

Nurit Haspel

University of Massachusetts Boston
Department of Computer Science
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Boston, MA 02125

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Education

- 2002-2006 **Ph.D.** Computer Science
Tel Aviv University, Tel Aviv, Israel
Advisors: Prof. Ruth Nussinov and Prof. Haim Wolfson
Thesis title: Computational modeling and prediction of self-assembling beta-sheet rich protein structures
- 1999-2002 **M.Sc.** Structural Bioinformatics at the Department of Human Genetics (Summa Cum Laude)
Tel Aviv University, Tel Aviv, Israel
Advisors: Prof. Ruth Nussinov and Prof. Haim Wolfson
Thesis title: Computational study of protein folding pathways using the building blocks folding model
- 1995-1998 **B.Sc.** Chemistry and Computer Science (Cum Laude)
Tel Aviv University, Tel Aviv, Israel

Employment

- 2016-present **Associate Professor**, Department of Computer Science
University of Massachusetts Boston
- 2009-2016 **Assistant Professor**, Department of Computer Science
University of Massachusetts Boston
- 2007-2009 **Postdoctoral Research Associate**, Department of Computer Science
Rice University, Houston, TX
Advisor: Prof. Lydia Kaviraki
- 2002-2006 **Research and Teaching Assistant**, School of Computer Science
Tel-Aviv University, Tel-Aviv, Israel
- 2001-2005 **Visiting Researcher**, Center for Cancer Research Nanobiology Program
National Cancer Institute Frederick, MD
- 1999-2001 **Research Assistant**, Department of Human Genetics, School of Medicine
Tel-Aviv University, Tel-Aviv, Israel

Publications

Peer Reviewed Journal Publications

1. Farhoodi, R., Akbal-Delibas, B., and Haspel, N. (2017). Machine learning approaches for predicting protein structure similarity. *J. Comp. Biol.*, 24(1):40–51
2. Luo, D., González, E., and Haspel, N. (2016). Detecting intermediate protein conformations using algebraic topology. *BMC Bioinformatics*, Submitted
3. Akbal-Delibas, B., Farhoodi, R., Pomplun, M., and Haspel, N. (2016). Accurate refinement of docked protein complexes using evolutionary information and deep learning. *J. Bioinf.*

- Comp. Biol.*, 14(3):1642002
4. Akbal-Delibas, B., Pomplun, M., and Haspel, N. (2015a). Accurate prediction of docked protein structure similarity. *J. Comp. Biol.*, 22(9):892–904
 5. Murase, S. K., Haspel, N., del Valle, L. J., Perpete, E. A., Michaux, C., Nussinov, R., Puiggali, J., and Aleman, C. (2014). Molecular characterization of l-phenylalanine terminated poly(l-lactide) conjugates. *RSC Advances*, 4(44):23231–23241
 6. Akbal-Delibas, B. and Haspel, N. (2013). A conservation and biophysics guided stochastic approach to refining docked multimeric proteins. *BMC Struct. Biol.*, 13(Suppl 1):S7
 7. B. Akbal-Delibas, F. Jagodzinski, and Haspel, N. (2013). A conservation and rigidity based method for detecting critical protein residues. *BMC Struct. Biol.*, 13(Suppl 1):S6
* – Equal contribution
 8. Zanuy, D., Kotla, R., Nussinov, R., Teesalu, T., Sugahara, K. N., Aleman, C., and Haspel, N. (2013). Sequence dependence of c-end rule peptides in binding and activation of neuropilin-1 receptor. *Journal of Structural Biology*, 182(2):78 – 86
 9. Haspel, N., Laurent, A. D., David, Z., Ruth, N., Carlos, A., Jordi, P., and Guillem, R.-L. (2012a). Conformational exploration of two peptides and their hybrid polymer conjugates: Potentialities as self-aggregating materials. *The Journal of Physical Chemistry B*, 116(48):13941–13952
 10. Akbal-Delibas, B., Hashmi, I., Shehu, A., and Haspel, N. (2012a). An evolutionary conservation-based method for refining and reranking protein complex structures. *J. Bioinformatics and Computational Biology (JBCB)*, 10(3):1242002
 11. Hashmi, I., Akbal-Delibas, B., Haspel, N., and Shehu, A. (2012). Guiding protein docking with geometric and evolutionary information. *J. Bioinformatics and Computational Biology (JBCB)*, 10(3):1242008
 12. Haspel, N., Zanuy, D., Nussinov, R., Teesalu, T., Ruoslahti, E., and Aleman, C. (2011d). Binding of a c-end rule peptide to the neuropilin-1 receptor: a molecular modeling approach. *Biochemistry*, 50(10):1755–1762
 13. Haspel, N., Moll, M., Baker, M., Chiu, W., and Kaviraki, L. E. (2010b). Tracing conformational changes in proteins. *BMC Structural Biology*, Suppl1:S1
 14. Haspel, N., Geisbrecht, B., Lambris, J., and Kaviraki, L. (2010a). Multi-scale characterization of the energy landscape of proteins with application to the c3d/efb-c complex. *Proteins: Structure, function and bioinformatics*, 78(4):1004–1014
 15. Zanuy, D., Ballano, G., Jimenez, A. I., Casanovas, J., Haspel, N., Cativiela, C., Curco, D., Nussinov, R., and Aleman, C. (2009). Protein segments with conformationally restricted amino acids can control supramolecular organization at the nanoscale. *J. Chemical and Information Modeling*, 49(7):1623–1629
 16. Haspel*, N., D. Ricklin*, Geisbrecht, B., Lambris, J., and Kaviraki, L. (2008). Electrostatic contributions drive the interaction between staphylococcus aureus protein efb-c and its complement target c3d. *Protein Science*, 17(11):1894–1906
* – Equal contribution
 17. Zanuy, D., Rodriguez-Roperero, F., Haspel, N., Zheng, J., Nussinov, R., and Aleman, C. (2007). Stability of tubular structures based on beta-helical proteins: self-assembled versus polymer-

- ized nanoconstructs and wild-type versus mutated sequences. *Biomacromolecules*, 8(10):3135–3146
18. Tsai, C., Zheng, J., Zanuy, D., Haspel, N., and Nussinov, R. (2007). Principles of nanostructure design with protein building blocks. *Proteins: Structure, function and bioinformatics*, 68:245–253
 19. Haspel, N., Zanuy, D., Zheng, J., Aleman, C., Wolfson, H., and Nussinov, R. (2007b). Changing the charge distribution of beta-helical based nanostructures can provide the conditions for charge transfer. *Biophys. J.*, 93:245–253
 20. Zheng, J., Zanuy, D., Haspel, N., Tsai, C., Aleman, C., and Nussinov, R. (2007). Nanostructure design using protein building blocks enhanced by conformationally constrained synthetic residues. *Biochemistry*, 46(5):1205–1218
 21. Aleman, C., Zanuy, D., Jimenez, A., Cativiela, C., Haspel, N., Zheng, J., Casanovas, J., Wolfson, H., and Nussinov, R. (2006). Concepts and schemes for the re-engineering of physical protein modules: generating nanodevices via targeted replacements with constrained amino acids. *Phys. Biol.*, 3(1):S54–62
 22. Haspel, N., Zanuy, D., Aleman, C., Wolfson, H., and Nussinov, R. (2006). De-novo tubular nanostructure design based on self-assembly of beta-helical protein motifs. *Structure*, 14:1137–1148
 23. Wainreb, G., Haspel, N., Wolfson, H., and Nussinov, R. (2006). A permissive secondary structure-guided superposition tool for clustering of protein fragments toward protein structure prediction via fragment assembly. *Bioinformatics*, 22:1343–1352
 24. Haspel, N., Zanuy, D., Ma, B., Wolfson, H., and Nussinov, R. (2005a). A comparative study of amyloid fibril formation by residues 15-19 of the human calcitonin hormone: A single beta-sheet model with a small hydrophobic core. *J. Mol. Biol.*, 345(5):1213–1227
 25. Tsai, H., Zanuy, D., Haspel, N., Gunasekaran, K., Ma, B., Tsai, C., and Nussinov, R. (2004). The stability and dynamic of the human calcitonin amyloid peptide dfnkf. *Biophys. J.*, 87(1):146–158
 26. D. Zanuy*, Haspel*, N., Tsai, H., Ma, B., Kannan, G., Wolfson, H., and Nussinov, R. (2004). Side chain interactions determine the amyloid organization: A single layer beta-sheet molecular structure of the calcitonin peptide segment 15-19. *Phys. Biol.*, 1:89–99
* – Equal contribution
 27. Haspel, N., Tsai, C., Wolfson, H., and Nussinov, R. (2003b). Reducing the computational complexity of protein folding via fragment folding and assembly. *Protein Science*, 12:1177–1187
 28. Haspel, N., Tsai, C., Wolfson, H., and Nussinov, R. (2003a). Hierarchical protein folding pathways: A computational study of protein fragments. *Proteins: Structure, function and bioinformatics*, 51:203–215
 29. Schneidman-Duhovny, D., Inbar, Y., Polak, V., Shatsky, M., Halperin, I., Benyamini, H., Barzilai, A., Dror, O., Haspel, N., Nussinov, R., and Wolfson, H. (2003). Taking geometry to its edge: Fast unbound rigid (and hinge-bent) docking. *Proteins: Structure, function and genetics*, 52(1):107–112

Peer Reviewed Conference Proceedings

1. Andersson, E., Hsieh, R., Szeto, H., Farhoodi, R., Jagodzinski, F., and Haspel, N. (2016). Assessing how multiple mutations affect protein stability using rigid cluster size distributions. In *proc. of IEEE-ICCABS (International Conference on Computational Advances in Bio and Medical Sciences)*
2. Vajdi, A. and Haspel, N. (2016). Clustering protein conformations using a dynamic programming based similarity measurement. In *proc. of BICoB (8th international conference on Bioinformatics and Computational Biology)*
3. Vajdi, A., Banaee, H., and Haspel, N. (2015a). A new dp algorithm for comparing gene expression data using geometric similarity. In *Workshop on Computational Regulatory Genomics and Metagenomics, in conjunction with IEEE-BIBM 2015*, pages 1157–1161
4. Farhoodi, R., Akbal-Delibas, B., and Haspel, N. (2015). Accurate prediction of docked protein structure similarity using neural networks and restricted boltzmann machines. In *CSBW (Computational Structural Bioinformatics Workshop), in conjunction with IEEE-BIBM 2015*, pages 1296–1303
5. Akbal-Delibas, B., Pomplun, M., and Haspel, N. (2015b). Accurefiner: A machine learning guided refinement method for protein-protein docking. In *proc. of BICoB (7th international conference on Bioinformatics and Computational Biology)*
6. Vetro, R., Farhoodi, R., Kotla, R., Haspel, N., Weisman, D., Rosen, J., and Simovici, D. (2014). Tide: Inter-chromosomal translocation and insertion detection using embeddings. In *The 2014 Workshop on Big Data in Bioinformatics and Healthcare Informatics (BBH14), held in conjunction with the 2014 IEEE International Conference on Big Data*, pages 64–70
7. Akbal-Delibas, B., Pomplun, M., and Haspel, N. (2014). Accurmsd: A machine learning approach to predicting structure similarity of docked protein complexes. In *proc. of ACM-BCB (5th ACM International conference on Bioinformatics and Computational Biology)*, pages 289–296
8. Jagodzinski, F., Akbal-Delibas, B., and Haspel, N. (2013). An evolutionary conservation & rigidity analysis machine learning approach for detecting critical protein residues. In *CSBW (Computational Structural Bioinformatics Workshop), in proc. of ACM-BCB (ACM International conference on Bioinformatics and Computational Biology)*, pages 780–786
9. Luo, D. and Haspel, N. (2013b). Multi-resolution rigidity-based sampling of protein conformational paths. In *CSBW (Computational Structural Bioinformatics Workshop), in proc. of ACM-BCB (ACM International conference on Bioinformatics and Computational Biology)*, pages 787–793
10. Luo, D. and Haspel, N. (2013a). Efficient coarse-grained geometry-based sampling of protein conformational paths. In *Proc. 5th Int. Conf. on Bioinformatics and Computational Biology (BiCOB)*, Honolulu, HI, USA
11. Haspel, N., Luo, D., and Gonzalez, E. (2013). Detecting intermediate structures in protein conformational pathways. In *Proc. 5th Int. Conf. on Bioinformatics and Computational Biology (BiCOB)*, Honolulu, HI, USA
12. Haspel, N. and Gonzalez, E. (2012). Topological properties of the configuration spaces of proteins. In *Proc. 4th Int. Conf. on Bioinformatics and Computational Biology (BiCOB)*,

Las Vegas, NV, USA

13. Vetro, R., Haspel, N., and Simovici, D. (2012). Characterizing intermediate conformations in protein conformational space. In *Proc. of the Ninth International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics*, Houston, TX, USA
14. Akbal-Delibas, B. and Haspel, N. (2012b). Refining multimeric protein complexes using conservation, electrostatics and probabilistic selection. In *IEEE Intl Conf on Bioinf and Biomed Workshops (BIBMW)*, pages 102–108
15. B. Akbal-Delibas*, F. Jagodzinski*, and Haspel, N. (2012). Towards a hybrid method for detecting critical protein residues. In *IEEE Intl Conf on Bioinf and Biomed Workshops (BIBMW)*, pages 82–85
* – Equal contribution
16. Akbal-Delibas, B., Hashmi, I., Shehu, A., and Haspel, N. (2011). Refinement of docked protein complex structures using evolutionary traces. In *2011 IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW)*, pages 400–404. IEEE
17. Hashmi, I., Akbal-Delibas, B., Haspel, N., and Shehu, A. (2011). Protein docking with information on evolutionary conserved interfaces. In *Proc. Computational Structural Biology workshop (CSBW), in conjunction with IEEE Int. Conference on Bioinformatics and Biomedicine (BIBM)*, pages 358–365, Atlanta, GA, USA
18. Haspel, N. (2010). Tracing conformational changes in proteins represented at a coarse level. In *BIONETICS 2010, Bioinformatics track*, Boston, MA, USA
19. Haspel, N., Moll, M., Baker, M., Chiu, W., and Kavraki, L. (2009a). Tracing conformational changes in proteins. In *Proc. Computational Structural Biology workshop (CSBW), in conjunction with IEEE Int. Conference on Bioinformatics and Biomedicine (BIBM)*, pages 120–127, Washington DC, USA

Book Chapters

1. Haspel, N., Zheng, J., Zanuy, D., Aleman, C., and Nussinov, R. (2017). A protocol for the design of protein and peptide nanostructure self- assemblies exploiting synthetic amino acids. In Samish, I., editor, *Methods Mol. Biol.*, volume on Computational Protein Design, chapter 17, pages 323–352. Springer, NY, USA
2. Haspel, N. and Jagodzinski, F. (2016). Methods for detecting critical residues in proteins. In Reeves, A., editor, *Methods Mol. Biol.*, volume on In Vitro Mutagenesis, pages 227–242. Springer, NY, USA
3. Haspel, N. (2015). Methods for detecting protein binding interfaces. In Zhang, W., editor, *Method in Pharmacology and Toxicology*, volume on Computer aided drug discovery, pages 133–152. Springer, NY, USA
4. Haspel, N., Shell, A., and Deutsch, C. (2012b). Computational approaches to measurement of visual attention: Modeling over-selectivity in intellectual and developmental disability. In Pomplun, M. and Suzuki, J., editors, *Developing and applying biologically inspired vision systems: Interdisciplinary concepts*, pages 31–43. IGI Global, Hershey, PA, USA
5. Haspel, N., Wainreb, G., Inbar, Y., Tsai, H., Tsai, C., Wolfson, H., and Nussinov, R. (2007a). A hierarchical protein folding scheme based on the building block folding model. *Methods Mol. Biol.*, 350:189–204

6. Haspel, N., Zanuy, D., Tsai, H., Ma, B., Wolfson, H., and Nussinov, R. (2005b). Computational approaches and tools for establishing structural models for short amyloid-forming peptides. In *Amyloid Proteins*, volume 1, pages 301–318. Ed. Jean D. Sipe. Wiley-VCH
7. Haspel, N., Tsai, C., Wolfson, H., and Nussinov, R. (2002). From the building blocks folding model to protein structure prediction. In *Protein Structure Prediction: Bioinformatics approach*, chapter 8, pages 201–226. Ed. Tsigelny I
8. Kumar, S., Barzilai, A., Haspel, N., Sham, Y., Tsai, C., Wolfson, H., and Nussinov, R. (2002). Critical building blocks in proteins: a common theme in folding and binding. In *Recent Research Developments in Protein Folding, Stability and Design.*, chapter 15. Gromiha, M. KH. and Selvarage, S., Trivadruram, India

Refereed Abstracts

1. Campbell, K., Nouduri, I., and Haspel, N. (2016). Protein hormones as nested information systems: Computational analysis of interleukins and cxc chemokines reveal alignments of family domains and proteolytic cleavage sites. In *Endocrine Society Meeting* (Abstract + poster)
2. Vajdi, A., Banaee, H., and Haspel, N. (2015b). A new dp algorithm for comparing gene expression data using geometric similarity. In *IEEE Intl Conf on Bioinf and Biomed (BIBM)*, page To appear (abstract+poster, selected for oral presentation)
3. Campbell, K., Haspel, N., Ford, V., and Gabriel-Richards, T. (2015). Hormone signal modulators among protein hormone pro-peptides and hormone fragments. In *47th Annual Society for the Study of Reproduction Meeting*, page 690 (Abstract + poster)
4. Campbell, K., Haspel, N., Dominas, B., Mason, B., Calixte, W., Bigos, R., Taguzem, G., Vadher, U., Palmstrom, N., Stenbruck, J., Solchenberger, S., and Diallo, F. (2014). Protein hormone proteolysis in target cell endosomes and lysosomes and release of previously unrecognized signaling information. In *World Congress of Reproductive Biology Meeting* (Abstract + poster)
5. B. Akbal-Delibas, M. P. and Haspel, N. (2014). An artificial neural network to predict rmsds of docked protein complexes. In *Intelligent Systems in Molecular Biology (ISMB)* (Abstract + poster)
6. Akbal-Delibas, B. and Haspel, N. (2012a). An evolutionary-guided iterative refinement approach for protein multimers. In *IEEE Intl Conf on Bioinf and Biomed (BIBM)* (Abstract + poster)
7. Akbal-Delibas, B., Jagodzinski, F., and Haspel, N. (2012b). Combining conservation and rigidity methods to detect critical residues in proteins. In *IEEE Intl Conf on Bioinf and Biomed (BIBM)* (Abstract + poster)
8. Diallo, F. B., Campbell, K., and Haspel, N. (2012). Discovering proteins potentially participating in novel protein hormone signal transduction pathways. In *ABRCMS (Annual biomedical research conference for minority students)* (Abstract + oral presentation)
9. Campbell, K., Haspel, N., Palmstrom, N., Steinbruck, J., Vadher, U., and Solchenberger, S. (2012a). Progress in identifying possible targets for a novel signal transduction pathway for protein hormones involving products of λ cathepsin proteolysis of the hormones. In *Society for the Study of Reproduction (SSR) meeting* (Abstract + poster)

10. Campbell, K., Haspel, N., Palmstrom, N., Steinbruck, J., Vadher, U., and Solchenberger, S. (2012b). Proteomic exploration of potential bioactivities of proteolytic peptides of protein hormones. In *ENDO 2012: The Endocrine Society's 94th Annual Meeting & Expo* (Abstract + poster)
11. Diallo, F. B., Gonzalez, E., and Haspel, N. (2011a). Analyzing the conformational space of proteins using mathematical and computational tools. In *ABRCMS (Annual biomedical research conference for minority students)* (Abstract + oral presentation)
12. Diallo, F. B., Gonzalez, E., and Haspel, N. (2011b). Analyzing the conformational space of proteins using mathematical and computational tools. In *NURDS(4th Annual Northeast Undergraduate Research and Development Symposium)* (Abstract + poster)
13. Haspel, N., Zanuy, D., Aleman, C., and Nussinov, R. (2011c). Binding of a c-end rule peptide to neuropilin-1 receptor: A molecular modeling approach and computational mutant study. In *Protein Society 25th meeting* (Abstract + poster)
14. Haspel, N., Campbell, K., and Vadher, U. (2011a). Proteolytic fragments of follicle stimulating hormone (fsh) show homologies to transducers and metabolic proteins: Are the peptide fragments biologically active? In *11th Hunter meeting* (Abstract + poster)
15. Haspel, N., Revilla-Lopez, G., Zanuy, D., Zheng, J., R, N., and Aleman, C. (2011b). Towards rational design of amyloid-based peptides to self-assemble into ordered nano- or microstructures with distinct morphology. In *Biophysical Society 55th meeting* (Abstract + poster)
16. Haspel, N., Moll, M., Chiu, W., and Kaviraki, L. (2009b). Tracing conformational changes in medium resolution protein structures. In *26th annual houston conference on biomedical engineering research (HSEMB)* (Abstract + poster)
17. Ricklin, D., Ricklin-Lichtsteiner, S. K., Sfyroera, G., Chen, H., Tzekou, A., Magotti, P., Wu, Y.-Q., Garcia, B. L., McWorther, W. J., Haspel, N., Kaviraki, L. E., Geisbrecht, B. V., and Lambris, J. D. (2008). Novel insights into target specificities and molecular mechanisms for two potent complement evasion proteins from staphylococcus aureus. In *Biophysical Society 55th meeting*, pages 4114–4115 (Abstract + oral presentation)
18. Gunasekaran, K., Haspel, N., Tsai, C., Kumar, S., Wolfson, H., and Nussinov, R. (2003). Extended disordered proteins: An elegant solution to having large intermolecular interfaces, yet keeping smaller genome and cell sizes. In *Biophysical Society 47th meeting*, volume 84(2), page S163A (Abstract + poster)
19. Haspel, N., Wolfson, H., and Nussinov, R. (2001). A study of protein folding pathways using the building block folding model. In *Protein Society 15th meeting* (Abstract + poster)

Selected Presentations

1. Tufts University, invited talk – CS department seminar, October 2013.
2. Umass Dartmouth, invited talk – CS department seminar, April 2012.
3. BU Medical school, invited talk – department seminar, March 2012.
4. Conquering the Complexity of Protein Data, invited talk, BioIT conference, Lehigh University.
5. Conquering the Complexity of Protein Data, BioIT 2011 (April 2011).
6. Affordable departmental supercomputing to calculate protein dynamics, Bio-IT 2011, (April

2011).

7. Computing Structural Changes in Proteins, College of Science and Math at UMass Boston, new faculty series.
8. Computing Structural Changes in Proteins, UMass Boston, Biology department seminar, Sep. 2009 (invited talk)
9. Computing Structural Changes in Proteins, George Mason University, CS department seminar, Nov. 2009 (invited talk).

Teaching

UMass Boston

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|---|---------------------------------------|
| CS187SL,CS188SL (Science Gateway Seminar) | Fall 2013, Spring 2014 |
| MOOC about Molecular Dynamics simulations | March 2013 (guest lecture) |
| CS612 (Algorithms in Bioinformatics) | Spring 2012, Spring 2014 |
| CS697 (Topics in Bioinformatics – Special topics) | Spring 2011 |
| CS624 (Analysis of Algorithms) | Spring 2010, Spring 2012, Spring 2015 |
| CS310 (Advanced data structures and algorithms) | Fall 2009–Fall 2016 |

Rice University

COMP 450 (Algorithmic Robotics) Fall 2008, Teaching assistant

Tel Aviv University

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|---|-----------|
| Programming for engineering students (lecturer) | 2006 |
| Introduction to Computer Science in Scheme (Teaching assistant) | 2005–2006 |
| Programming for engineering students (TA) | 2004–2005 |
| Programming for Chemistry students (lecturer) | 2005 |

Student Mentoring

- PhD students: Bahar Akbal-Delibas (2010-2014, graduated with PhD), Rohith Kotla (2011-2014, graduated with MSc), Dong Luo (2012-2015, graduated with MSc), Roshanak Farhoodi (2013-present), Amir Vajdi (2015-present), Ramin Dehghanpoor (2016-present)
- PhD thesis committee member: Saaid Baraty (2012-2013, graduated), Dan Pletea (2012-2013, graduated), Rosanne Vetro (2012-2015, graduated), Henry Lo (2012-2016), Shilpa Chakravartula (2011-2015), Jan Chang, Biology department (2010-2011, graduated), Alex Hwang (2009-2010, graduated)
- Kit Menlove, Graduate rotation project, Rice University (Advisor – Lydia Kaviraki), 2008
- Umaben Vadhar, MSc Student. Advisor – Kenneth Campbell, Biology, 2010-2011 (graduated)
- Wagner Calixte, NIH Bridges fellow, Roxbury community college, 2013
- Tara Gabriel-Richards, NIH Bridges fellow, Bunker Hill community college, 2014
- Fatoumata Binta Diallo, NIH Bridges fellow, Roxbury community college, 2011-2012
- Harold Gomez, Undergraduate honors thesis, 2010-2011

- Alex Jurgens, Undergraduate research project, 2009-2010
- Megha Sharma, Undergraduate research project, 2013
- Alex Valchev, Honors thesis committee member, 2012
- Nick Zhu, Undergraduate research project, Rice University, 2008

Grants and Sponsored Research

- **NSF-CCF 1421871** “AF: SMALL: Computational Framework for Characterizing Protein Conformational Landscapes” (PI), \$320,000, (July 1, 2014 - June 30, 2017)
- **MGHPCC (Massachusetts Green High Performance Computing Center) seed grant** “Genome-scale Characterization of Chromosomal Aberrations Using Parallelizable Compression Algorithms”. PI’s: N. Haspel, D. Simovici, D. Weisman D. (Biology) and J. Rosen (BU Medical School). \$60,000, (January 1 2013– December 31 2014)
- **NSF-CCF 1116060** “AF: SMALL: Developing Novel Computational Methods for Investigating Protein Dynamics Using a Multi-Scale Approach” (PI), \$249,774, (September 1, 2011 - December 31, 2014)
- **UMB Healey Grant** “Computational and Mathematical Analysis of Protein Conformational Spaces”– N. Haspel (PI), Eduardo Gonzalez, Math department(Co-PI) \$11,000 (July 1 2013 – December 31 2014)
- **UMB Proposal development grant** “Towards Rational Design of Amyloid-based Peptides to Self-assemble into Ordered Nano- or Micro-structures with Distinct Morphology”. N. Haspel (PI), Z. Zheng, U. of Akron (Co-PI), \$10,000, (April 2010 – December 2011).
- **UMB Healey grant** identification and Characterization of Biologically Active Metabolic Fragments of Pituitary Hormones: Has an Entire Area of Cell Signaling Been Missed? K. Campbell (Co-PI), N. Haspel (Co-PI), \$12,000 (April 2010 – June 2011).
- **UMB PII award for instruction innovation** “WUMP – women undergraduate mentoring program”. W. Ding (PI), N. Haspel (Co-PI), E. O’Neil (Co-PI), \$5,000, (Jan. 2010–Dec. 2010)
- **TeraGrid** Structural properties of peptides that penetrate cells and tissues through binding to the neuropilin-1 (NRP-1) receptor, (December 15, 2010 - December 14, 2011). Allocated 150,000 CPU cycles in the Texas Advanced Computing Center (TACC)

Awards and Fellowships

- 2009: Postdoctoral Fellow of NIH Nanobiology Training program of the Gulf Coast Consortia (declined).
- 2004, 2006: Tel Aviv University School of Computer Science PhD fellowship.
- 2005: Don and Sara Marejn award for PhD students.
- 2005: Dan David prize for PhD students.
- 2002,2003: Tel Aviv University Rector Scholarship for excellent PhD students.
- 1999-2001: Tel Aviv University School of Medicine MSc Fellowship.
- 1997: Tel Aviv University commemoration fellowship.
- 1997: Undergraduate training scholarship, School of Chemistry, Tel Aviv University

- 1996,1997: Dean's honor list, School of Chemistry, Tel Aviv University.

Service

Department

- CS faculty search committee – 2011,2013
- Alumni relation committee – 2011-present
- Department personnel committee – 2012-2013
- Curriculum committee – 2011-2012
- Student recruitment and retention committee – 2009-present
- RTF (Research Trust Fund) committee – 2009-2010

College and University

- CSM committee for drafting phase II of the interdepartmental PhD program in Integrative biosciences – 2013-2016
- CSM committee for drafting phase II of the interdepartmental PhD program in Computational sciences – 2013-2016
- UMB CIO search committee – 2013-2015
- CSM committee for drafting phase I of the interdepartmental PhD program in Integrative biosciences – 2012-2013
- CSM committee for drafting phase I of the interdepartmental PhD program in Computational sciences – 2012-2013
- Physics faculty search committee – 2011,2012
- CSM committee for drafting a white paper for an inter-departmental PhD program – 2011-2012
- University advisory committee on academic computing – 2011-present
- Research computing manager search committee – 2011
- Biology faculty search committee – 2010
- University subcommittee on mission statement (part of the Chancellor's strategic planning task force) – 2010

Professional

Journal and Conference Reviewer

- 2014 – JBCB (Journal of Bioinformatics and Computational Biology) – special issue for BiCOB 2014 – one paper, RSS 2014 Workshop on Robotics Methods for Structural and Dynamic Modeling of Molecular Systems (RMMSW 14) – three papers, ACM-BCB 2014 – 6 papers, Protein Science – one paper, Journal of Chemical Information and Modelling – one paper, PLoS one – one paper.
- 2013 – CSBW (Computational Structural Bioinformatics Workshop) 2013 – 3 papers, Journal of Chemical Information and Modeling, PLoS One, TCBB (ACM Transactions on Computational Biology and Bioinformatics), JBCB (Journal of Bioinformatics and Computational Biology) – special issue for BiCOB 2013 – 2 papers, BMC Structural Biology – special issue

for CSBW 2012 – 3 papers, ACS Chemical Neuroscience, Biointerphases, Journal of Molecular Graphics and Modelling, International Journal of Molecular Sciences

- 2012 – CSBW (Computational Structural Bioinformatics Workshop) 2012, Biochemistry Journal, PLoS One (twice), Current Pharmaceutical Design Journal, Proteins: Structure, function and bioinformatics, Journal of Bioinformatics and Computational Biology (JBCB) – special issue for CSBW 2011 – 4 papers, JMMOL (Journal of molecular modeling), PLoS Computational Biology
- 2011 – CSBW (Computational Structural Bioinformatics Workshop) 2011, Langmuir Journal (2 papers), Proteins: Structure, function and bioinformatics, PLoS One (4 papers), Bioinformatics journal, Journal of Bioinformatics and Computational Biology (JBCB) – special issue for BIONETICS 2010 – 5 papers, Biomacromolecules journal
- 2010 – International Journal of Data Mining and Bioinformatics (IJDMB), BIONETICS conference – special tracks on Bioinformatics and on Bio-inspired machine vision (6 papers total), Polymers journal

Conference Organization

- ACM-BCB 2017 (international conference on Bioinformatics, Computational biology and biomedicine), general co-chair.
- BiCOB 2016 (8th international conference on Bioinformatics and Computational Biology), Program co-chair.
- BiCOB 2015 (7th international conference on Bioinformatics and Computational Biology), Program co-chair.
- BiCOB 2014 (6th international conference on Bioinformatics and Computational Biology), Publicity chair.
- CSBW (Computational Structural Bioinformatics Workshop), co-chair and organizer. Held in conjunction with IEEE BIBM (International Conference on Bioinformatics and Biomedicine) 2011-2012, 2014, and ACM-BCB (ACM international conference on Bioinformatics and Computational Biology), 2013, 2015
- Robotics in Structural Biology tutorial co-organizer, ACM-BCB (2013)
- Conference PC member: BIONETICS special track on bioinformatics (2010), BIONETICS special track on visual systems (2010), BiCOB (2014), CSBW (2011-2016), ACM-BCB (2014-2016), IEEE-BIBM (2014-2016)
- Conference session chair: BIO-IT (2011), CIBB (2012), CSBW (2011-2013), BIBM (2012), BIONETICS special track on bioinformatics (2010)
- BIONETICS 2010, chair of a Bioinformatics special track, 2010

Journal and Book Editorial

- International Journal of Computational and Medicinal Chemistry (IJCMC), journal editorial board (2013-present)
- JBCB Special issue for BiCoB 2015, guest editor (2015)
- JCB (Journal of Computational Biology) Special issue for the Computational Structural Bioinformatics Workshop (CSBW 2014, held in conjunction with ACM-BCB), guest editor (2015)

- BMC Structural Biology Special issue for the Computational Structural Bioinformatics Workshop (CSBW 2012, held in conjunction with IEEE BIBM), guest editor (2013)
- JBCB Special issue for the Computational Structural Bioinformatics Workshop (CSBW 2011, held in conjunction with IEEE BIBM), guest editor (2012)
- JBCB Special issue for The 5th International Conference on Bio-Inspired Models of Network, Information and Computing Systems (BIONETICS 2010) special track on bioinformatics, guest editor (2011)
- Developing and Applying Biologically-Inspired Vision Systems: Interdisciplinary Concepts. Editors: M. Pomplun and J. Suzuki. Publishers: IGI Global (2011). Editorial review board member, reviewed 2 chapters.

Grant Proposal Reviewer

- NIH study section – 2014.
- NSF review panel – 2011, 2012, 2015.
- Alzheimer’s association, grant proposal review – 2011.

Professional Membership

- Biophysical Society
- IEEE
- ACM
- ISCA (International Society for Computers and Their Applications)

Community and Outreach

- UMB Women in Science club (WINS) co-organizer and faculty advisor.