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ResercherID: <http://www.researcherid.com/rid/D-3383-2011>

Education:

Ph.D. College of Engineering/Computational Science and Engineering, Koç University, Turkey, Oct 2010.

M.Sc. College of Engineering/Computational Science and Engineering, Koç University, Turkey, Sept 2007.

B.Sc. College of Engineering/Chemical Engineering, Istanbul Technical University, Turkey, 2005

Professional Positions:

Feb 2021–still Associate Professor, jointly at Chemical and Biological Engineering and Medical School, Koç University, Turkey

2017–Feb 2021 Associate Professor, Informatics Institute, Dept. of Health Informatics, METU/Turkey

2016–2017 Assistant Professor, Informatics Institute, Dept. of Health Informatics, METU/Turkey

2014–2016 Principal Investigator, Informatics Institute, Dept. of Health Informatics, METU/Turkey

2010–2014 Postdoctoral Associate, College of Engineering/ Department of Biological Engineering, Massachusetts Institute of Technology/ USA

Visiting Positions:

Mar 2016 Visiting Researcher, Biological Engineering, Massachusetts Institute of Technology/ USA

Jan 2012 Visiting Researcher, Microsoft New England Research and Development/USA

In collaboration with Jennifer Chayes and Christian Borgs

Jan 2011 Visiting Researcher, Politecnico di Torino/Italy

In collaboration with Prof Riccardo Zecchina

July 2009 Visiting Researcher, National Cancer Institute/Center for Cancer Research, National Institute of Health/USA

Awards and Fellowships:

2020 Selected as a member of Global Young Academy for 5 years.

2017 – 2020 METU Faculty Performance Award (3 consecutive years)

2019 UNESCO-L’Oreal International Rising Talent Award, UNESCO-L’Oréal Foundation/France

2019 Health Institutes of Turkey (TUSEB) Young Scientist Award/Turkey

2018 UNESCO-L’Oreal National for Women in Science Award, UNESCO-L’Oréal Turkey/Turkey

2018 TUBA GEBIP Young Investigator Award, Turkish Academy of Sciences /Turkey

2017 Young Scientist Award, Parlar Foundation /Turkey

2017 Young Scientist Award (BAGEP), Science Academy/Turkey

2014 – 2016 FP7 Marie Curie – TUBITAK Cofunded Brain Circulation Scheme Fellowship (Every year, this fellowship is given to 25 exceptional researchers from all research fields)

2006 – 2010 Graduate Scholarship, Scientific Council of Turkey (TUBITAK)/ Turkey

2007 ISMB/ECCB, Vienna, Austria – Student Council Travel Award, sponsored by European Bioinformatics Institute (EBI) granted only to five people all over the Europe

Grants

- 2019 – 2022 TÜBİTAK 1001 (Researcher) Project title: “Identification of SETD3 dependent alterations in gene expression during the differentiation of Mouse Embryonic Stem Cells to Endoderm”
- 2019 – 2022 TÜBİTAK International Joint Projects (Advisor) Project title: “Investigation of Cerebral Cortical Disorders with Multi-Omics”
- 2019 – 2022 TÜBİTAK 1001 (Researcher) Project title: “Modeling the Off-target Effects of the Drugs in Hepatocellular Carcinoma via Computational Systems Biology Approaches”

- 2017 – 2020 TÜBİTAK 1001 (Researcher) Project Title: “Identification and Validation of the Dynamic Protein Interaction Network of Ypel2”
- 2017 – 2020 TUBITAK 3501 Career Development Program Grant (Principle Investigator), Project Title: “Reconstruction of the Tumor-Specific Protein Interaction Networks in Human Cancers via Alternative Splicing Events”
- 2016 – 2017 METU Scientific Research Projects Grant (Principle Investigator), Project Title: “Structural Modeling of the Patient Specific Networks in Glioblastoma”
- 2014 – 2016 FP7 the Marie Curie Action and TUBITAK Co-funded Brain Circulation Scheme Fellowship (Principle Investigator), Project Title: “Multi-dimensional modelling of the disease networks in atomic detail by data integration across several cancer types”

Citations

Total Times Cited: 1411 (WoS) / 2104 (Google Scholar)

h-index: 17 (WoS) / 19 (Google Scholar)

Supervision of Graduate Students:

M.Sc. Alumni:

- Gungor Budak, MSc., Sept 2015, Department of Bioinformatics, METU Turkey
 - Now a Research Scientist at Seven Bridges Genomics
- Poorya Parvizi, MSc, Sept 2016, Department of Biology, METU Turkey
 - Now a PhD Student at The University of Edinburgh, UK
- Gokce Senger, MSc, March 2019, Department of Bioinformatics, METU Turkey
 - Now a PhD Student at European Institute of Oncology, Italy
- Cansu Demirel, MSc, July 2019, Department of Bioinformatics, METU Turkey
 - Now a PhD Student at Department of Health Informatics, METU Turkey
- Cansu Dincer, MSc, August 2019, Department of Bioinformatics, METU Turkey
 - Now a PhD student at Wellcome Sanger Institute, UK

Current Ph.D. students

Seyma Unsal (Medical Informatics), Bengi Ruken Yavuz (Medical Informatics), Kaan Arici (Medical Informatics), Melike Caglayan (Medical Informatics), Gungor Budak (Computer Engineering), Cansu Demirel (Medical Informatics) at METU Informatics Institute

Teaching

Taught 2 graduate courses per semester at METU since 2014. Developed new graduate courses in: Bioinformatics, Programming, Biological Databases and Structural Bioinformatics. The students are taking the course from very different departments including medical school (Hacettepe and Ankara Universities), chemical engineering, computer engineering, architecture, civil engineering, food engineering, geological engineering, industrial design, bioinformatics, molecular biology which shows the interdisciplinary aspect of my courses.

Conference Organizing:

Co-chair of International Symposium of Health Informatics and Bioinformatics (HIBIT) 2017(130 participants) / Cyprus, Organizer in HIBIT) 2018(150 participants), Antalya, Turkey

Program Committee Member:

- 2020 Proteomics Conference in Turkey,

- 2015 – 2019 International Symposium of Health Informatics and Bioinformatics (HIBIT),
- 2014 – 2016 ACM Conference on Bioinformatics, Computational Biology and Health Informatics

Institutional Responsibilities -- University Service

3. 2016 – present Graduate Program Coordinator of Bioinformatics, METU/ Informatics Institute/ Turkey
 2. 2017 – present Organizer of the Internal Seminars, METU/Informatics Institute Bioinformatics Seminar Series/Turkey
 1. 2017–present Organization of the Open Research Day METU/ Informatics Institute/ Turkey

Grant Proposal Reviewing / Panelist:

- Qatar National Research Fund and Qatar Genome Programme Calls,
- EJP Rare Diseases 2020,
- The Scientific Council of Turkey (TUBITAK), 2015- still,
- The Institutes of Health in Turkey (TUSEB), 2019-still, Science Academy Turkey, 2017.

Reviewer in International Journals

iScience (*Cell Press*), Scientific Reports(*Nature Publishing Group*), PLOS Computational Biology, Bioinformatics (*Oxford Journals*), PLOS One, Proteins: Structure, Function & Bioinformatics, Transactions on Computational Biology and Bioinformatics (*IEEE Computer Society*), BMC Structural Biology, BMC Bioinformatics, OMICS, Nucleic Acids Research, Briefings in Bioinformatics (*Oxford Journals*), Trends in Biotechnology (*Cell Publishing Group*), Molecular Biosystems, Computers in Biology and Medicine, ACM Conference on Bioinformatics, Computational Biology and Health Informatics, PeerJ, Frontiers Series.

Memberships in Scientific Societies

1. 2019 - Founding Member, Turkish Bioinformatics Society, 2. 2018-present Member of Turkish Proteomic Society, 3. 2015-present a member of the Young Academy of Science Academy in Turkey, 4. 2011 - Founding Member of Regional Student Group in Turkey of ISCB, 5. 2008–2010 Member of Biophysical Society, 2007-present Member of ISCB

Major Collaborations

1. Prof. Ruth Nussinov, Analysis of Cancer Mutations, National Cancer Institute/Center for Cancer Research, National Institute of Health/USA 2. Prof. Ernest Fraenkel, Developing Network Modeling Techniques, College of Engineering/ Department of Biological Engineering, Massachusetts Institute of Technology/ USA 3. Assoc. Prof. Nurhan Ozlu, Proteomics and Post-translational Modifications in Cancer, College of Science/Molecular Biology and Genetics, Koc University/Turkey 4. Assist. Prof. Ferah Yildirim, Single Cell Transcriptomics in Huntington Disease, Medical School, Charite University/Germany 5. Dr. Esko Kankuri, Multi-omic modelling of Cardiovascular Diseases to Evaluate the Benefit from the Surgery, University of Helsinki/Finland 6. COSBI Lab (directed by Prof. Ozlem Keskin and Prof Attila Gursoy) Koc University/Turkey

Invited Talks (selected):

- NCBI Computational Biology Branch Seminar Series, August 22, 2019 (Invited Talk)
- National Cancer Institute/National Health Institute (NCI/NIH), August 20, 2019 (Invited Talk)
- International Symposium on Health Informatics and Bioinformatics (HIBIT) 2019
- Great Lakes Bioinformatics Conference, May 15 - 17, 2017 (Selected Talk)
- X Annual Congress of the European Proteomics Association, June 22-25, 2016 (Invited Talk)
- University of Zurich, von Mering Lab, October 2015 (Invited Talk)

Manuscripts Under Review and in Preparation

1. Yavuz B.R., Tsai C.J., Nussinov R., **Tuncbag N.** Discovery of Latent Drivers from Double Mutations in Pan-Cancer Data Reveal their Clinical Impact, *Genome Medicine*, *under review*.
2. Paraskevopoulou F., Parvizi P., Senger G., **Tuncbag N.**, Rosenmund C., Yildirim F. Impaired inhibitory GABAergic synaptic transmission and gene transcription studied in single neurons by Patch-seq in Huntington's disease, *PNAS*, *under review*.
3. Arici M.K., **Tuncbag N.** A critical assessment of the performance of network reconstruction approaches based on interactome data sets, *Frontiers in Molecular Biosciences*, *under review*.
4. Mulari S., Eskin A., Lampinen M., Nummi A., Nieminen T., Teittinen K., Ojala T., Kankainen M., Vento A., Laurikka J., Kupari M., Harjula A., **Tuncbag N.**, Kankuri E. Atrial Appendage Signature RNAs Associated with Ischemic Heart Disease Severity and Surgical Outcome, *in manuscript*.
5. Senturk A., Sahin A., Armutlu A., Kiremit M., Acar O., Erdem S., Bagbudar S., Esen T., **Tuncbag N.**, Ozlu N., Quantitative proteomics identifies secreted diagnostic biomarkers as well as tumor-dependent prognostic targets for clear cell Renal Cell Carcinoma, *in manuscript*.

Publications in Peer-Reviewed Journals

1. Dincer C, Kaya T, Keskin O, Gursoy A, **Tuncbag N.** (2019) 3D spatial organization and network-guided comparison of mutation profiles in Glioblastoma reveals similarities across patients. *PLOS Computational Biology*. 15(9):e1006789. doi: 10.1371/journal.pcbi.1006789.
2. Uretmen Kagiali ZC, Sanal E, Karayel Ö, Polat AN, Saatci Ö, Ersan PG, TrappeK, Renard BY, Önder TT, **Tuncbag N.**, Şahin Ö, Ozlu N. (2019) Systems-level analysis reveals multiple modulators of epithelial-mesenchymal transition and identifies DNAJB4 and CD81 as novel metastasis inducers in breast cancer. *Mol Cell Proteomics*. pii: mcp.RA119.001446. doi: 10.1074/mcp.RA119.001446.
3. Demirel HC, Dogan T, **Tuncbag N.** (2018) A Structural Perspective on the Modulation of Protein-Protein Interactions with Small Molecules. *Curr Top Med Chem.*;18(8):700-713. doi: 10.2174/1568026618666180601080824.
4. Atas H, **Tuncbag N.** Doğan T. (2018) Phylogenetic and Other Conservation-Based Approaches to Predict Protein Functional Sites. *Methods Mol Biol.*;1762:51-69. doi: 10.1007/978-1-4939-7756-7_4.
5. Karayel O, Sanal E, Giese SH, Uretmen Kagiali ZC, Polat AN, Hu CK, Renard BY, **Tuncbag N.**, Ozlu N (2017) Comparative phosphoproteomic analysis reveals signaling networks that regulate cytokinesis, *Scientific Reports* 8(1):2269. doi: 10.1038/s41598-018-20231-5..
6. Kacar B, Garmendia E, **Tuncbag N.**, Andersson DI, Hughes D. (2017) Functional Constraints on Replacing an Essential Gene with Its Ancient and Modern Homologs, *mBio*, doi: 10.1128/mBio.01276-17
7. Khurana V, Peng J, Chung CY, Auluck PK, Fanning S, Tardiff DF, Bartels T, Koeva M, Eichhorn SW, Benyamini H, Lou Y, Nutter-Upham A, Baru V, Freyzo Y, **Tuncbag N.**, Costanzo M, San Luis B, Schöndorf DC, Barrasa MI, Ehsani S, Sanjana N, Zhong Q, Gasser T, Bartel DP, Vidal M, Deleidi M, Boone C, Fraenkel E, Berger B, Lindquist S (2017) Genome-scale networks link neurodegenerative disease genes to alpha-synuclein through specific molecular pathways, *Cell Systems*, doi:10.1016/j.cels.2016.12.011.
8. **Tuncbag N.**, Keskin O, Nussinov R, Gursoy A (2017) Prediction of Protein Interactions by Structural Matching: Prediction of PPI Networks and the Effects of Mutations on PPIs that Combines Sequence and Structural Information, *Methods in Molecular Biology*, 1558:255-270. (book chapter).

9. **Tuncbag N**, Milani P, Pokorný JL, Johnson H, Sio TT, Dalin S, Iyekegbe DO, White F, Sarkaria JN, Fraenkel E (2016) Network Modeling Identifies Patient-specific Pathways in Glioblastoma, *Scientific Reports*, 6:28668. doi: 10.1038/srep28668.
10. **Tuncbag N**, Gursoy A, Keskin O, Nussinov R. The potential impact of recent developments in three-dimensional quantitative interaction proteomics on structural biology. *Expert Rev Proteomics*. 2016 May;13(5):447-9. doi: 10.1080/14789450.2016.
11. **Tuncbag N**, Gosline SJC, Kedaigle A, Soltis AR, Gitter A, Fraenkel E. Network-based interpretation of diverse high-throughput datasets through the Omics Integrator software package, *PLOS Comp Bio*, 2016, 12(4):e1004879. doi: 10.1371/journal.pcbi.1004879.
Out of all 2016 articles, it was in the top 50 most downloaded.
12. Keskin O, **Tuncbag N**, Gursoy A. Predicting Protein-Protein Interactions from the Molecular to the Proteome Level. *Chemical Reviews*. 2016 Apr 27;116(8):4884-909. doi: 10.1021/acs.chemrev.5b00683.
13. Budak G, Eren-Ozsoy O, Aydin-Son Y, Can T, **Tuncbag N**. Modeling and reconstruction of temporal signaling networks in Salmonella-infected human cells, *Frontiers in Microbiology*, 2015, 20(6):730.
14. Ersahin T, **Tuncbag N**, Cetin-Atalay R. The PI3K/AKT/mTOR interactive pathway, *Molecular Biosystems*, 2015, 11(7):1946-54.
15. **Tuncbag N**, Braunstein A, Pagnani A, Huang SSC, Chayes J, Borgs C, Zecchina R, Fraenkel E. Simultaneous reconstruction of multiple signaling pathways via the prize-collecting Steiner forest problem, *Journal of Computational Biology*, 2013, 20, pp. 1-13.
16. **Tuncbag N**, McCallum S, Huang SSC, Fraenkel E. SteinerNet: A Web Server for Integrating “Omic” data to Discover Hidden Components of Response Pathways, *Nucleic Acids Research (Web Server Issue)*, 2012, doi: 10.1093/nar/gks445.
17. **Tuncbag N**, Keskin O, Nussinov R, Gursoy A. Fast and Accurate Modeling of Protein-Protein Interactions by Combining Template-Interface-Based Docking with Flexible Refinement, *Proteins: Structure, Function and Bioinformatics*, 2012, 80(4):1239-49.
18. **Tuncbag N**, Gursoy A, Nussinov R, Keskin O. Predicting Protein-Protein Interactions on a Proteome Scale by Matching Evolutionary and Structural Similarities at Interfaces Using PRISM, *Nature Protocols*, 2011, 6(9):1341-54.
Labelled “Highly cited paper” at Web of Science.
19. **Tuncbag N**, Gursoy A, Keskin O. Prediction of protein-protein interactions: Unifying evolution and structure at protein interfaces, *Physical Biology*, 2011, 8(3):035006.
20. **Tuncbag N**, Keskin O, Gursoy A. “HotPoint: Hot Spot Prediction Server for Protein Interfaces” *Nucleic Acids Research*, 2010, 38(Web Server issue):W402-6.
21. **Tuncbag N**, Salman FS, Keskin O, Gursoy A. “Analysis and network representation of hot spots in protein interfaces using minimum cut trees” *Proteins: Structure, Function and Bioinformatics*, 2010, 78(10):2283-94.
22. **Tuncbag N**, Kar G, Gursoy A, Keskin O, Nussinov R. “Towards inferring time-dimensionality in protein-protein interaction networks by integrating structures: the p53 example” *Molecular Biosystems*, 2009, 5:1770-1778.
Amongst the top ten accessed articles in June, July, August 2011 and in February 2012.
23. **Tuncbag N**, Gursoy A, Keskin O. “Identification of computational hot spots in protein interfaces: Combining solvent accessibility and inter-residue potentials improves the accuracy” *Bioinformatics*, 2009, 25(12):1513-1520.
“Fast Breaking Paper in Engineering” by Thomson Reuters and Science Watch in December 2010 in the field of Computer Science

Labelled “Highly cited paper” at Web of Science.

24. **Tuncbag N**, Kar G, Gursoy A, Keskin O, Nussinov R. “A survey of available tools and web servers for analysis of protein–protein interactions and interfaces” *Briefings in Bioinformatics*, 2009, 10:217-232.
25. Guney E, **Tuncbag N**, Keskin O, Gursoy A. “HotSprint: database of computational hot spots in protein interfaces” *Nucleic Acids Research*, 36(Database Issue):D662-666, 2008.
26. Keskin O, **Tuncbag N**, Gursoy A. “Characterization and Prediction of Protein Interfaces to Infer Protein-Protein Interaction Networks” *Curr. Phar. Biotech.*, 9(2):67-76, 2008.
27. **Tuncbag N**, Guney E, Gursoy A, Keskin O, Nussinov R. “Architectures and Functional Coverage of Protein-Protein Interfaces” *Journal of Molecular Biology*, 381:785-802, 2008.

Refereed Conferences (Proceedings/Posters)

1. Unsal Beyge S, Tuncbag N. Integrative network modelling of drug responses for revealing mechanism of action, HIBIT 2020, October 2020.
2. Basaran E., Tuncbag N. Impact of Pan-Cancer mutation profiles in signaling pathways through phosphorylation events, HIBIT 2020, October 2020.
3. Eskin A., Mulari S., Tuncbag N., Kankuri E., Cardiac atrial transcriptomic landscaping reveals defects in various pathways in patients with ischemic heart disease or heart failure, HIBIT 2020, October 2020.
4. Demirel H.C., Tuncbag N., Modeling the tumor specific network rewiring through alternative isoforms of proteins, HIBIT 2020, October 2020.
5. Demirel H.C., Tuncbag N., Modeling the Tumor Specific Network Rewiring by Integrating Alternative Splicing Events with Structural Interactome, ISMB/ECCB 2019, Basel Switzerland.
6. Kutnu M., Özcengiz G., Tunçbağ N. Biological network modeling based on differentially expressed proteins in a bacilysin-deficient strain of *Bacillus subtilis*, 20th International Conference on Bacilli and Gram-Positive Bacteria, Washington, USA, 23 - 26 Temmuz 2019.
7. Sinoplu E. , Tuncbag N. , Kahraman D. C. , Atalay R. C. In silico modeling and in vitro validation of undefined off-target of drugs in hepatocellular carcinoma, Annual Meeting of the American-Association-for-Cancer-Research (AACR), Georgia, USA, 29 Mart - 03 Nisan 2019.
8. Kaya T., Tuncbag N. Integrative Modeling of the Tumor Specific Structural Networks in Human Cancers, EMBO Workshop In situ Methods in Cell Biology and Cellular Biophysics, July 2018, Berlin Germany.
9. Demirel H. C. , Tunçbağ N., Modeling the tumor specific structural networks by integrating alternative splicing events, European Conference on Computational Biology, 8 - 12 Eylül 2018.
10. Budak G., Fraenkel E., Tunçbağ N., Identification of the Ischemic Pathway Level Changes by Integrating Temporal Phosphoproteome in Ovarian Cancer, 5th International Congress of the Molecular Biology Association of Turkey, 8 - 10 Eylül 2017.
11. Demirel H. C. , Tunçbağ N. The Effect of Alternative Splicing on Tumor Specific Protein Networks HIBIT 2017, 28 - 30 Haziran 2017.
12. Senger G., Tunçbağ N. Network Modeling of the Dasatinib Treatment in Glioblastoma Stem Cells by Data Integration, HIBIT 2017, 28 - 30 Haziran 2017
13. Dincer C., Tunçbağ N. Structural Modeling of the Patient-Specific Signaling Networks in Glioblastoma, HIBIT 2017, 28 - 30 Haziran 2017

14. Fayetorbay R., Atalay R. , Tunçbağ N. Network-Based Discovery of Drug Treatments in Hepatocellular Carcinoma, HIBIT 2017, 28 - 30 Haziran 2017
15. Olgun Ç. E. , Tunçbağ N. , Muyan M. Towards proteomic analysis of YPEL2 interacting partners identified with proximity dependent biotinylation, HIBIT2017, 28 - 30 Haziran 2017
16. Tunçbağ N. Integrative Modeling of the Tumor Specific Structural Networks in Human Cancers GLBIO 2017, 15 - 17 Mayıs 2017.
17. Erşahin T., Tunçbağ N. , Acar A. C. , Atalay R. Combination Therapy For Hepatocellular Carcinoma: A Systems Biology Perspective On The Synergistic Antitumor Activity Of Sorafenib With Pi3k/Akt Pathway Inhibitors, 50th International Liver Congress of the European-Association-for-the-Study-of-the-Liver, Vienna, Austria, 22 - 26 Nisan 2015.
18. Tunçbağ N. , Braunstein A., Pagnani A., Huang S. S. C. , Chayes J., Borgs C., et al. Simultaneous reconstruction of multiple signaling pathways via the prize collecting Steiner forest problem, 16th Annual International Conference on Research in Computational Molecular Biology, 21 - 24 Nisan 2012.
19. Tunçbağ N. , Gürsoy A., Keskin Özkaya Z. Ö. , Nussinov R. Structural proteome scale prediction of protein protein interactions using interfaces, 3dSig Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), 15 - 16 Temmuz 2011.
20. Tunçbağ N. , Gürsoy A., Nussinov R., Keskin Özkaya Z. Ö. Prediction of Protein Protein Interactions at Genome Scale, 55th Annual Meeting of the Biophysical-Society, 5 - 09 Mart 2011
21. Tunçbağ N. , Keskin Özkaya Z. Ö. , Gürsoy A. HotPOINT Hot Spot Prediction Server for Protein Interfaces, Research in Computational Molecular Biology (RECOMB), LIZBON, Portekiz, 12 - 15 Ağustos 2010
22. Tunçbağ N. , Gürsoy A., Nussinov R., Keskin Özkaya Z. Ö. Large scale construction of three dimensional protein protein complex structures, Research In Computational Molecular Biology (RECOMB), Lizbon, Portekiz, 12 - 15 Ağustos 2010.
23. Tunçbağ N. , Gürsoy A., Nussinov R., Keskin Özkaya Z. Ö. Large scale combinatorial docking of the proteome for functional predictions, Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), Boston, Amerika Birleşik Devletleri, 11 - 13 Temmuz 2010
24. Tunçbağ N. , Keskin Özkaya Z. Ö. , Gürsoy A. HotPoint A web server for prediction of hot spots in protein interfaces, 5th International Symposium on Health Informatics and Bioinformatics, Antalya, Türkiye, 20 - 22 Nisan 2010.
25. Tunçbağ N. , Gürsoy A., Nussinov R., Keskin Özkaya Z. Ö. Architectures and Functional Coverage of Protein Protein Interface, ISMB/ECCB 3dSig, Stockholm, İsveç, 20 Haziran - 02 Temmuz 2009
26. Tunçbağ N. , Gürsoy A., Keskin Özkaya Z. Ö. Identification of Computational Hot Spots in Protein Interfaces Using Solvent Accessibility and Inter Residue Potentials Poster Presentation, Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)& European Conference on Computational Biology (ECCB), Stockholm, İsveç, 27 Haziran - 02 Temmuz 2009
27. Güney E, Tunçbağ N, Keskin Ö, Gürsoy A (2008). Large Scale Identification of Spatial Motifs on the Protein-Protein Interfaces. International Symposium on HealthInformatics and Bioinformatics (HIBIT)
28. Tunçbağ N. , Keskin Özkaya Z. Ö. , Nussinov R., Gürsoy A. Large Scale Prediction of Computational Hot Spots in Protein Interfaces, 53rd Annual Meeting of the Biophysical-Society, 28 Şubat - 04 Mart 2009, cilt.96, ss.650-651
29. Güney E., Tunçbağ N. , Keskin Özkaya Z. Ö. , Gürsoy A. Large Scale Prediction of Hot Spots at Protein Interfaces, European Conferance on Computational Biology, SARDINIA, 22 - 26 Eylül 2008
30. Tunçbağ N. , Güney E., Ulubaş M. C. , Keskin Özkaya Z. Ö. , Gürsoy A. PRISM A Web Server for Prediction and Visualization of Protein Protein Interactions, 15th Annual International Conference on

Intelligent Systems for Molecular Biology (ISMB)& 6th European Conference on Computational Biology (ECCB), VIYANA, Avusturya, 21 - 25 Temmuz 2007

31. Tunçbağ N. , Gürsoy A., Guney E., Nussinov R., Tsai C. J. , Keskin Özkaya Z. Ö. A new dataset of protein protein interfaces, 51st Annual Meeting of the Biophysical-Society, 3 - 07 Mart 2007