish collaboration with Prof Ranjith Padinhateeri (Indian Institute of Technology Bombay) and to organise a workshop “Biophysics of Chromatin”, July 8, 2019, Colchester, UK.

20) The Royal Society Partnership Grant, 2018, **Co-PI** with Dr Mari Chikvaidze, **£3,000**.

21) LabArchives Development Grant, 2017-2021, **PI, $6,200**

HONOURS, AWARDS & FELLOWSHIPS

2023: Overall Supervisor of the Year, University of Essex, 2023
2018: Publons award for top peer-reviewers (top 1% reviewers in 2018)
2014: Helmholtz-Israel Cooperation in Personalized Medicine Short-Term Exchange Grant.
2011: BIOMS Fellowship, DKFZ and BioQuant, Germany, 2011-2015
2009: German Excellence Cluster Cellnetworks Fellowship, BioQuant, Germany, 2009-2010
2009: DKFZ Guest Scientist Grant, DKFZ and BioQuant, Germany, 2008-2009
2008: CTBP Visiting Scientist Grant, University of California at San Diego, USA, 02-06/2008
2008: SFI Visiting Scientist Grant, Institute of Complex Systems, Santa Fe, USA, 04/2008
2007: Boehringer Ingelheim Short-Term Fellowship, DKFZ, Germany 10/2007
2007: UNESCO Visiting Scientist, International Center of Theoretical Physics, Trieste, 09/2007
2007: President’s Fellowship (top 100 young scientists of Belarus)
2007: FEBS Short-Term Fellowship, Hebrew University, Jerusalem, Israel
2006: Golda Meir Fellowship, Hebrew University, Jerusalem (not taken for family reasons)
2004: Fellow of the Belarus National Academy of Sciences, 2004
2002: INTAS Young Scientist Ph.D. Fellowship, CEA/Saclay, France, 2002-2004
2000-2016: 14 Young Scientist Travel Awards (see page 7); 1 best student poster award.

PROFESSIONAL SERVICE

Management Committee Member:

COST action International Nucleome Consortium https://e-services.cost.eu/action/CA18127

Biophysical Society's subgroup Multiscale Genome Organisation https://www.biophysics.org/subgroups/multiscale-genome-organization

Organiser of conferences/workshops/seminar series:

"Biophysics of Chromatin" workshop, University of Essex, 08/07/2019
"Chromatin and Epigenomics" workshop, University of Essex, 14/09/2017; 13/09/2019.
"Fragile Nucleosome" seminars, 2020-21 https://generegulation.org/fragile-nucleosome
"INC Academy" seminars, courses & workshops, 2020-21 https://inc-cost.eu/inc-academy

Conference session chair, Biomolecular Structure and Dynamics, Albany 2015, the 19th Conversation, the State University of New York, Albany, NY, USA, June 9-13, 2015.

Associate Editor for *Frontiers in Genetics (since 2013)*; *AIMS Biophysics (since 2014)*. Also edited special issue "Chromatin and Epigenetics" http://www.aimspress.com/newsinfo/133.html

Guest Editor for PLoS Computational Biology (since 2021).

Reviewed grants for BBSRC, CRUK, Breast Cancer NOW and Daphne Jackson (UK), ANR (France), DFG (Germany), ISF (Israel), NSERC (Canada), NWO (Netherlands), PNF (Poland).

Reviewed for > 40 journals including *Cell, NAR, PNAS, Genome Research, PLoS Comput. Biol., Bioinformatics, BMC Bioinformatics, BMC Biology, BMC Genomics, Briefings in Bioinformatics, Biophysical Journal, etc. See* https://publons.com/author/1308717/vladimir-teif

PhD examiner:

Dr Pavel Artemov, Imperial College London, 2024
Dr Yucheng Wang, University of Essex, 2023
Dr Dominic Hall, University of Cambridge, 2022
Dr Jareth Wolfe, University of Essex, 2022
Dr Luca Nanni, Politechnico di Milano, 2021
Dr Patrick Martin, University of Essex, 2020
Dr Ilya Flyamer, University of Edinburgh, 2019
Dr Joanna Mitchelmore, University of Cambridge, 2018

STEM Ambassador: scientific outreach activities for the Claremont High School Academy.

PATENT APPLICATIONS, analysis of cell-free DNA: P050691-GB (2022), P050465-GB (2021)

PUBLICATIONS*

**Asterisk indicates the corresponding author. Last updated: October 6, 2024*

1. Takahashi N., Pongor L., Agrawal S. P., Shtumpf M., Rajapakse V. N., Shafiei A., Schultz C. W., Kim S., Roame D., Carter P., Vilimas R., Nichols S., Desai P., Figg W. D. Sr, Bagheri M, **Teif V. B.***, Thomas A.* (2024) Genomic alterations and transcriptional phenotypes in circulating tumor DNA and matched metastatic tumor. bioRxiv 2024.06.02.597054.
2. Tajmul Md, Bhatt D. N, Ruje L., Price E., Ji Y., Loukinov D., **Teif V. B.**, Lobanenkov V. V., Pugacheva E. M (2024). CTCF binding landscape is established by the epigenetic status of the nucleosome, well-positioned relative to CTCF motif orientation. bioRxiv 2024.09.25.614770.

3. Gautam P., Ciuta I., **Teif V. B.***, Sinha S. K.* (2024) Predicting p53-dependent cell transitions from thermodynamic models. *J. Chem. Phys.* **161**, 135101.
4. Shtumpf M., Jeong S., Bikova M., Mamayusupova H., Ruje L. and **Teif V.B.*** (2024) Aging clock based on nucleosome reorganisation derived from cell-free DNA. *Aging Cell,* **23**, e14100
5. Jacob D.R., Guiblet W. M., Mamayusupova H., Shtumpf M., Ruje L., Ciuta I., Gretton S., Correa C., Dellow E., Agrawal S. P., Shafiei N., Drobysevskaja A., Armstrong C. M., Lam J. D. G., Vainshtein Y., Clarkson C. T., Thorn G. J., Sohn K., Madapura M. P., Chandrasekharan S., Brooke G.N., Klenova E., Zhurkin V. B.*, **Teif V.B.*** (2024) Nucleosome reorganisation in breast cancer tissues. *Clinical Epigenetics* **16**, 50.
6. Peng Y., Song W., **Teif V.B**, Ovcharenko I., Landsman D., Panchenko A.R. (2023) Detection of new pioneer transcription factors as cell-type specific nucleosome binders. *eLife* **13**, RP88936.
7. Piroeva K. V., McDonald C., Xanthopoulos C., Fox C., Clarkson C. T., Mallm J.-P., Vainshtein Y., Ruje L., Klett L. C., Stilgenbauer S., Mertens D., Kostareli E.*, Rippe K.* and **Teif V. B.*** (2023) Nucleosome repositioning in chronic lymphocytic leukaemia. *Genome Research* **33**, 1649-1661.
8. Thorn G.J., Clarkson C.T., Rademacher A., Mamayusupova H., Schotta G., Rippe K.* and **Teif V.B.*** (2022) DNA sequence-dependent formation of heterochromatin nanodomains. *Nature Communications* **13**, 1861.
9. Shtumpf M., Piroeva K.V., Agrawal S.P., Jakob D.R., **Teif V.B.*** (2022) NucPosDB: a database of nucleosome positioning in vivo and nucleosomics of cell-free DNA. *Chromosoma.* **131***,* 19-28.
10. Belokopytova P., Viesná E., Chiliński M., Qi Y., Salari H., Di Stefano M., Esposito A., Conte M., Chiariello A.M., **Teif V.B.**, Plewczynski D., Zhang B., Jost D., Fishman V. (2022). 3DGenBench: a web-server to benchmark computational models for 3D Genomics. *Nucleic Acids Res* **50**, W1, W4–W12.
11. Hedley J.G., **Teif V.B.***, Kornyshev A.A.* (2021) Nucleosome induced homology recognition in chromatin. *J Royal Soc Interface* **18**, 20210147*.*
12. Cucinotta C.E.*, Martin B.J.E.*, Noé González M.*, Raman P.*, **Teif V.B.***, Vlaming H.* (2021) Strength in engagement: the rise of online scientific communities during COVID-19 pandemic. *EMBO Reports* **22,** e52612.
13. Mohr A., Tianyuan C., Clarkson C.T., Brooke G.N, **Teif V.B.**, Zwacka R.M. (2020). Fas-threshold signalling in MSCs causes tumour progression and metastasis. *Cancer Letters* **519**, 63-67.
14. **Teif V.B.**,*, Gould T.J., Clarkson C.T., Boyd L., Antwi E.B., Ishaque N., Olins A.L. & Olins D.E.* (2020) Linker histone epitopes are hidden by in situ higher-order chromatin structure. *Epigenetics and Chromatin*, **13**, 26.
15. **Teif V.B.*** (2020) Soft power of non-consensus protein-DNA binding. *Biophys. J.* **118**, 1797-1798.
16. Antwi E.B., Olins A., **Teif V.B.**, Bieg M., Bauer T., Gu Z., Brors B., Eils R., Olins D., Ishaque N. (2020) Whole-genome fingerprint of the DNA methylome during chemically induced differentiation of the human AML cell line HL-60/S4. *Biology Open*, **9**, bio044222*.*
17. Clarkson C.T., Deeks E.A., Samarista R., Mamayusupova H., Zhurkin V.B.,* **Teif V.B.*** (2019) CTCF-dependent chromatin boundaries formed by asymmetric nucleosome arrays with decreased linker length. *Nucleic Acids Res*. **47**, 11181-1196. **REF2020.**
18. Wiehle L., Thorn G.J., Raddatz G., Clarkson C.T., Rippe K., Lyko F., Breiling A.*, **Teif V.B.*** (2019) DNA (de)methylation in embryonic stem cells controls CTCF-dependent chromatin boundaries. *Genome Research* **29**, 750-761. **Featured on the journal cover**. **REF2020.**

19. Mallm J.-P., Iskar M., Ishaque N., Klett L.C., Kugler S.J., Muino J.M., **Teif V.B.**, Poos A.M., Großmann S., Erdel F., Tavernari D., Koser S.D., Schumacher S., Brors B., König R., Remondini D., Vingron M., Stilgenbauer S., Lichter P., Zapatka M., Mertens D., Rippe K. (2019) Linking aberrant chromatin features in chronic lymphocytic leukemia to transcription factor networks. *Mol Syst Biol* **15**, e8339. **Featured on the journal cover**.
20. **Teif V.B.*** and Clarkson C.T. (2019) Nucleosome Positioning. In: Guenther, R. and Steel, D. (eds.), *Encyclopedia of Bioinformatics and Computational Biology*, vol. 2, pp. 308–317. Oxford: Elsevier.
21. Pavlaki I., Docquier F., Chernukhin I., Kita G., Gretton S., Clarkson C.T., ***Teif V.B.**, *Klenova E. (2018) Poly(ADP-ribosyl)ation dependent changes in CTCF-chromatin binding and gene expression in breast cells. *Biochim Biophys Acta (BBA) – Gene Regulatory Mechanisms* **1861**, 718-730.
22. Vainshtein Y., Rippe K. and **Teif V.B.*** (2017). NucTools: analysis of chromatin feature occupancy profiles from high-throughput sequencing data. *BMC Genomics* 18, 158.
23. **Teif V.B.***, Mallm J.-P., Sharma T., Mark Welch D.B., Rippe K., Eils R., Langowski J., Olins A.L. and Olins D.E.* (2017). Nucleosome repositioning during differentiation of a human myeloid leukemia cell line. *Nucleus* **8**, 188-204.
24. **Teif V.B.*** (2016) Nucleosome positioning: resources and tools online. *Briefings in Bioinformatics* 17, 745-757.
25. **Teif V.B.*** and Cherstvy A.G. (2016). Chromatin and epigenetics: current biophysical views. *AIMS Biophysics* **3**, 88-98.
26. **Teif V.B.***, Kepper N., Yserentant K., Wedemann G., Rippe K. (2015). Affinity, stoichiometry and cooperativity of heterochromatin protein 1 (HP1) binding to nucleosomal arrays. *J. Phys.: Condens. Matter.* **27**, 064110
27. Salih B.*, **Teif V.B.**, Tripathi V., Trifonov E.N. (2015) Strong nucleosomes of mouse genome in recovered centromeric sequences. *J. Biomol. Struct. & Dynam.* **33***,* 1164-75.
28. **Teif V.B.***, Beshnova D.A., Marth C., Vainshtein Y., Mallm J.-P., Höfer T. and Rippe K.* (2014). Nucleosome repositioning links DNA (de)methylation and differential CTCF binding during stem cell development. *Genome Research*. **24**, 1285-1295. **REF2020**
29. Beshnova D.A., Cherstvy A.G. Vainshtein Y. and **Teif V.B.*** (2014). Regulation of the nucleosome repeat length *in vivo* by the DNA sequence, protein concentrations and long-range interactions. *PLoS Comput. Biol*. **10**(7):e1003698. **REF2020**
30. Cherstvy A.G.* and **Teif V.B.** (2014). Electrostatic effect of H1 histone binding on the nucleosome repeat length. *Phys. Biol.* **11**, 044001.
31. **Teif V.B.*** (2014). On the Sociology of Science 2.0. In "Opening Science: the evolving guide on how the Internet is changing research, collaboration and scholarly publishing", Eds. S. Bartling, S. Friesike. Springer, 2014, IX, 335 p. 43 illus. | ISBN 978-3-319-00026-8.
32. Schöpflin R., **Teif V.B.**, Müller O., Weinberg C., Rippe K., Wedemann G.* (2013). Modeling nucleosome distributions from experimental nucleosome positioning maps of cell ensembles. *Bioinfomatics*. **29**, 2380-2386.
33. Cherstvy A.G.* and **Teif V.B.** (2013) Structure-driven homology pairing of chromatin fibers: The role of electrostatics and protein bridging. *J. Biol. Phys.* **39**, 363-385.
34. **Teif V.B.***, Erdel F., Beshnova D.A., Vainshtein Y., Mallm J.-P., Rippe K. (2013) Taking into account nucleosomes for predicting gene expression. *Methods* **62**, 26-38.
35. **Teif V.B.*** (2013). Science 3.0: Corrections to the Science 2.0 paradigm. ArXiv:1301.2522.
36. **Teif V.B.***, Vainshtein Y., Caudron-Herger M., Mallm J.-P., Marth C., Höfer T., *Rippe K. (2012) Genome-wide nucleosome positioning during embryonic stem cell development. *Nature Struct. Mol. Biol.* **19**, 1185-92.

37. **Teif V.B.*** and Rippe K. (2012) Calculating transcription factor binding maps for chromatin. *Briefings in Bioinformatics* **13**, 187-201.
38. **Teif V.B.***, Shkrabkou A.V., Egorova V.P., Krot V.I. (2012) Nucleosomes in gene regulation: theoretical approaches. *Molecular Biology* **46***,* 1-10*.*
39. **Teif V. B.*** and Bohinc K. (2011). Condensed DNA: condensing the concepts. *Progress in Biophysics and Molecular Biology* **105**, 208-222.
40. **Teif V.B.*** and Rippe K.* (2011) Nucleosome mediated crosstalk between transcription factors at eukaryotic enhancers. *Physical Biology* **8**, 044001*.*
41. Längst G.*, **Teif V.B.** and Rippe K.* (2011). Chromatin remodeling by translocation of nucleosomes. In "Genome organization and function in the cell nucleus", Ed. K. Rippe, Wiley-VCH, Weinheim. P. 111-139.
42. **Teif V. B.*** (2010). Predicting gene-regulation functions: Lessons from temperate bacteriophages. *Biophys. J.* **98**, 1247-1256.
43. **Teif V.B.***, Ettig R. and Rippe K.* (2010). A lattice model for transcription factor access to nucleosomal DNA. *Biophys. J.* **99**, 2597-2607.
44. **Teif V.B.*** and Rippe K.* (2010). Statistical-mechanical lattice models for protein-DNA binding in chromatin. *J. Phys.: Condens. Matter.* **22**, 414105.
45. **Teif V. B.***, Harries D., Lando D.Y. and Ben-Shaul A. (2010). Matrix formalism for sequence-specific polymer binding to multicomponent lipid membranes. In "Membrane-active peptides: methods and results on structure and function", Ed. M. Castanho, International University Line, La Jolla. P. 29-52.
46. **Teif V. B.*** and Rippe K.* (2009). Predicting nucleosome positions on the DNA: combining intrinsic affinities and remodeler activities. *Nucleic Acids Res.* **37**, 5641-5655.
47. **Teif V. B.***, Harries D., Lando D. Y. and Ben-Shaul A. (2008). Matrix formalism for site-specific binding of unstructured proteins to multicomponent lipid membranes. *J. Pept. Sci.* **14**, 368-373.
48. **Teif V. B.*** (2007). General transfer matrix formalism to calculate DNA-protein-drug binding in gene regulation: Application to O_R operator of phage λ. *Nucleic Acids Res.* **35**, e80.
49. **Teif V. B.*** (2005). Ligand-induced DNA condensation: choosing the model. *Biophys. J.* **89**, 2574-2587.
50. **Teif V. B.** and Lando D. Y.* (2003). DNA condensation caused by ligand binding. In "Bioregulators: investigation and application", Ed. F.A. Lakhvich, Technoprint, Minsk, P. 116-128.
51. Lando D. Y.* and **Teif V. B.** (2002). Modeling of DNA condensation and decondensation caused by ligand binding. *J. Biomol. Struct. Dynam.* **20**, 215-222.
52. **Teif V. B.**, Haroutunian S. H., Vorob'ev V. I. and Lando D. Y.* (2002). Short-range interactions and size of ligands bound to DNA strongly influence adsorptive phase transition caused by long-range interactions. *J. Biomol. Struct. Dynam.* **19,** 1103-1110.
53. **Teif V. B.** and Lando D. Y.* (2001). Calculation of DNA condensation caused by ligand adsorption. *Molecular Biology* **35**, 117-119.
54. **Teif V. B.***, Lando D. Y. (2001). DNA condensation caused by ligand binding may serve as a sensor. In "Sensor Technology 2001", ed. M. Elwenspoek, Kluver, Dordrecht, P. 155-160.
55. Lando D. Y.* and **Teif V. B.** (2000). Long-range interactions between ligands bound to a DNA molecule give rise to adsorption with the character of phase transition of the first kind. *J. Biomol. Struct. Dynam.* **17**, 903-911.

INVITED TALKS

1. Liquid biopsies based on nucleosomics of cell-free DNA, Imperial College London, September 4, 2024.
2. Nucleosome repositioning in cancer and ageing. “Chromatin Modeling: Integrating Mathematics, Physics, and Computation for Advances in Biology and Medicine”, University of Vienna, March 4-15, 2024
3. Nucleosome repositioning in cancer, University of Birmingham, November 5, 2023.
4. Nucleosome repositioning in cancer, “The Genome in Space and Time”, Corfu, Greece, September 10-13, 2023
5. Transcription factors and nucleosomes: playmates, competitors and more, “Protein-DNA Interactions: from Biophysics to Cell Biology”, Rehovot, Israel, October 18-20, 2022.
6. Nucleosomes and CTCF: together forever, University of Sheffield, February 23, 2022
7. Nucleosome repositioning in cell differentiation and cancer, University of Liverpool, October 19, 2021
8. Nucleosome repositioning in cancer, National Institutes of Health (NIH, USA), May 25, 2021.
9. DNA sequence-dependent formation of heterochromatin nanodomains, Biophysical Society’s subgroup Multiscale Genome Organisation, April 28, 2021.
10. Nucleosomes and chromatin boundaries in cell differentiation and cancer, University of Exeter, March 18, 2021.
11. Chromatin reorganisation in cell differentiation and cancer: focus on nucleosomes and CTCF, “Chromatin Modeling: Integrating Mathematics, Physics, and Computation for Advances in Biology and Medicine”, Erwin Schrödinger International Institute for Mathematics and Physics (ESI), University of Vienna, Austria, March 16-20, 2020.
12. Chromatin reorganisation in cell differentiation and cancer: focus on nucleosomes and CTCF, University of Manchester, UK, March 2, 2020.
13. Microdomain formation in chromatin, “Biophysics of Chromatin”, University of Essex, UK, July 8, 2019.
14. Microdomain formation in chromatin, Biophysics of Epigenetics and Chromatin Workshop, Edinburgh, April 16-17, 2018.
15. Interplay of epigenetic modifications, TF binding and nucleosome positioning, CECAM-Lorentz Workshop “Multiscale-modelling of nucleosomes and their positioning on DNA”, January 15-19, 2018, Lausanne.
16. Microdomain formation in chromatin, Multiscale Modeling and Experimental Approaches to Genome Organization, April 2-7, 2017, Ecole de Physique, Les Houches, France.
17. Predicting differential transcription factor binding in cell transformations, Collège de France, Paris, November 2, 2015
18. Predicting differential transcription factor binding in cell transformations, University of Strasbourg, France, 25 September, 2015.
19. Predicting differential transcription factor binding in cell transformations, CNRS, Paris, April 1, 2015.
20. Predicting differential transcription factor binding in cell transformations, University of Würzburg, Germany, 13 January 2015.
21. Predicting differential transcription factor binding during cell transformations, University of Essex, UK, November 6, 2014.
22. Deciphering the rules of stem cell development, Centre d'Immunologie de Marseille-Luminy, University of Marseille, France, September 24, 2014.
23. Interplay of CTCF binding, DNA methylation and nucleosome positioning, Weizmann Institute of Science, Israel, September 16, 2014.
24. Interplay of CTCF binding, DNA methylation and nucleosome positioning, Hebrew University, Israel, September 14, 2014.
25. Interplay of CTCF binding, DNA methylation and nucleosome positioning, University of Haifa, Israel, September 11, 2014.
26. Deciphering epigenetic mechanisms of stem cell differentiation, University of Gdansk, Poland, 27 June 2014.

27. Deciphering epigenetic mechanisms of stem cell differentiation, Max F. Perutz Laboratories, Vienna, Austria, May 28, 2014.
28. Macromolecule assembly on the DNA, Friedrich-Alexander-Universität Erlangen-Nürnberg, Fürth, Germany, March 4, 2014.
29. Deciphering rules of epigenetic regulation using modeling and high-throughput sequencing experiments, Institute of Systems and Synthetic Biology, Evry, France, February 15, 2014.
30. Interplay between DNA methylation, nucleosome positioning and transcription factor binding during stem cell development, Max Plank Institute for Molecular Genetics, Berlin, 5th November 2013.
31. Deciphering epigenetic mechanisms of stem cell differentiation, Humboldt University, Berlin, 4th November 2013.
32. Deciphering epigenetic mechanisms of stem cell differentiation, University of Sheffield, UK, October 16, 2013.
33. Deciphering epigenetic mechanisms of stem cell differentiation, CNRS, Gif-sur-Yvette, France, October 10, 2013.
34. Deciphering epigenetic mechanisms of stem cell differentiation, BIOTEC, TU Dresden, April 29, 2013.
35. Deciphering epigenetic mechanisms of stem cell differentiation, Bar Ilan University, Israel, 24 July 2013.
36. Deciphering epigenetic mechanisms of stem cell differentiation, Ecole Normale Supérieure de Lyon, France, July 6, 2013
37. Nucleosome positioning in cell differentiation. Max-Plank-Institute for the Physics of Complex Systems, Dresden, March 20, 2012.
38. Quantitative description of gene regulation in chromatin. Institut de cancérologie Gustave Roussy, Villejuif, France, October 4, 2011.
39. Calculating transcription factor binding in chromatin. Gene Center, LMU, Munich, Germany, 18 April, 2011.
40. Deciphering epigenetic algorithms of the cell. Center of Quantitative Biology, Düsseldorf University, December 16, 2010.
41. Deciphering epigenetic algorithms of the cell. International Symposium on Biological Physics, Max-Plank-Institute for the Physics of Complex Systems and Max-Plank-Institute of Molecular Cell Biology and Genetics, Dresden, December 2-3, 2010.
42. Predicting gene-regulation functions, University College Dublin, December 3, 2009.
43. Predicting gene-regulation functions, University of Warwick, July 6, 2009.
44. Quantitative description of gene regulation. Imperial College London, May 7, 2008.
45. Lattice models for stat.-mech. description of gene regulation, Institute of Complex Systems, Santa Fe, NM, USA, March 25, 2008.
46. Lattice models for gene regulation, UCSD, San Diego, USA, February 10, 2008.
47. Lattice models for DNA-ligand binding, Hebrew University, Jerusalem, January 5, 2006.
48. DNA condensation induced by polyamines and metal ions, Engelhard Institute of Molecular Biology, Moscow, Russia, March 27, 2004.

CONTRIBUTED TALKS

1. Nucleosome repositioning in cancer, Transcription and Chromatin UK, October 3-5, 2023.
2. Microdomain formation in chromatin, Quantitative Methods in Gene Regulation IV, December 18-19, 2017, Cambridge, UK.
3. Nucleosome repositioning in cancer transitions, Genome 10K and Genome Science Conference, 29 August – 1 September 2017, Norwich, UK.
4. Interplay of nucleosome positioning, covalent modifications and transcription factor binding, European Conference on Mathematical and Theoretical Biology, Nottingham, UK, 16 July, 2016.
5. Chromatin rearrangement and differential CTCF binding during cell transformations. London Chromatin Club, Kings College London, 30 June, 2016

6. Integrative analysis of combinatorial chromatin interactions using high-throughput sequencing data, 12th International Symposium on Bioinformatics Research and Applications, Minsk, Belarus, June 5-8, 2016.
7. Developing a software suite to analyze the interplay between nucleosome arrangement, DNA methylation and transcription factor binding, "The next NGS Challenge", May 14-16, 2013, Valencia, Spain. Published: Teif V.B., Beshnova D., Vainshtein Y., Höfer T., Rippe K. (2013). Developing a software suite to analyze the interplay between nucleosome arrangement, DNA methylation and transcription factor binding. *EMBnet.journal* 19A, 39-40.
8. Nucleosome re-arrangement as a feedback mechanism between DNA methylation and transcription factor binding. Joint International Meeting of the German Society for Cell Biology (DGZ) and the German Society for Developmental Biology (GfE), Heidelberg, March 20 – 23, 2013.
9. Calculating transcription factor binding maps for chromatin. International Chromosome Conference, Manchester, September 2, 2011.
10. Chromatin remodeling during differentiation of mouse embryonic stem cells. 4th Workshop “Epigenetics at DKFZ”, DKFZ, Heidelberg, January 16, 2012.
11. Why biological logic is NOT Boolean? ERASysBio Summer School, Universidad de Verano de Adeje, Tenerife, Spain, July 29, 2010. Calculating transcription factor binding in chromatin. Summer School on Systems Biology, Kloster Seeon, Germany, 16-18 March, 2011.
12. Predicting nucleosome positions on the DNA: combining intrinsic affinities and remodeler activities. Biophysics of Chromatin Workshop, February 4-6, 2009, Heidelberg, Germany.
13. Polyamine-induced DNA condensation. International Summer School “Multiple aspects of DNA and RNA: from biophysics to bioinformatics”, Les Houches, France, 2 August – 24 August, 2004.

Presentations selected for young scientist travel awards:

1. Lando D. Y. and **Teif V. B.** Influence on double helix stability of the antibiotics, linked to DNA by flexible polymeric molecules. Third Meeting of Belarusian Society of Biophysicists and Photobiologists, Minsk, October 21-23, 1998. P. 206. **Best Student Poster Award.**
2. **Teif V. B.** and Lando D. Y. Conditions for DNA phase transition induced by ligand binding. 10th International Congress of Human Genetics, May 15-19, 2001, Vienna, Austria. Published in *Europ. J. Human Genet.* 9 suppl. 1, 241 (2001).
3. **Teif V. B.** and Lando D. Y. Modeling of DNA condensation and decondensation caused by ligand binding. “DNA in Chromatin: at the Frontiers of Biology, Biophysics and Genomics”, Arcachon, France, March 23-29, 2002. P. 189.
4. **Teif V. B.** and Lando D. Y. DNA condensation-decondensation transition caused by ligand binding. 14th World Biophysics Congress, Buenos Aires, Argentina, April 27 – May 1, 2002. P. 42.
5. **Teif V. B.**, Vorob’ev V. I. and Lando D. Y. A Single DNA chemical modification by cisplatin may cause long-range changes in protein binding to DNA. Results of computer modeling. European Human Genetics Conference 2002, Strasbourg, France, May 25 – 28, 2002. Published in *Europ. J. Human Genet.* 10 suppl. 1, 104 (2002).
6. **Teif V. B.**, Lando D. Y. On the cooperativity of metal ion binding to the bases of single-stranded DNA. 29th FEBS Congress, Warsaw, 26 June – 1 July, 2004. In *Europ. J. Biochem.* 271(1), 19 (2004).
7. Soft condensed matter physics in molecular and cell biology, Edinburgh, UK, 29 March – 8 April, 2004.
8. International Summer School “Multiple aspects of DNA and RNA: from biophysics to bioinformatics”, Les Houches, France, 2 August – 24 August, 2004.
9. **Teif V. B.** General transfer matrix formalism for protein-DNA binding. International Congress of Biochemistry and Molecular Biology, June 16-23, 2006, Kyoto, Japan. **IUBMB Award.**

10. Teif V.B., Lando D.Y., Ben-Shaul A.. A transfer matrix model for the binding of the unfolded MARCKS protein to a mixed fluid lipid membrane. 2nd Workshop on Biophysics of Membrane-Active Peptides, Lisbon, 1-4 April, 2007. **FEBS Award.**
11. **Teif V. B.** General transfer matrix formalism for protein-DNA binding. Biophysical Congress, 2008, Long Beach, USA. **Biophysical Society International Travel Award**
12. **Teif V. B.** and Rippe K. (2009). Predicting nucleosome positions on the DNA: combining intrinsic affinities and remodeler activities. Advanced Lecture Course "New Developments in Quantitative Molecular Bioscience", Spetses, 10-17 Sept. 2008. **FEBS Award.**
13. **Teif V. B.** and Rippe K. (2009). Predicting nucleosome positions on the DNA: combining intrinsic affinities and remodeler activities. International Conference “From DNA-Inspired Physics to Physics-Inspired Biology”, Trieste, 1-5 June, 2009.
14. **Teif V. B.** (2016) Microdomain formation in chromatin. EMBO Conference “From Functional Genomics to Systems Biology”, Heidelberg, November 12-15 2016, **EMBL Travel Grant**.

TEACHING (University of Essex)

BS222 Genome Science (Module supervisor); BS220 Medical Genetics;
BS312 Genome Bioinformatics; BS320 Human Molecular Genetics
BS349 Molecular Basis of Cancer; 3rd Year BSc Research Projects
BS932 Advanced Cancer Biology; BS933 Practical Skills in Cancer Research
BS984 MSc Molecular Medicine; BS986 MSc Biotechnology
Graduate courses: “Online tools for researchers”; “Next Generation Sequencing Analysis"

Teaching before coming to the University of Essex:

- “Interactions of Proteins and Nucleic Acids - Techniques and Applications”, Heidelberg University, Germany, 2009-2012 (assisted Prof. Karsten Rippe).
- “Introduction to Biophysics of Nucleic Acids”, Institute of Molecular and Atomic Physics, Minsk, 2000-2002 (independently developed and delivered a new course).

Supervision of postdocs:

Dr. Hulkar Mamayusupova, 2022 – 2023 (CRUK funded);
Dr. Graeme Thorn, 2017 – 2018 (Wellcome Trust funded)*;*
Dr. Svetlana Gretton, 2016 – 2017 (joint supervision with Prof Elena Klenova);
Dr. Ioanna Pavlaki, 2015 – 2016 (joint supervision with Prof Elena Klenova)
Dr. Daria Beshnova, 2012 – 2013 (scientific programmer, DKFZ funded)

Supervision of PhD students:

Isabella Ciuta, 2024 – current;
Negin Behboodi, 2023 – current;
Dr. Christopher Clarkson, 2017 – 2020.

Supervision of MSD (master by dissertation) research projects:

- *Amishasingh Beeharry (2023-current);*
- *Isabella Ciuta (2021-2024);*
- *Clark Correa (2021-2024);*
- *Dyvia Rose Jacob (2021-2023);*
- *Mariya Shtumpf (2021-2023)*;
- *Varvara Koraki Folli (2019-2021);*

Supervision of MSc (taught) research projects (incomplete list)**:**

Usama Akram (2022), Ankita Gurjar (2022), Jesmi Pullely Poulose (2022), Ahmed Mohammed (2022), Eldhose Makkithadathil (2022), Kaveesa Jayaratnam (2021), Thomas Hickson (2021), Shivam Agrawal (2021), Anastasija Drobysevskaja (2020); Jonathan Lam (2019); Christopher Armstrong (2018); Navid Shafiei (2017); Joshua Burton (2016); Tanvi Sharma (2016).

Supervision of undergraduate students funded by competitive fellowships:

- *Amishasingh Beeharry* (Frontrunner fellowship, 2023),
- *Milena Bykova* (Frontrunner fellowship, 2023; Genetics Society Fellowship, 2023)
- *Seihee Jeong* (Frontrunner fellowship, 2023)
- *Liminita Ruje* (Genetics Society Fellowship, 2021);
- *Mariya Shtumpf (2021-2023)* (Genetics Society Fellowship, 2020);
- *Kristan Piroeva* (UROP Fellowship, 2020; Genetics Society Fellowship, 2019);
- *Emma Deeks* (Frontrunner Plus Fellowship, 2018/19);
- *Ralph Samarista* (Wellcome Trust Vacation Fellowship, 2018).

OTHER ACTIVITIES

- Co-founder of the startup company PiligrimXXI (http://www.piligrimxxi.com). It was awarded a number of prizes including $60k Microsoft Startup Award, 2014.
- Awarded a Royal Society STEM Partnership Grant (2018) in collaboration with Dr Mari Chikvaidze for the use of Augmented Reality (AR) for scientific outreach. Developed and conducted a course “Can we construct drugs with computers?” for year 8 students in the Claremont High School (London).
- Founder of @generegulation Twitter hub for academic community

  (>14k followers including ~30% PIs, ~30% postdocs, ~30% students, ~3% journal editors