

## **Emre GUNEY**

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### **RESEARCH & WORK EXPERIENCE**

- Aug 2016 – present*      **Maastricht University**, *Affiliate Research Fellow*  
Pharmacology and Personalised Medicine Group  
Maastricht, the Netherlands
- Oct 2015 – present*      **Institute for Biomedical Research**, *Beatriu de Pinós Fellow*  
Structural Bioinformatics and Network Biology Lab  
Barcelona, Spain
- Sept 2015 – present*      **DZZOM**, *Scientific Advisor*  
Boston, MA, USA
- Oct 2015 – June 2016*      **Northeastern University**, *Affiliate Research Fellow*  
Center for Complex Network Research, Department of Physics  
Boston, MA, USA
- June 2013 – Sept 2015*      **Northeastern University**, *Postdoctoral Research Associate*  
Center for Complex Network Research, Department of Physics  
Boston, MA, USA
- June 2013 – Sept 2015*      **Dana Farber Cancer Institute**, *Affiliate Research Associate*  
Center for Cancer System Biology  
Boston, MA, USA
- Sept 2008 – April 2013*      **Pompeu Fabra University**, *Research and Teaching Assistant*  
Structural Bioinformatics Lab  
Barcelona, Spain
- Apr 2010 – Sept 2010*      **University of California, San Diego**, *Visiting Researcher*  
Trey Ideker Lab  
San Diego, CA, USA
- Sept 2005 – June 2007*      **Koc University**, *Research and Teaching Assistant*  
COSBI Lab, Department of Computer Engineering  
Istanbul, Turkey

### **EDUCATION**

- Sept 2008 – Sept 2012*      **Pompeu Fabra University (UPF)**, Barcelona, Spain  
PhD. in Biomedicine  
*Advisor: Prof. Baldo Oliva*
- Sept 2005 – Nov 2007*      **Koc University (KU)**, Istanbul, Turkey  
M.S. in Electrical and Computer Engineering  
*Advisor: Prof. Attila Gursoy*
- Sept 2001 – June 2005*      **Middle East Technical University (METU)**, Ankara, Turkey  
B.S. in Computer Engineering

## **PUBLICATIONS**

Rubio-Perez C\*, Guney E\*, Aguilar D, Garcia-Garcia J, Piñero J, Iadarola B, Sanz F, Fernandez-Fuentes N, Furlong L, Oliva B. Genetic and functional characterization of disease associations explains comorbidity. *Scientific Reports*, 2017, 7:6207.

Menche J\*, Guney E\*, Sharma A, Branigan P, Loza M, Baribaud F, Dobrin R, Barabási AL. Integrating personalized gene expression profiles into predictive disease-associated gene pools. *Npj Systems Biology and Applications*, 2017, 3:10.

Garcia-Garcia J, Valls-Comamala V, Guney E, Andreu D, Muñoz FJ, Fernandez-Fuentes N, Oliva B. iFraG: a protein-protein interface prediction server based on sequence fragments. *Journal of Molecular Biology*, 2017, 429(3):382-389.

Guney E. Reproducible drug repurposing: When similarity does not suffice. *Pacific Symposium on Biocomputing*, 2016, 22:132-143.

Kitsak M, Sharma A, Menche J, Guney E, Ghiassian S, Loscalzo J, Barabási AL. Tissue Specificity of Human Disease. *Scientific Reports*, 2016, 6, 35241.

Sieberts SK, Zhu F, García-García J, Stahl E, Pratap A, Pandey G, Pappas D, Aguilar D, Anton B, Bonet J, Eksi R, Fornés O, Guney E, et al. Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. *Nature Communications*, 2016, 7:12460.

Guney E, Menche J, Vidal M, Barabási AL. Network-based *in silico* drug efficacy screening. *Nature Communications*, 2016, 6:10331.

Martínez-Aranda A, Hernández V, Guney E, Muixí L, Foj R, Baixeras N, Cuadras D, Moreno V, Urruticoechea A, Gil M, Oliva B, Moreno F, González E, Vidal N, Andreu X, Seguí MA, Ballester R, Castella E, and Sierra A. FN14 and GRP94 expression are prognostic/predictive biomarkers of brain metastasis outcome that open up new therapeutic strategies. *Oncotarget*, 2015, 6(42):44254-73.

Hänzelmann S, Wang J, Guney E, Tang Y, Zhang E, Axelsson AS, Nenonen H, Salehi AS, Wollheim CB, Zetterberg E, Berntorp E, Costa IG, Castelo R, Rosengren AH. Thrombin stimulates insulin secretion via protease-activated receptor-3. *Islets*, 2015, 7:4.

Guney E, Oliva B. Analysis of the Robustness of Network-Based Disease-Gene Prioritization Methods Reveals Redundancy in the Human Interactome and Functional Diversity of Disease-Genes. *PLoS ONE*, 2014, 9(4): e94686.

Guney E, Garcia-Garcia J, Oliva B. GUILDify: A web server for phenotypic characterization of genes through biological data integration and network-based prioritization algorithms. *Bioinformatics*, 2014, 30(12):1789-90.

Di Domenico T, Prudence C, Vicedo E, Guney E, Jigisha A and Shanmugam A. Highlights from the ISCB Student Council Symposium 2013. *BMC Bioinformatics*, 2014, 15(Suppl 3):A1.

Engin HB, Guney E, Keskin O, Oliva B, Gursoy A. Integrating Structure to Protein-Protein Interaction Networks That Drive Metastasis to Brain and Lung in Breast Cancer. *PLoS ONE*, 2013, 8(11), e81035.

Santana-Codina N, Carretero R, Sanz-Pamplona R, Cabrera T, Guney E, Oliva B, Clezardin P, Olarte OE, Loza P, Méndez-Lucas A, Perales JC, and Sierra A. A transcriptome-proteome integrated network identifies ERp57 as a hub that mediates bone metastasis. *Molecular and Cellular Proteomics*, 2013, 12(8), 2111-2125.

Guney E, Oliva B. Exploiting Protein-Protein Interaction Networks for Genome-wide Disease-Gene Prioritization. *PLoS ONE*, 2012, 7(9): e43557.

Garcia-Garcia J, Bonet J, Guney E, Fornes O, Planas-Iglesias J, Oliva B. Networks of Protein-Protein Interactions: from uncertainty to molecular details. *Molecular Informatics*, 2012, 31(5): 342-362.

Planas-Iglesias J, Guney E, Garcia-Garcia J, Robertson KA, Raza S, Freeman TC, Ghazal P and Oliva B. Extending signalling pathways with protein-interaction networks. Application to apoptosis. *OMICS: A journal of Integrative Biology*, 2012, 16(5): 245-256.

Garcia-Garcia J, Guney E, Aragues R, Planas-Iglesias J, Oliva B. BIANA: A software framework for compiling biological interactions and analyzing networks. *BMC Bioinformatics*, 2010, 11:56.

Tuncbag N, Gursoy A, Guney E, Nussinov R, Keskin O. Architectures and functional coverage of protein-protein interfaces. *Journal of Molecular Biology*, 2008, 381(3), 785-802.

Guney E, Tuncbag N, Keskin O, Gursoy A. HotSprint: database of computational hot spots in protein interfaces. *Nucleic Acids Research*, 2008, 36:D662-D666.

### **MANUSCRIPTS in preparation**

Anupama J, Francescato M, Rahman F, Fatima N, Santos A, Kolekar P, Shanmugam AK, Satagopam VP, DeBlasio D, Michaut M, Guney E. The ISCB Student Council Internship Program: Expanding computational biology capacity worldwide. *Submitted*.

Langhauser F, Casas AI, Dao VT, Guney E, Menche J, Geuss E, Kleikers PWM, López MG, Barabási AL, Kleinschnitz C, Schmidt HHHW. Disease-driven repurposing of apo-soluble guanylate cyclase as a mechanism-based neuroprotective target in stroke. *Submitted*.

Cuadrado A, Manda G, Ahmed H, Alcaraz MJ, Barbas C, Daiber A, Ghezzi P, León R, López MG, Oliva B, Pajares M, Rojo AI, Valverde AM, Guney E, Schmidt H. Transcription factor NRF2 as a therapeutic target for degenerative diseases: a systems medicine approach. *Submitted*.

### **BOOK CHAPTERS**

Guney E. Investigating side effect modules in the interactome and their use in drug adverse effect discovery. *Workshop on Complex Networks CompleNet, Springer Proceedings in Complexity. Springer*, 2017, Pages 239-250.

Guney E, Sanz R, Angels S, Oliva B. Understanding Cancer Progression Using Protein Interaction Networks. *Systems Biology in Cancer Research and Drug Discovery, Springer*, 2012, Pages 167-195.

### **THESES**

Guney E. Role of network topology based methods in discovering novel gene-phenotype associations. *Ph.D. thesis submitted to Experimental and Health Sciences of Pompeu Fabra University*, 2012.

Guney E. Large scale characterization of protein interactions: Identification of hot spots and spatial motifs in protein-protein interfaces. *Dissertation thesis submitted to Graduate School of Koc University*, 2007.

## SELECTED TALKS

Integrating personalized gene expression profiles into predictive disease-associated gene pools. *Intelligent Systems for Molecular Biology (ISMB) & European Conference on Computational Biology (ECCB)*, Prague, July, 2017

Should I stay or should I go, NOW? *RSG-Turkey Student Symposium*, Guzelyurt, June, 2017.

Challenges and opportunities in systems pharmacology. *The International Symposium on Health Informatics and Bioinformatics, (HIBIT)*, Guzelyurt, June, 2017.

Investigating side effect modules in the interactome and their use in drug adverse effect discovery. *Conference on Complex Networks (CompleNet)*, Dubrovnik, March, 2017.

Reproducible drug repurposing: When similarity does not suffice. *Pacific Symposium on Biocomputing (PSB)*, Big Island of Hawaii, January, 2017.

Revisiting drug discovery through integrative network pharmacology in the era of precision medicine. *European Conference on Computational Biology (ECCB)*, The Hague, September, 2016.

Interactome-based disease gene prioritization and drug discovery. *Center for Proteomics Research, Disease Systems Biology Department, NNF, Copenhagen, Denmark*, April, 2016.

Precision medicine through integrative network pharmacology. *Barcelona Super Computing Center, Life Sciences Seminar Series, Barcelona*, February, 2016.

Rational drug design through interactome analysis: Are we there yet? *the Division of Pharmacoepidemiology and Pharmacoeconomics Brigham and Women's Hospital, Harvard Medical School*, August, 2015.

Network-based relative proximity: A novel measure for quantifying the closeness between two sets of nodes and its application to network pharmacology. *NetSci'15 - Zaragoza*, June, 2015.

Systematic drug efficacy screening using network-based drug-disease proximity, *Channing Division of Network Medicine - Network Science Seminar*, March, 2015.

Analyzing drug mechanism of action through underlying protein-protein interaction network. *NetSci - Network Medicine Symposium, UC Berkeley*, June, 2014.