

Samad Jahandideh

Origent Data Sciences, Inc.

Phone: (619) 823-3790, E-mail: samad_jahandideh@yahoo.com

Updated at July/2016

SUMMARY:

I am a Data Scientist with extensive training in personalized predictive modeling. After graduation, I did a postdoctoral fellowship in department of biostatistics at University of Alabama. Then I moved to Sanford Burnham Prebys Medical Discovery Institute, La Jolla, CA. Now, I am a Data Scientist at Origent Data Sciences, Inc. I have over 10 years of experience in predictive modeling using machine learning and statistical learning technologies. Recently, I have examined my predictive modeling skills in competitive crowdsourcing challenges and I have shown very promising results. Also, I have authored multiple publications in peer-viewed journals and book chapters in the field of applied machine learning and bioinformatics.

ACADEMIC TRAINING:

2016-present **Data Scientist**, Origent Data Sciences, Inc., Vienna, VA.

Duties including:

- Developing novel advanced machine-learning-based personalized predictive models to design efficient clinical trials.
- Preparing applications for FDA approval to market new algorithms.
- Active involvement in hiring new employees.
- Regular meeting with customers and collaborators from industry and academia.
- Active involvement in grant application and writing scientific reports and publications.

2012-2016 **Senior Postdoctoral Research Fellow in Computational Structural Genomics**, Sanford Burnham Prebys Medical Discovery Institute, La Jolla, CA

- Mentor – Adam Godzik

Achievement: Development of several advanced machine-learning-based methods for feature selection and predictive model. In collaboration with *Aaron Ciechanover* (nobel prize winner) we have deciphered structural disorder as a key feature in discrimination of poly- and mono-ubiquitination in human. As another notable research, we have developed a predictive model for prediction of protein sequence crystallizability.

2010-2012 **Postdoctoral Research Fellow in Bioinformatics**, Statistical Genetics Section, Department of Biostatistics, School of Public Health, University of Alabama at Birmingham, AL

- Mentor – Degui Zhi

2010 **Ph.D., Biophysics**, Tarbiat Modares University, Tehran, Iran

2005 **M.Sc., Biophysics**, Tarbiat Modares University, Tehran, Iran

2003 **B.S., Cell and Molecular Biology (Genetics)**, Shahid Chamran University, Ahvaz, Iran

RESEARCH INTERESTS:

Big data science, Machine Learning, Bioinformatics, Data mining, Modeling and Molecular Dynamics, Systems Biology, Structural Genomics, De novo protein design, Structure-Activity relationship (*SAR* and *QSAR*), Network biology

5 TOP PAPERS:

Samad Jahandideh, Ian Wilson, Adam Godzik and Lukasz Jaroszewski. An algorithmic approach to construct design for protein structure determination by x-ray crystallography. *Acta Crystallographica Section D* (under revision).

Samad Jahandideh, Lukasz Jaroszewski, and Adam Godzik. Improving chances of successful protein structure determination with Random Forest classifier. *Acta Crystallographica Section D*, (2014) 70(Pt 3), 627-35.

Ori Braten, Ido Livneh, Tamar Ziv, Arie Admon, Izhak Kehat, Lilac H. Caspi, Hedva Gonen, Beatrice Bercovich, Adam Godzik, **Samad Jahandideh**, Lukasz Jaroszewski, Thomas Sommer, Yong Tae Kwon, Mainak Guharoy, Peter Tompa, and Aaron Ciechanover. Numerous proteins with unique characteristics are degraded by the 26S proteasome following monoubiquitination. *PNAS*, 2016.

Samad Jahandideh, and Degui Zhi. Systematic investigation of predicted effect of nonsynonymous SNPs in human prion protein gene: A molecular modeling and molecular dynamics study. *Journal of Biomolecular Structure and Dynamics*, (2014) 32(2), 289-300.

Mehdi Pour Sheikh Ali Asgary, **Samad Jahandideh**, Parviz Abdolmaleki, and Anoshirvan Kazemnejad. Analysis and prediction of {beta}-turn types using multinomial logistic regression and artificial neural network. *Bioinformatics*, 23 (2007) 3125-30.

ACADEMIC POSITION AND RESPONSIBILITIES:

- 2013 **Session Chair**, 113th OMICS group conference, International conference on integrative biology summit, August 5-7 Las Vegas, USA
- 2010 **Vice-Chancellor for Research**, Medical Physics Department, Shiraz University of Medical Sciences, Shiraz, Iran
- 2010 **Assistant Professor**, Department of Medical Physics, Shiraz University of Medical Sciences, Shiraz, Iran
- 2010 **Membership in the supreme scientific evaluation committee**, 1st Research Scientific Congress for the National Students of Radiation Biology Science Congress in Shiraz University of Medical Sciences, Shiraz, Iran

POPULAR BIOINFORMATICS PACKAGE AND WEB SERVERS:

- 2015 XtalCoDe: A construct design WEB server for protein structure determination by X-ray crystallography, available at <http://ffas.burnham.org/XtalPred-cgi/xtal.pl>. XtalCoDe is the first algorithm that provides a single score assessing the suitability of specific positions in the sequence as construct start and end positions.
- 2015 PROPER: a package for performance visualization for optimizing and comparing ranking classifiers in MATLAB available at <https://sourceforge.net/projects/PROPER-Package>.

- 2013 XtalPred-RF: A WEB server for crystallization classification by Random Forest Classifier, available at <http://ffas.burnham.org/XtalPred-cgi/xtal.pl>. XtalPred-RF is expected to further reduce cost of structure determination in structural genomics projects up to 30% where optimal target(s) can be selected from a larger pool of proteins. Also, XtalPred-RF is almost two-times more reliable for prediction of single crystallizable protein than original XtalPred version from 2007 as a widely used algorithm for prediction of crystallization success.
- 2009 CRYSTALP2: A WEB server for sequence-based protein crystallization propensity prediction, available at <http://biomine-ws.ece.ualberta.ca/CRYSTALP2.html>.

CONTINUING EDUCATION:

- 2015 Workshop on Science Communication presentations by *Thomas O. Baldwin*, the dean of the College of Natural and Agricultural Sciences at the University of California, Riverside
- 2013 Workshop on creating and delivering exceptional scientific presentations by *Jean-luc Doumont*
- 2011 GRD 717: Principles of Scientific Integrity, UAB (Grade 4.0/4.0)
- 2011 Initial training in the protection of human subjects in research, UAB
- 2011 BST 695: Special Notes on Statistical Genetics, SSG, UAB (Grade 4.0/4.0)
- 2009 I have passed a few educational courses during my PhD at the Tarbiat Modares University including educational psychology, logic and methodology of science, Teaching methods, and educational technology.

INVITED TALKS AND PRESENTATIONS:

- 2014 “Classification and survival curve prediction of cancers using functional proteomic data”, Cancer Center Retreat, Sanford-Burnham Medical Research Institute, La Jolla, CA
- 2013 “A systematic approach to investigate the predicted effect of nonsynonymous SNPs in the human prion protein gene: A molecular modeling and molecular dynamics study”, 113th OMICS group conference, International conference on integrative biology summit, August 5-7, Las Vegas, USA
- 2012 “Improving prediction of protein crystallizability”, PSI, Bethesda, MD
- 2012 “Annotation of protein function”, CCI, Emory University, GA
- 2012 “An introduction to some of the important topics in bioinformatics”, Division of Informatics, Department of Pathology, UAB, AL
- 2012 Journal Club presentation. Title: Machine Learning Prediction: Protein Active Sites or Medical Outcomes. SSG, UAB, AL
- 2011 SOPH research day poster presentation. Title: Application of density similarities to predict membrane protein types based on pseudo-amino acid composition, UAB, AL
- 2009 “Seminar on Systems Biology”, Department of Biochemistry, SUMS, Shiraz, Iran
- 2009 Monthly talks, Title: Systems biology and biological networks. Medical school, Shiraz University of Medical Sciences, Shiraz University, Shiraz, Iran
- 2007 9th Congress of Biochemistry and Second International Congress of Biochemistry and Molecular Biology, Shiraz, Iran
- 2006 1st Iranian Congress of Biotechnology, Tehran University, Tehran, Iran
- 2006 14th International Congress of Biology, TMU, Tehran, Iran

GRANTS AND DISTINCTIONS:

2015 DREAM ALS Stratification Prize4Life Challenge

Our group was one of the best performers in the main sub-challenge (PREDICTOMIX group). The final results available at <https://www.synapse.org/#!/Synapse:syn2873386/wiki/266773>. We will be co-author of a paper for publication in Nature Biotechnology and the best performers group's method will be compared and discussed in this paper.

2015 STRIVE research support

STRIVE is a new program at Sanford Burnham Prebys Medical Discovery Institute, which is aimed at providing knowledge and cost-effective support to facilitate the translation of innovative academic discoveries made by Sanford Burnham Prebys investigators into therapeutic leads or diagnostics addressing timely, unmet clinical needs.

2015 The first place out of 351 participants in the [2015 Microsoft-sponsored international machine-learning competition \(Tweakathon1\)](#). We have been on top 5 best performers of 9 out of 10 questions (Tweakathon1 and Final1) among >120 groups including Intel (User ID: sjahandideh). The results are published in this paper:

I Guyon, K Bennett, G Cawley et al., AutoML Challenge 2015: Design and First Results, JMLR: Workshop and Conference Proceedings 1 (2015) 1-10.

2015 NIH NCI R21 (Unfunded)

- **Title:** Multilayer classifier for cancer survival prediction from functional proteomics.
(Role: Co-Investigator)

2015 NIH R01

- **Title:** Proteins Construct Design for Crystallography and NMR (1st Submission: Score 43; Percentile 44).
(Role: Co-Investigator; machine learning and computational biology scientist)

2014 NIH NCI K22 (Unfunded)

- **Title:** Classification and survival prediction of cancers using functional proteomic data.
(Role: Principal Investigator)

2014 NSF ABI (Not reviewed)

- **Title:** Multilayer classifier for cancer survival curve prediction from functional proteomic data.
(Role: Co-Principal Investigator)

2014 NIH K01 Biomedical Big Data Science (Resubmitted: Unfunded)

- **Title:** Classification and survival prediction of cancers using functional proteomic data.
(Role: PI)

2012 NIH R01 GM095847 (PIs: David Eisenberg, Adam Godzik, and Zygmunt S. Derewenda)

- **Title:** Rational protein engineering for crystallography.
05/30/2012 – 05/30/2015 (Role: Postdoctoral Fellow)

2010 NIH R00 RR024163 (PI: Degui Zhi)

- **Title:** Algorithms for protein structural classification and function prediction.
07/15/2009 – 05/31/2012 (Role: Postdoctoral Fellow)

2014 Fishman Fund Award (finalist)

- 2013 Fishman Fund Award (finalist)
- 2009 Nation wide 1st rank in research by Iranian National Institute of Elite
- 2009 Certification of teaching from Tarbiat Modares University, Tehran, Iran
- 2008 Scholarship from the Ministry of Health and Sciences of Iran
- 2007 Fellow of National Institute of Elite, Iran
- 2005 Member of Science council of Tarbiat Modares University
- 2005 2nd rank in PhD entrance exam
- 2003 Nation wide 30th rank among over 5000 applicants in Master of Science entrance exam
- 1999 Nation wide 1290th rank among over 300,000 applicants in university entrance exam

TEACHING:

- 2010 Seminar (M.Sc. students of Medical Physics and Bio-medical Engineering), SUMS, Iran
- 2010 Electricity, Magnetism and applications in medicine (M.Sc. students of Medical Physics), SUMS, Iran
- 2010 Thermodynamics and heat transport (B.Sc. students), SUMS, Iran
- 2010 Non-ionizing radiations (M.Sc. students of Medical Physics), SUMS, Iran
- 2010 Biophysics (B.Sc. students), SUMS, Iran
- 2010 Radiobiology (M.Sc. students of Medical Physics), SUMS, Iran
- 2010 Health Physics (M.Sc. students), SUMS, Iran
- 2009 Structural Bioinformatics (Ph.D. students), Shahid Beheshti University of Medical Science, Iran
- 2009 Cell and Molecular Biology (M.Sc. Students of Medical Physics), SUMS, Iran
- 2009 Health Physics (B.Sc. students), SUMS, Iran
- 2009 Non-ionizing radiations (M.Sc. Students of Medical Physics), SUMS, Iran
- 2009 Medical physics (M.D. students), SUMS, Iran
- 2007 Biophysics and Radiational Biology (B.Sc. students), Azad University of Arak, Iran

MENTORSHIP:

- 2015- Ehsan Saghapour (PhD Candidate in Biomedical Engineering, Esfahan University of Medical Science, Co-Advisor)
 - 2015 Pun Wai Tong (PhD Candidate in Mathematics, UC San Diego, Summer intern)
- Outcome: Samad Jahandideh, Pun Wai Tong, Adam Godzik, A random forest-based approach to predict Head and Neck Squamous Cell Carcinoma progression using functional proteomic data (submitted to BBRC). Current position: researcher at Fujitsu America, Inc.

COMPUTER SKILLS:

Programming Languages and packages: MATLAB, R, SPSS, Python, and C⁺⁺

Molecular modeling tools: SPDBV, Sirius, and macPyMol

Molecular Dynamics package: Gromacs

Genome analysis tools: FASTQ format, SAM tools, and VCF tools

Software development tools: SVN, and wiki

Microsoft Office: Word, Excel, and Power Point

ACADEMIC SERVICE:

Manuscript review to:

- 2016 Oncotarget, Thorax, Analytical Biochemistry, Bioinformatics
- 2015 Bioinformatics, Thorax, Prion, Analytical Biochemistry (2 Manuscripts), Genomics (2 Manuscripts), Chemometrics and Intelligent Laboratory Systems, BMC Bioinformatics, Journal of Molecular Graphics and Modelling, PeerJ, Journal of Biomolecular Structure & Dynamics (2 Manuscript), Molecular Genetics and Genomics, Computational Biology and Chemistry, International Journal of Molecular Sciences, Molecular Simulation, Analytical Biochemistry
- 2014 Analytical Biochemistry, Bioinformatics, Frontiers in Genetics, The Scientific World Journal, International Journal of Molecular Sciences, BioMed Research International, PLOS ONE (2 Manuscript), Molecular BioSystems, Biochimie (3 Manuscript), Journal of Biomolecular Structure & Dynamics (2 Manuscripts), Computational Biology and Chemistry (2 Manuscripts)
- 2013 Biochimie, Neural Computing and Applications, The Scientific World Journal (6 Manuscripts)
- 2012 Chemical Biology & Drug design, The Scientific World Journal (3 Manuscripts), IEE/ACM Transactions on Computational Biology and Bioinformatics
- 2011 Computers in Biology and Medicine, Amino acids, Fresenius Environmental Bulletin, Scientia Iranica, Theoretical Computer Science
- 2010 BMC Bioinformatics, Bioinformatics, Iranian Journal of Chemistry & Chemical Engineering
- 2009 Neurocomputing, Computers in Biology and Medicine, Computer Methods and Programs in Biomedicine
- 2008 BMC Genomics, The Open Bioinformatics Journal

Lead Guest Editor:

For a Special Issues entitled “Sequence-based prediction of structure and function of protein” in The Scientific World Journal [<http://www.tswj.com/si/625074/cfp/>]. Up to now, we accepted three papers.

Editorial Board:

- 2016- Journal of Pulmonology and Respiratory Research
- 2015- Peertechz Journal of Bioinformatics and Biostatistics
- 2013- The Scientific World Journal, computational biology section

Interviews:

- 2014 Sanford-Burnham Science Blog
<http://beaker.sanfordburnham.org/2014/11/meet-our-postdocs-samad-jahandideh/>

PUBLICATIONS (*Corresponding author, and #Equal contribution):

Journal articles:

Ori Braten, Ido Livneh, Tamar Ziv, Arie Admon, Izhak Kehat, Lilac H. Caspi, Hedva Gonen, Beatrice Bercovich, Adam Godzik, **Samad Jahandideh**, Lukasz Jaroszewski, Thomas Sommer, Yong Tae Kwon, Mainak Guharoy, Peter Tompa, and Aaron Ciechanover*. Numerous proteins with unique characteristics are degraded by the 26S proteasome following monoubiquitination. PNAS, 2016 (Accepted).

Samad Jahandideh, Ian Wilson, Adam Godzik and Lukasz Jaroszewski*. An algorithmic approach to construct design for protein structure determination by x-ray crystallography. Acta Crystallographica Section D (In revision).

Samad Jahandideh*, Fatemeh Sharifi, Lukasz Jaroszewski, and Adam Godzik*. PROPER: Performance visualization for optimizing and comparing ranking classifiers in MATLAB. Source Code for Biology and Medicine, (2015) 10:15.

Samad Jahandideh*, and Degui Zhi. Systematic investigation of predicted effect of nonsynonymous SNPs in human prion protein gene: A molecular modeling and molecular dynamics study. Journal of Biomolecular Structure and Dynamics, (2014) 32(2), 289-300 [Impact Factor: 9.35 in 2011; **JBSD ranks 5 out of 185 in all molecular biology journals**, Times Cited 2]

- **Highlighted by ASPH Friday Letter #1776**
http://archives.fridayletter.asph.org/article_view.cfm?fl_index=1776&fle_index=20897

Samad Jahandideh, Lukasz Jaroszewski, and Adam Godzik*. Improving chances of successful protein structure determination with Random Forest classifier. Acta Crystallographica Section D, (2014) 70(Pt 3), 627-35 [Impact Factor: 14.103 in 2013; **ACSD ranks first out of 73 journals in the category of biophysics**, Times Cited 7]

- **Featured by PSI/Nature Structural Biology Knowledgebase. The highlight written by Tal Nawy is available at** <http://sbkb.org/update/research/predicting-protein-crystal-candidates>

Samad Jahandideh*. Diversity in Structural Consequences of MexZ Mutations in Pseudomonas aeruginosa. Chemical Biology and Drug Design (2013) 81, 600-6. [Impact Factor: 2.469; Times Cited 0]

Soheila Shokrollahzade, Fatemeh Sharifi, Akbar Vaseghi, Maryam Faridounnia, **Samad Jahandideh***. Protein cold adaptation: role of physico-chemical parameters in adaptation of proteins to low temperatures. Journal of Theoretical Biology, (2015) 383:130-7.

- **Highlighted by Atlas of Science** <http://atlasofscience.org/how-do-microorganisms-survive-in-extreme-conditions/>

Samad Jahandideh*, Mostafa Jamalan, and Maryam Faridounnia. Molecular dynamics study of the dominant-negative E219K polymorphism in human prion protein. Journal of Biomolecular Structure and Dynamics, (2014) 33 (6), 1315-1325. Times Cited 2]

Mohammad Ali Ghaffari, Majid Zeinali, Ebrahim Barzegari Asadabadi, Mostafa Jamalan*, **Samad Jahandideh***. Affinity maturation of HER2-binding Z(HER2:342) affibody via rational design approach: a molecular dynamic simulation study. Journal of Biomolecular Structure and Dynamics. [Impact Factor: 9.35 in 2013; **JBSD ranks 5 out of 185 in all molecular biology journals**, Times Cited 2]

Samad Jahandideh*, Vinodh Srinivasasainagendra, and Degui Zhi*. Comprehensive comparative analysis and identification of RNA-binding protein domains: multi-class classification and feature selection. Journal of Theoretical Biology, (2012) 312, 65-75. [5-Year Impact Factor: 2.496; Times Cited 3]

Samad Jahandideh*, Abbas Mahdavi. RFCRYS: Sequence-based protein crystallization propensity prediction by means of random forest. Journal of Theoretical Biology, (2012) 306, 115-119. [5-Year Impact Factor: 2.496; Times Cited 0]

Sedigheh Mahdavi, Ali Mohades, Ali Salehzadeh Yazdi, **Samad Jahandideh**, and Ali Masoudi-Nejad*. Computational Analysis of RNA-Protein Interaction interfaces via the Voronoi Diagram. *Journal of Theoretical Biology*, (2011) 10;293C:55-64. [5-Year Impact Factor: 2.496; Times Cited 2]

Esmail Behmard, Parviz Abdolmaleki*, Ebrahim Barzegari Asadabadi, and **Samad Jahandideh**. Prevalent Mutations of Human Prion Protein: A Molecular Modeling and Molecular Dynamics Study. *Journal of Biomolecular Structure and Dynamics*, 29(2) (2011) 379-89. [Impact Factor: 4.986; Times Cited 11]

Abbas Mahdavi[#], and **Samad Jahandideh^{#,*}**. Application of density similarities to predict membrane protein types based on pseudo-amino acid composition. *Journal of Theoretical Biology*, 276 (2011) 132–37. [5-Year Impact Factor: 2.496; Times Cited 5]

Samad Jahandideh, Parviz Abdolmaleki*, and Mohammad Mehdi Movahedi. Prediction of melatonin excretion patterns in the rat exposed to ELF magnetic fields based on support vector machine and linear discriminant analysis. *Micron*, 41(7) (2010) 882-5. [5-Year Impact Factor: 1.912; Times Cited 5]

Samad Jahandideh, Parviz Abdolmaleki*, and Mohammad Mehdi Movahedi. Comparing Performances of Logistic Regression and Neural Networks for predicting Melatonin Excretion Patterns in the Rat Exposed to ELF Magnetic Fields. *Bioelectromagnetics*, 31(2) (2010) 164-71. [Impact Factor: 2.291; Times Cited 13]

Fatemeh Saberian, and **Samad Jahandideh***. Introduction of novel research area in the field of bioelectromagnetics. *Bioelectromagnetics newsletter*, Published, Sep 2010.

Ebrahim Barzegari Asadabadi, Parviz Abdolmaleki*, Seyyed Mohsen Hosseini Barkooie, **Samad Jahandideh**, Mohammad Ali Rezaei, Marziyeh Fadaie, and Shahrokh Safarian. A combinatorial feature selection approach to describe the QSAR of dual site inhibitors of acetylcholinesterase, *Computers in Biology and Medicine*, 39 (2009) 1089–95. [5-Year Impact Factor: 1.359; Times Cited 3]

Samad Jahandideh*, Somayyeh Hoseini, Mina Jahandideh, Afsaneh Hoseini, and Fatemeh Miri Disfani. γ -turn types prediction in proteins using the two-stage hybrid neural discriminant model, *Journal of Theoretical Biology*, 259(3) (2009) 517-22. [5-Year Impact Factor: 2.496; Times Cited 8]

Lukasz Kurgan*, Ali A Razib, Sara Aghakhani, Scott Dick, Marcin Mizianty, and **Samad Jahandideh**. CRYSTALP2: sequence-based protein crystallization propensity prediction. *BMC structural biology*, 31 (2009) 9:50. [Impact Factor: 2.10; Times Cited 19]

Sepideh Jahandideh, **Samad Jahandideh***, Ebrahim Barzegari Asadabadi, Mehrdad Askarian, Mohammad Mehdi Movahedi, Somayyeh Hosseini, and Mina Jahandideh. The use of artificial neural networks and multiple linear regression to predict rate of medical waste generation. *Waste Management*, 2009 29(11):2874-9. [5-Year Impact Factor: 2.926; Times Cited 12]

Samad Jahandideh*, Somayyeh Hoseini, and Mina Jahandideh. Toward more accuracy in protein structural bioinformatics: Have novel hybrid modeling procedures been born? *Journal of Theoretical Biology*, 256 (2009) 147. [5-Year Impact Factor: 2.496; Times Cited 1]

Mina Jahandideh, Seyyed Mohsen Hosseini Barkooie, **Samad Jahandideh**, Parviz Abdolmaleki*, Mohammad Mehdi Movahedi, Somayyeh Hoseini, Ebrahim Barzegari

Asadabadi, Fatemeh Javani Jouni, Zahra Karami, and Nader Hodjati Firoozabadi. Elucidating the protein cold adaptation: Investigation of the parameters enhancing protein psychrophilicity. *Journal of Theoretical Biology*, 255 (2008) 113-18. [5-Year Impact Factor: 2.496; Times Cited 7]

Samad Jahandideh, Amir Sabet Sarvestani, Parviz Abdolmaleki*, and Mina Jahandideh. γ -turn types prediction in proteins using the Support Vector Machine. *Journal of Theoretical Biology*, 249(4) (2007) 785-90. [5-Year Impact Factor: 2.496; Times Cited 21]

Samad Jahandideh, Ebrahim Barzegari Asadabadi, Parviz Abdolmaleki*, and Mina Jahandideh. Protein psychrophilicity: Role of residual structural properties in adaptation of proteins to low temperatures. *Journal of Theoretical Biology*, 248(4) (2007) 721-6. [5-Year Impact Factor: 2.496; Times Cited 6]

Mehdi Pour Sheikh Ali Asgary, **Samad Jahandideh**, Parviz Abdolmaleki*, and Anoshirvan Kazemnejad. Analysis and prediction of $\{\beta\}$ -turn types using multinomial logistic regression and artificial neural network. *Bioinformatics*, 23 (2007) 3125-30. [5-Year Impact Factor: 6.911; **Bioinformatics ranks first out of 47 journals in the category of Mathematical and Computational Biology**, Times Cited 10]

Samad Jahandideh, Parviz Abdolmaleki*, Mina Jahandideh, and Ebrahim Barzegari Asadabadi. Novel two-stage hybrid neural discriminant model for predicting proteins structural classes. *Biophysical Chemistry*, 128 (2007) 87-93. [5-Year Impact Factor: 2.094; Times Cited 58] **SELECTED AS TOP TEN HIGHLY CITED PAPER**

Samad Jahandideh*, Parviz Abdolmaleki, and Ebrahim Barzegari Asadabadi. Prediction of future citations of a research paper from number of its internet downloads. *Medical Hypotheses* doi: 10. 1016/j.mehy.(2007).01.007. [5-Year Impact Factor: 1.157; Times Cited 7]

Samad Jahandideh, Parviz Abdolmaleki*, Mina Jahandideh, and Ebrahim Barzegari Asadabadi. Sequence and structural parameters enhancing adaptation of proteins to low temperatures. *Journal of Theoretical Biology*, 246(1) 2007 159-6. [5-Year Impact Factor: 2.496; Times Cited 12]

Samad Jahandideh, Parviz Abdolmaleki*, Mina Jahandideh, and Sayyed Hamed Sadat Hayatshahi. Novel hybrid method for the evaluation of parameters contributing in determination of protein structural classes. *Journal of Theoretical Biology*, 244(2) (2007) 275-81. [5-Year Impact Factor: 2.496; Times Cited 25]

Book chapters:

Akbar Vaseghi, Maryam Faridounnia, Soheila Shokrollahzade, **Samad Jahandideh**, Kuo-Chen Chou, Pattern recognition in quaternary structures. Mourad Elloumi and Albert Y. Zomaya (eds). John Wiley (2016).

OTHER INFORMATION:

Current visa status: US permanent resident.