

Hosein Mohimani

Employment

- October 2017 - Present **Assistant Professor, Computational Biology Department, Carnegie Mellon University .**
- February 2015 - September 2017 **Scientist, Department of Computer Science and Engineering, University of California, San Diego.**
- August 2013 - February 2015 **Bioinformatics Scientist, Advanced research department, Illumina Inc., San Diego.**

Education

- Fall 2008 - Fall 2013 **PhD in Communication Theory and Systems, Department of Electrical and Computer Engineering, University of California, San Diego.**
- Fall 2003 - Fall 2008 **B.Sc. in dual degrees, Electrical Engineering and Mathematical Sciences, Sharif University of Technology, Tehran, Iran.**

Honors and Awards

- 2019 **National Institute of Health Director's New Innovator Award.**
- 2019 **Alfred P. Sloan Research Fellowship in Computational and Evolutionary Biology.**
- 2010 **Rita L. Atkinson Graduate Fellowship , UC San Diego.**
- 2008 **Departmental fellowship from Electrical and Computer Engineering Department, UC San Diego.**
- 2003 **Bronze medal of 44th International Mathematics Olympiad, Tokyo, Japan.**
- 2002 **Gold medal of Iranian National Mathematics Olympiad, Tehran, Iran.**

Journal Papers

"*" indicates lead/corresponding author, H-index=19.

- Justin J. J. van der Hooft, **Hosein Mohimani**, Anelize Bauermeister, Pieter C. Dorrestein, Katherine R. Duncan, Marnix Medema, *Linking genomics and metabolomics to chart specialized metabolic diversity*, in press, Chem. Soc. Rev., 2020.
- Louis-Felix Nothias et. al. including **Hosein Mohimani**, *Feature-based Molecular Networking in the GNPS Analysis Environment*, accepted, Nature Methods, 2020.
- Bahar Behsaz, **Hosein Mohimani**, Alexey Gurevich, Andrey Prjibelski, Mark Fisher, Fernando Vargas, Larry Smarr, Pieter Dorrestein, Joshua Mylne, Pavel Pevzner, *De Novo Peptide Sequencing Reveals Many Cyclopeptides in the Human Gut and Other Environments*, Cell Systems, 2020, 10 (1), 99-108.e5.
- Liu Cao et.al., **Hosein Mohimani***, *MetaMiner: A Peptidogenomics Approach for the Discovery of Ribosomally Synthesized and Post-translationally Modified Peptides from Microbial Communities*, Cell Systems, 2019, 9 (6) 600-608.e4.
- Liu Cao, Egor Shcherbin, **Hosein Mohimani***, *Metabolome-metagenome-wide association network reveals microbial natural products and microbial biotransformations from the human microbiota*, mSystems 2019, 4 (4) e00387-19; DOI: 10.1128/mSystems.00387-19.
- Dima Meleshko, **Hosein Mohimani***, Vittorio Tracanna, Iman Hajirasouliha, Marnix Medema, Anton Korobeynikov, Pavel Pevzner, *BiosyntheticSPAdes : reconstructing biosynthetic gene clusters from assembly graphs*, Genome Research, 2019, doi:10.1101/gr.243477.118.

- **Hosein Mohimani***, Alexey Gurevich, Alexander Shlemov, Alla Mikheenko, Anton Korobeynikov, Liu Cao, Egor Shcherbin, Louis-Felix Nothias, Pieter Dorrestein, Pavel Pevzner, *In silico Identification of Microbial Natural Products Through Database Search of Mass Spectra*, Nature Communications, 2018, 9, 4035.
- Alexey Gurevich, Alla Mikheenko, Alexander Shlemov, Anton Korobeynikov, **Hosein Mohimani**, Pavel Pevzner, *Modification-tolerant database search reveals surprising diversity of peptidic natural products*, Nature Microbiology, 2018, 3, 319–327.
- Daniel McDonald et. al. including **Hosein Mohimani**, *American Gut: an Open Platform for Citizen-Science Microbiome Research*, mSystems, 2018, 10.1128/mSystems.00031-18.
- Eric Stava, Jens Gundlach, Jeffrey Mandell, Kevin Gunderson, Ian Derrington, **Hosein Mohimani**, *Compositions and methods for polynucleotide sequencing.*, US. patents, Illumina Inc., June 27th, 2017.
- Anna Edlund, Neha Garg, **Hosein Mohimani**, Alexey Gurevich, Xuesong He, Wenyan Shi, Pieter C. Dorrestein, Jeffrey S. McLean, *Metabolic Fingerprints from the Human Oral Microbiome Reveal a Vast Knowledge Gap of Secreted Small Peptidic Molecules*, mSystems, 2017, 2, e00058-17.
- **Hosein Mohimani**, Alexey Gurevich, Alla Mikheenko, Neha Garg, Louis-Felix Nothias, Akihiro Ninomiya, Kentaro Takada, Pieter C. Dorrestein, Pavel A. Pevzner, *Dereplication of Peptidic Natural Products Through Database Search of Mass Spectra*, Nature Chemical Biology, 2017, 13, 30-37.
- Ming Wang et. al. including **Hosein Mohimani**, *Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking*, Nature Biotechnology, 2016, 34, 828-837.
- Neha Garg, Yi Zeng, Anna Edlund, Alexey Melnik, Laura Sanchez, **Hosein Mohimani**, Alexey Gurevich, Vivian Miao, Stefan Schiffler, Yan Wei Lim, Tal Luzzatto-Knaan, Shengxin Kai, Forest Rohwer, Pavel Pevzner, Robert Cichewicz, Theodore Alexandrov, Pieter Dorrestein, *The spatial molecular structure of the microbial community of Peltigera Lichen*, mSystems, 2016, 1, e00139-16.
- **Hosein Mohimani** and Pavel A. Pevzner, *Dereplication, Sequencing and Identification of Peptidic Natural Products: from Genome Mining to Peptidogenomics to Spectral Networks*, Nat Prod Rep, 2016, 33, 73-86.
- **Hosein Mohimani**, Wei-Ting Liu, Roland Kersten, Bradley Moore, Pieter C. Dorrestein, and Pavel A. Pevzner, *NRPquest: Coupling Mass Spectrometry and Genome Mining for Nonribosomal Peptide Discovery*, Journal of Natural Products, 2014, 77, 1902–1909.
- **Hosein Mohimani**, Roland D. Kersten, Wei-Ting Liu, Mingxun Wan, Samuel O. Purvine, Si Wu, Heather M. Brewer, Ljiljana Pasa-Tolic, Nuno Bandeira, Bradley S. Moore, Pavel A. Pevzner, and Pieter C. Dorrestein, *Automated Genome Mining of Ribosomal Peptide Natural Products*, ACS Chemical Biology, 2014, 9, 1545–1551.
- **Hosein Mohimani**, Sangtae Kim, and Pavel A. Pevzner, *A new approach to evaluating statistical significance of spectral identifications*, Journal of Proteome Research, 2013, 12, 1560-1568.
- **Hosein Mohimani**, Wei-Ting Liu, Joshua S. Mylne, Aaron G. Poth, Michelle Colgrave, Michael Selsted, Pieter C. Dorrestein, and Pavel A. Pevzner., *Cycloquest: Identification of cyclopeptides via database search of their mass spectra against genome databases*, Journal of Proteome Research, 2011, 10, 4505-4512.
- **Hosein Mohimani**, Yu-Liang Yang, Wei-Ting Liu, Pei-Wen Hsieh, Pieter C. Dorrestein, and Pavel Pevzner, *Sequencing Cyclic Peptides by Multistage Mass Spectrometry*, Journal of Proteomics, 2011, 11, 3642-50.
- **Hosein Mohimani**, Wei-Ting Liu, Yu-Liang Yang, Susana P. Gaudenico, William Fenical, Pieter C. Dorrestein, and Pavel Pevzner, *Multiplex De Novo Sequencing of Peptide Antibiotics*, Journal of Computational Biology, 2011, 18, 1371-1381.

- Emily Mevers, Wei-Ting Liu, Niclas Engene, **Hosein Mohimani**, Tara Byrum, Pavel A. Pevzner, Pieter C. Dorrestein, Carmenza Spadafora, and William H. Gerwick, *Cytotoxic veraguamides, alkynyl bromide-containing cyclic depsipeptides from the marine cyanobacterium cf. Oscillatoria margaritifera*, *Journal of Natural Products*, 2011, 74, 928-936.
- Massoud Babaie-Zadeh, Christian Jutten, **Hosein Mohimani**, *On the error of estimating the sparsest solution of underdetermined linear systems*, *IEEE Trans. On Information Theory*, 2011, 57, 7840-7855.
- **Hosein Mohimani**, Massoud Babaie-Zadeh and Christian Jutten, *A fast approach for over-complete sparse decomposition based on smoothed L0 norm*, *IEEE Trans. On Signal Processing*, 2009, volume 57, 289-301.
- **Hosein Mohimani**, Farid Ashtiani, Adel Javanmard, Mazyiar Hamdi, *Mobility Modeling, Spatial Traffic Distribution, and Probability of Connectivity for Sparse and Dense Vehicular Ad-Hoc Networks*, *IEEE Trans. On Vehicular Technology*, 2009, 58, 1998-2007.
- **Hosein Mohimani**, Massoud Babaie-Zadeh, Irina Gorodnitsky, Christian Jutten, *SL0 : A convergence analysis*, arXiv:1001.5073.
- Farid Movahedi Naini, **Hosein Mohimani**, Massoud Babaie-Zadeh and Christian Jutten, *Estimating the mixing matrix in Sparse Component Analysis (SCA) based on partial k-dimensional subspace clustering*, *Neurocomputing*, 2008, vol. 71, 10-12, 2330-2343.

Journal Papers in preparation

- Arash Davoudi, Anubhav Bajewa, **Hosein Mohimani**^{*}, *Forest-wise Distribution Sensitive hashing: Efficient Maximum likelihood Classification by joint dimensionality reduction in known probabilistic settings*, under revision at *Data Mining and Knowledge Discovery*, 2020.

Refereed Conference Papers

- Mohsen Ferdosi, Arash Davoudi, **Hosein Mohimani**^{*}, *Measuring Mutual Information Between All Pairs of Variables in Subquadratic Complexity*, AISTAT2020, Palermo, Sicily, Italy (accepted).
- Mihir Mongia, Benjamin Soudry, Arash Davoudi, **Hosein Mohimani**^{*}, *Measuring Mutual Information Between All Pairs of Variables in Subquadratic Complexity*, PAKDD2020, Singapore (accepted).
- Liu Cao, Egor Shcherbin, **Hosein Mohimani**^{*}, *Metabolome-metagenome-wide association network reveals microbial natural products and microbial biotransformations from the human microbiota*, ASMS2019, Atlanta, USA (Oral session).
- **Hosein Mohimani**, *Modification-tolerant database search reveals surprising diversity of peptidic natural products*, RECOMB2018, Paris, France (Highlight talk).
- **Hosein Mohimani**, Sangtae Kim, Pavel Pevzner, *MS-DPR: An algorithm for computing statistical significance of spectral identifications of non-linear peptides*, Workshop on Algorithms in Bioinformatics (WABI2012), Ljubljana, Slovenia, *Lecture Notes in Computer Science*, Volume 7534, 2012, pp 301-313.
- **Hosein Mohimani**, Wei-Ting Liu, Yu-Liang Yang, Susana P. Gaudenico, William Fenical, Pieter C. Dorrestein, and Pavel Pevzner, *Multiplex De Novo Sequencing of Peptide Antibiotics*, Vancouver, *Research in Computational Molecular Biology (RECOMB2011)*, *Lecture Notes in Computer Science*, 2011, Volume 6577, 267-281.
- **Hosein Mohimani**, Wei-Ting Liu, Joshua S. Mylne, Aaron G. Poth, Michelle Colgrave, Michael Selsted, Pieter C. Dorrestein, and Pavel A. Pevzner, *Cycloquest: Identification of cyclopeptides via database search of their mass spectra against genome databases*, *American Society of Pharmacognosy 2011 (ASP2011)*, San Diego (invited talk).
- Jayadev Acharya, Hirakendu Das, **Hosein Mohimani**, Alon Orlitsky, Shengjun Pan, *Exact calculation of pattern probabilities*, *IEEE International Symposium on Information Theory (ISIT2010)*, Austin, Texas, June 13 – 18, page 1498-1502.

- Massoud Babaie-Zadeh, **Hosein Mohimani**, Christian Jutten, *An upper bound on the estimation error of the sparsest solution of underdetermined linear systems*, in Proceedings of SPARS2009, Saint-Malo, France, 2009.
- **Hosein Mohimani**, Massoud Babaie-Zadeh and Christian Jutten, *Complex-valued Sparse Representation based on Smoothed L0 Norm*, 33rd IEEE International Conference on Acoustics, Speech and Signal Processing (ICASSP 2008), March 30 - April 4, Las Vegas.
- **Hosein Mohimani**, Massoud Babaie-Zadeh and Christian Jutten, *Fast Sparse Representation based on Smoothed L0 norm*, 7th International Conference on Independent Component Analysis and Signal Separation (ICA 2007), 9th - 12th September, London, UK, LNCS 4666, pp. 389-396.
- Hadi Zayyani, Massoud Babaie-Zadeh, **Hosein Mohimani**, Christian Jutten, *Sparse Component Analysis in Presence of Noise Using an Iterative EM-MAP Algorithm*, 7th International Conference on Independent Component Analysis and Signal Separation (ICA 2007), 9th - 12th September, London, UK, LNCS 4666, pp. 438-445.
- Elham Azizi, **Hosein Mohimani**, Massoud Babaie-Zadeh, *Adaptive Sparse Source Separation With Application To Speech Signals*, 2007 IEEE International Conference on Signal Processing and Communications (ICSPC 2007), 24th - 27th November, Dubai, UAE.
- Farid Movahedi Naini, **Hosein Mohimani**, Massoud Babaie-Zadeh, Christian Jutten, *Estimating the mixing matrix in Sparse Component Analysis (SCA) based on multidimensional subspace clustering*, 14th IEEE International Conference On Telecommunications and 8th IEEE Malaysia International Conference on Communications (ICT-MICC 2007), 14th - 17th May, Penang, Malaysia.

Teaching

Algorithm and Advance Data Structure, 15-351, 15-650, 02-613 (90 students), Spring 2019, Spring 2020.

Computational Biology Seminar, 02-402, 02-702, Fall 2018, Spring 2019, Fall 2019.

Computational Methods in Proteomics and Metabolomics, 02-425, 02-725 (6 students), Spring 2018, Fall 2019.

Advising

PostDocs **Arash Gholami Davoudi (Lane Fellow, Current).**

PhD students **Liu Cao (started 2017, Current), Mihir Mongia (started 2018, Current), Mohsen Ferdosi (started 2018, Current), Mustafa Guller (started 2019, current), Donghui Yan (started 2019, current) .**

Master students **Chengze Shen (MSCB student, Current), Ian Lee (MSCB student, Current), Neel Mittal (MSCB student, current).**

Undergraduate students **Anubhav Bajewa, Benjamin Sourdi (Current), Sean Chang (Current), Hyungon Yoo, Heng Zhang (current).**

Research Software

TreeDSH, *Efficient maximum likelihood classification by joint dimensionality reduction in known probabilistic setting, with interface for mass spectrometry database search*, <https://github.com/mohimanilab/TreeDSH>.

AssociationNetworks, *Associating metabolomics features to metagenomics features accross multiple microbiomes for natural product discovery*, <https://github.com/mohimanilab/AssociationNetworks>.

MetaMiner, *Discovering ribosomally synthesized and post translationally modified peptides from mass spectrometry and metagenomics data* , <https://github.com/mohimanilab/MetaMiner> .

Dereplicator+, *Identification of mass spectra of natural products through database search*, <https://github.com/ablab/npdtools>.

Dereplicator, *Identification of mass spectra of peptide natural products through database search*, <https://github.com/ablab/npdtools>.

Varquest, *Error tolerant identification of mass spectra of peptide natural products through database search*, <https://github.com/ablab/npdtools>.

NRPquest, *Discovering non-ribosomal peptides from mass spectrometry and genomics data*, <https://github.com/ablab/npdtools>.

RiPPquest, *Discovering ribosomally synthesized and post translationally modified peptides from mass spectrometry and genomics data*, <https://github.com/ablab/npdtools>.

Web service, *All the antibiotic discovery projects are available as a web service at <http://gnps.ucsd.edu/ProteoSAFe/static/gnps-theoretical.jsp> (sign up is required)*.

Invited Talks

- April 2019 **Integrating computational mass spectrometry and metagenome mining for natural product discovery**, *Simons Microbiome Workshop*.
- Feb 2019 **Integrating computational mass spectrometry and metagenome mining for natural product discovery**, *University of Pittsburgh*.
- Nov 2018 **Antibiotics Discovery:From Genome Sequencing to Genome Mining to Peptidogenomics**, *Google, Pittsburgh*.
- April 2018 **Antibiotics Discovery:From Genome Sequencing to Genome Mining to Peptidogenomics**, *UPMC Enterprise, Pittsburgh*.
- Jan 2017 **Antibiotics Discovery:From Genome Sequencing to Genome Mining to Peptidogenomics**, *University of Southern California, Carnegie Mellon University, Duke University, University of Illinois, Urbana-Champaign*.
- Nov, 2015 **Dereplication, Sequencing and Identification of Peptidic Natural Products: from Genome Mining to Peptidogenomics to Spectal Networks**, *ICCP2015, Queensland, Australia*.

Reviewing activities

Nature Chemical Biology, FEMS Microbiology, Analytical Chemistry, Journal of Proteome Research, Bioinformatics Journal, IEEE Transactions on Signal Processing, IEEE Transactions on Information Theory, IEEE signal processing letters.

Departmental Service

- 2018,2019 **PhD admission Committee**, *Computational Biology Department*.
- 2018,2019 **Faculty Hiring Committee**, *Computational Biology Department*.

Professional Services

- 2020 **RECOMB**, *PC-member*.
- 2019,2020 **ISMB**, *PC-member*.
- 2019 **RECOMB-Seq**, *PC-member*.
- 2019 **ACM-BCB**, *PC-member*.
- 2016 **COMNAP**, *Organizing 2016 Workshop on computational methods in natural product discovery, UC San Diego*.

Research Funding

- 2019-2020 **Alfred P. Sloan Foundation's Research Fellowship**.
- 2019-2024 **NIH Director's New Innovator Award**.